

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 2598.22 Seconds

(without alignments)  
5321.503 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319

Sequence: 1 gaaatgcgataagtaagtgc.....sgaataccgcgtgaactta 319

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_hcg:\*

3: gb\_in:\*

4: gb\_ov:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sbs:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vt:\*

15: em\_da:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sbs:\*

28: em\_un:\*

29: em\_vt:\*

30: em\_hcg\_hum:\*

31: em\_hcg\_inv:\*

32: em\_hcg\_other:\*

33: em\_hcg\_mus:\*

34: em\_hcg\_pln:\*

35: em\_hcg\_rtd:\*

36: em\_hcg\_mam:\*

37: em\_hcg\_vrt:\*

38: em\_hcg\_hum:\*

39: em\_hcg\_mus:\*

40: em\_hcg\_hum:\*

41: em\_hcg\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319	100.0	319	6 AR206400	AR206400 Sequence
2	319	100.0	319	6 BD083591	BD083591 Nucleic a
3	319	100.0	319	6 AF117921	AF117921 Nectria h
4	317	99.4	559	8 AY429048	AY429048 Chaetomiu
5	317	99.4	551	8 AY429053	AY429053 Chaetomiu
6	317	99.4	575	8 AY310442	AY310442 Nectria h
7	315.4	98.9	569	8 AY429049	AY429049 Chaetomiu
8	309.2	96.9	501	8 AY273332	AY273332 Unculture
9	308	96.6	509	8 AF165874	AF165874 Nectria h
10	300.2	94.1	582	8 AF455451	AF455451 Nectria h
11	298.6	93.6	550	8 AF178394	AF178394 Nectria h
12	298.6	93.6	550	8 AF178401	AF178401 Nectria h
13	297	93.1	549	8 AF178397	AF178397 Fusaarium
14	294.6	92.4	549	8 AF178398	AF178398 Nectria i
15	292	91.5	298	8 AY226096	AY226096 Nectria h
16	288.6	90.5	546	8 AF178413	AF178413 Neocosmos
17	288.2	90.3	548	8 AF178402	AF178402 Fusaarium
18	287	90.0	547	8 AF178412	AF178412 Neocosmos
19	286	89.7	566	8 NHA317959	AJ317959 Nectria h
20	285.6	89.5	544	8 NEXIRS	L36627 Neocosmospo
21	280.2	87.8	550	8 AF178406	AF178406 Fusaarium
22	279	87.5	480	8 AF150466	AF150466 Nectria h
23	279	87.5	480	8 AF150467	AF150467 Nectria h
24	279	87.5	480	8 AF40567	AF40567 Nectria h
25	277.2	86.9	550	8 AF178422	AF178422 Fusaarium
26	276.2	86.6	552	8 AF178411	AF178411 Nectria h
27	275.6	86.4	550	8 AF178407	AF178407 Fusaarium
28	275.6	86.4	550	8 AF178408	AF178408 Fusaarium
29	275.6	86.2	547	8 NECTRSA	L36619 Nectria hae
30	270.6	84.6	549	8 AF178409	AF178409 Fusaarium
31	269.2	84.4	483	8 AY273333	AY273333 Unculture
32	269.2	84.4	418	8 AF178416	AF178416 Nectria h
33	268	84.0	548	8 AY243054	AY243054 Ascomycet
34	268	84.0	548	8 AF178395	AF178395 Nectria h
35	268	84.0	548	8 AF178404	AF178404 Fusaarium
36	268	84.0	566	8 AF130142	AF130142 Nectria h
37	267.4	83.8	518	8 AF437761	AF437761 Fungal is
38	265.8	83.3	547	8 AF178410	AF178410 Nectria h
39	265.8	83.1	545	8 NECTRSB	L36620 Nectria hae
40	265	83.1	552	8 AF178421	AF178421 Nectria h
41	263.6	82.6	540	8 AY332483	AY332483 Stenocarp
42	263.6	82.6	1157	8 AY188918	AY188918 Nectria h
43	263.6	82.5	535	8 AY332486	AY332486 Stenocarp
44	263.2	82.4	544	8 AF178399	AF178399 Fusaarium
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## ALIGNMENTS

RESULT 1

AR206400

LOCUS AR206400

DEFINITION Sequence 6 from patent US 6372430.

ACCESSION AR206400

VERSION AR206400.1 GI:21504990

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 319)

AUTHORS Morrison,C.J., Reiss,E., Alderevich,L. and Choi,J.Soo.

TITLE Nucleic acids for detecting Aspergillus species and other filamentous fungi

JOURNAL Patent: US 6372430-A 6 16-Apr-2002;

FEATURES  
source

ORIGIN

Location/Qualifiers  
1..319  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 319; DB 6; Length 319;

Best Local Similarity 100.0%; Pred. No. 1.4e-79; Mismatches 0; Indels 0; Gaps 0;

Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CCCCCGCGCTGGCGGATCGGCGGAGCCCGCTGCGGGGACAAACGCGCTCCCCCA 180  
DB 121 CCCCCGCGCTGGCGGATCGGCGGAGCCCGCTGCGGGGACAAACGCGCTCCCCCA 180  
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DB 241 GAGCGGCGGCGCGACCGCTTAAACACCACTTCTGAATGTTGACCTCGAATGAGTAG 300  
QY 301 GAATACCGCGCTGAACCTTAA 319  
DB 301 GAATACCGCGCTGAACCTTAA 319

RESULT 2  
BD083591  
LOCUS

DEFINITION Nucleic acids for detecting *Aspergillus* species and other filamentous fungi.  
ACCESSION BD083591  
VERSION BD083591.1  
KEYWORDS JP 2001525665-A/6.  
SOURCE Fusarium solani  
ORGANISM Fusarium solani

REFERENCE  
AUTHORS Morrison, C.J., Reiss, E., Aidorevich, L. and Choi, J.S.  
TITLE Nucleic acids for detecting *Aspergillus* species and other filamentous fungi  
JOURNAL Parent: JP 2001525665-A 6 11-DEC-2001;

THE GOVERNMENT OF THE UNITED STATES OF AMERICA HAS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE

COMMENT

OS Fusarium solani  
PN JP 2001525665-A/6  
PD 11-DEC-2001  
PF 01-MAY-1998 JP 1998548275  
PI 02-MAY-1997 US 60/045400  
PI CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO CHOI  
PC C1201/68  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key

FEATURES  
source

Location/Qualifiers  
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/organism="Fusarium solani"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:169388"

ORIGIN

/note="Fusarium solani"

Query Match 100.0%; Score 319; DB 6; Length 319;

Best Local Similarity 100.0%; Pred. No. 1.4e-79; Mismatches 0; Indels 0; Gaps 0;

Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 CCCCCGCGCTGGCGGATCGGCGGAGCCCGCTGCGGGGACAAACGCGCTCCCCCA 180  
QY 181 AATACAGTGGCGGTCCCGCGACGCTTCATTGCGTAGTACTTAACACCTTGCACACTGGA 240  
DB 181 AATACAGTGGCGGTCCCGCGACGCTTCATTGCGTAGTACTTAACACCTTGCACACTGGA 240  
QY 241 GAGCGGCGGCGCGACCGCTTAAACACCACTTCTGAATGTTGACCTCGAATGAGTAG 300  
DB 241 GAGCGGCGGCGCGACCGCTTAAACACCACTTCTGAATGTTGACCTCGAATGAGTAG 300  
QY 301 GAATACCGCGCTGAACCTTAA 319  
DB 301 GAATACCGCGCTGAACCTTAA 319

RESULT 3  
AF117921  
LOCUS

DEFINITION Nucleic acids for detecting *Aspergillus* species and other filamentous fungi.  
ACCESSION AF117921  
VERSION AF117921.1  
KEYWORDS AF117921.1  
SOURCE Fusarium solani  
ORGANISM Fusarium solani

REFERENCE  
AUTHORS Morrison, C.J., Reiss, E., Aidorevich, L. and Choi, J.S.  
TITLE Nucleic acids for detecting *Aspergillus* species and other filamentous fungi  
JOURNAL Parent: JP 2001525665-A 6 11-DEC-2001;

THE GOVERNMENT OF THE UNITED STATES OF AMERICA HAS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE

COMMENT

OS Fusarium solani  
PN JP 2001525665-A/6  
PD 11-DEC-2001  
PF 01-MAY-1998 JP 1998548275  
PI 02-MAY-1997 US 60/045400  
PI CHRISTINE J MORRISON, ERROL REISS, LILIANA AIDOREVICH, JONG SOO CHOI  
PC C1201/68  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key

FEATURES  
source

Location/Qualifiers  
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/organism="Fusarium solani"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:169388"

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 Db 61 CATTGCGCCCGCAGTATTTCTGCGCGGCAATGCTGTTGCGAGGTATTAACAACCTTCAGG 120  
 QY 121 CCCCCCGGCTTGGGCGGATTCGGCGGAGACCCCTTCGCGGCAACAACCGCTGCCCA 180  
 Db 121 CCCCCCGGCTTGGGCGGATTCGGCGGAGACCCCTTCGCGGCAACAACCGCTGCCCA 180  
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 Db 181 AATACAGTGGCGGTGCTCCCGCAGCTTCATTCGCGGATGCTTAACACCTCGCACTGGA 240  
 QY 241 GAGCGGCGCGGACCGCCGTAAACACCACTTGTGAATGTTGACCTCGAATCAGGTAG 300  
 Db 241 GAGCGGCGCGGACCGCCGTAAACACCACTTGTGAATGTTGACCTCGAATCAGGTAG 300  
 QY 301 GAATACCGGCTGAACTTAA 319  
 Db 301 GAATACCGGCTGAACTTAA 319

RESULT 4  
 AY429048 559 bp DNA linear PLN 30-NOV-2003

LOCUS  
 DEFINITION Chaetomium globosum isolate Cg1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION  
 VERSION AY429048.1 GI:38503524

KEYWORDS  
 SOURCE Chaetomium globosum

ORGANISM Chaetomium globosum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.

REFERENCE  
 AUTHORS Aggarwal, R., Renu, S. and Singh, D. V.  
 TITLE Nucleotide sequence of full length ITS region of Cg1 isolate of Chaetomium globosum  
 JOURNAL Unpublished

REFERENCE  
 AUTHORS Aggarwal, R., Renu, S. and Singh, D. V.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-OCT-2003) Division of Plant Pathology, IARI, Pusa Road, New Delhi, Delhi 110012, India

FEATURES  
 SOURCE location/Qualifiers  
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 /organism="Chaetomium globosum"  
 /mol\_type="genomic DNA"  
 /isolate="Cg1"  
 /db\_xref="taxon:38033"

misc\_RNA

/note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

ORIGIN

Query Match 99.4%; Score 317; DB 8; Length 559;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-79; Indels 0; Gaps 0;  
 Matches 317; Conservative 0; Mismatches 0;

QY 3 AATGCGATAGTATGATGAGAAATTCAGATGATCATGGAATCTTTGAACGCA 62  
 Db 201 AATGCGATAGTATGATGAGAAATTCAGATGATCATGGAATCTTTGAACGCA 260  
 QY 63 TTGGCGCCCGCAGTATTTCTGCGCGGCAATGCTGTTGCGAGGTATTAACAACCTTCAGGCC 122  
 Db 261 TTGGCGCCCGCAGTATTTCTGCGCGGCAATGCTGTTGCGAGGTATTAACAACCTTCAGGCC 320

QY 123 CCGGCGCTGGCGTTGGGGATTCGGCGGAGGCCCTTCGCGGCAACAACGCGTCCCAAA 182  
 Db 321 CCGGCGCTGGCGTTGGGGATTCGGCGGAGGCCCTTCGCGGCAACAACGCGTCCCAAA 380  
 QY 183 TACAGTGGCGGTTCGCGCGCAGCTTCATTCGCGGATGCTTAACACCTCGCACTGGA 242  
 Db 381 TACAGTGGCGGTTCGCGCGCAGCTTCATTCGCGGATGCTTAACACCTCGCACTGGA 440  
 QY 243 GCGGCGCGGCAACCGCGTAAACCACTTGTGAATGTTGACCTCGAATCAGGTAGGA 302  
 Db 441 GCGGCGCGGCAACCGCGTAAACCACTTGTGAATGTTGACCTCGAATCAGGTAGGA 500  
 QY 303 ATACCGGCTGAACTTAA 319  
 Db 501 ATACCGGCTGAACTTAA 517

RESULT 5  
 AY429053 561 bp DNA linear PLN 30-NOV-2003

LOCUS  
 DEFINITION Chaetomium globosum isolate Cg6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION  
 VERSION AY429053.1 GI:38503529

KEYWORDS  
 SOURCE Chaetomium globosum

ORGANISM Chaetomium globosum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.

REFERENCE  
 AUTHORS Aggarwal, R., Renu, S. and Singh, D. V.  
 TITLE Nucleotide sequence of full length ITS region of Cg6 isolate of Chaetomium globosum  
 JOURNAL Unpublished

REFERENCE  
 AUTHORS Aggarwal, R., Renu, S. and Singh, D. V.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-OCT-2003) Division of Plant Pathology, IARI, Pusa Road, New Delhi, Delhi 110012, India

FEATURES  
 SOURCE location/Qualifiers  
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 /isolate="Cg6"  
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misc\_RNA

/note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

ORIGIN

Query Match 99.4%; Score 317; DB 8; Length 561;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-79; Indels 0; Gaps 0;  
 Matches 317; Conservative 0; Mismatches 0;

QY 3 AATGCGATAGTATGATGAGAAATTCAGATGATCATGGAATCTTTGAACGCA 62  
 Db 203 AATGCGATAGTATGATGAGAAATTCAGATGATCATGGAATCTTTGAACGCA 262  
 QY 63 TTGGCGCCCGCAGTATTTCTGCGCGGCAATGCTGTTGCGAGGTATTAACAACCTTCAGGCC 122  
 Db 263 TTGGCGCCCGCAGTATTTCTGCGCGGCAATGCTGTTGCGAGGTATTAACAACCTTCAGGCC 322  
 QY 123 CCGGCGCTGGCGTTGGGGATTCGGCGGAGGCCCTTCGCGGCAACAACGCGTCCCAAA 182  
 Db 323 CCGGCGCTGGCGTTGGGGATTCGGCGGAGGCCCTTCGCGGCAACAACGCGTCCCAAA 382  
 QY 183 TACAGTGGCGGTTCGCGCGCAGCTTCATTCGCGGATGCTTAACACCTCGCACTGGA 242  
 Db 383 TACAGTGGCGGTTCGCGCGCAGCTTCATTCGCGGATGCTTAACACCTCGCACTGGA 442

QY 243 GCGGCGGCGGCAACGCGCTTAAACACCACTTGTGATGTTGACCTCGAATCAGTAGGA 302  
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Db 443 GCGGCGGCGGCAACGCGCTTAAACACCACTTGTGATGTTGACCTCGAATCAGTAGGA 502  
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QY 303 ATACCGGCTGAATCTTAA 319  
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Db 503 ATACCGGCTGAATCTTAA 519  
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RESULT 6  
AY310442 576 bp DNA linear PLN 01-JUL-2003  
LOCUS Nectria haematococca 18S ribosomal RNA gene, partial sequence;  
DEFINITION internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal  
transcribed spacer 2, complete sequence; and 28S ribosomal RNA  
gene, partial sequence.  
ACCESSION AY310442  
VERSION AY310442.1 GI:32264972  
KEYWORDS  
SOURCE Nectria haematococca  
ORGANISM Nectria haematococca  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
AUTHORS Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
TITLE 1 (bases 1 to 576)  
JOURNAL Scott, P.T., Martin, H.L., Boreel, S.M., Wearing, A.H. and Maclean, D.J.  
REFERENCE Isolation and characterization of Nectria haematococca from table  
AUTHORS best grown in the Lockyer Valley, Queensland, Australia  
TITLE Unpublished  
JOURNAL 2 (bases 1 to 576)  
REFERENCE Scott, P.T.  
AUTHORS Direct Submission  
TITLE Submitted (02-JUN-2003) Agronomy and Horticulture, The University  
JOURNAL of Queensland, Warrego Highway, Gatton, QLD 4343, Australia  
FEATURES  
source location/Qualifiers  
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/db\_xref="taxon:140110"  
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RNA <1..38  
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rRNA 39..188  
/product="internal transcribed spacer 1"  
189..345  
/product="5.8S ribosomal RNA"  
misc\_RNA 346..518  
/product="internal transcribed spacer 2"  
519..576  
/product="28S ribosomal RNA"

ORIGIN  
Query Match 99.4%; Score 317; DB 8; Length 576;  
Best Local Similarity 100.0%; Pred. No. 5.4e-79;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 480 GCGGCGGCGGCAACGCGCTTAAACACCACTTGTGATGTTGACCTCGAATCAGTAGGA 539  
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QY 303 ATACCGGCTGAATCTTAA 319  
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Db 540 ATACCGGCTGAATCTTAA 556  
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RESULT 7  
AY429049 569 bp DNA linear PLN 30-NOV-2003  
LOCUS Chaetomium globosum isolate Cg2 18S ribosomal RNA gene, partial  
DEFINITION sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene,  
and internal transcribed spacer 2, complete sequence; and 28S  
ribosomal RNA gene, partial sequence.  
ACCESSION AY429049  
VERSION AY429049.1 GI:38503525  
KEYWORDS  
SOURCE Chaetomium globosum  
ORGANISM Chaetomium globosum  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
AUTHORS Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.  
TITLE 1 (bases 1 to 569)  
JOURNAL Aggarwal, R., Renu, S. and Singh, D.V.  
REFERENCE Nucleotide sequence of full-length ITS region of Cg2 isolate of  
AUTHORS Chaetomium globosum  
TITLE Unpublished  
JOURNAL 2 (bases 1 to 569)  
REFERENCE Aggarwal, R., Renu, S. and Singh, D.V.  
AUTHORS Direct Submission  
TITLE Submitted (07-OCT-2003) Division of Plant Pathology, IARI, Pusa  
JOURNAL Road, New Delhi, Delhi 110012, India  
FEATURES  
source location/Qualifiers  
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/organism="Chaetomium globosum"  
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/isolate="Cg2"  
/db\_xref="taxon:38033"  
misc\_RNA <1..>569  
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spacer 1, 5.8S ribosomal RNA, internal transcribed spacer  
2, and 28S ribosomal RNA"

ORIGIN  
Query Match 98.9%; Score 315.4; DB 8; Length 569;  
Best Local Similarity 99.7%; Pred. No. 1.5e-78;  
Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



AY273332 501 bp DNA linear PLN 30-OCT-2003  
 LOCUS  
 DEFINITION Uncultured ascomycete clone T7A6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
 ACCESSION AY273332  
 VERSION AY273332.1 GI:34420179  
 KEYWORDS  
 SOURCE uncultured ascomycete  
 ORGANISM Uncultured ascomycete  
 Eukaryota; Fungi; Ascomycota; environmental samples.  
 REFERENCE 1 (bases 1 to 501)  
 AUTHORS Roose-Amaele, C., Brygoo, Y. and Harry, M.  
 TITLE Marked discrepancy between fungal diversity in soil-feeding termitaries and tropical soils  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 501)  
 AUTHORS Roose-Amaele, C., Brygoo, Y. and Harry, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-APR-2003) UFR Sciences Universite Paris 12, UMR137-LBSE, Avenue du General de Gaulle, Creteil cedex 94010, France  
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 /db\_xref="taxon:175243"  
 /clone="T7A6"  
 /environmental\_sample  
 /country="Gabon: Doda, la Lope"  
 <1..141  
 /note="contains 18S ribosomal RNA and internal transcribed spacer 1"  
 142..292  
 /product="5.8S ribosomal RNA"  
 293..>501  
 /note="contains internal transcribed spacer 2 and 28S ribosomal RNA"  
 ORIGIN  
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 Best Local Similarity 99.0%; Pred. No. 8.7e-77;  
 Matches 311; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 3 AAATGCATTAAGTAATGTAATGCAATTCAGATCATCGAATCTTTGAACGACCA 62  
 Db 188 AAATGCATTAAGTAATGTAATGCAATTCAGATCATCGAATCTTTGAACGACCA 247  
 Oy 63 TTGGCGCCGCGCAGTAATTCGGCGGGCATGCTGTTGAGCGTCATTACAACCTCAGGCC 122  
 Db 248 TTGGCGCCGCGCAGTAATTCGGCGGGCATGCTGTTGAGCGTCATTACAACCTCAGGCC 307  
 Oy 123 CCCGGGCTTGCGCTGGGGATTCGGGGAGAGCCCTGCGGGCACAAGCCGCTCCGCCAAA 182  
 Db 308 CCCGGGCTTGCGCTGGGGATTCGGGGAGAGCCCTGCGGGCACAAGCCGCTCCGCCAAA 367  
 Oy 183 TACAGTGGCGGTCCCGCGCAGCTTCATTTGGTGTAGCTAACACCTCGCACTGGAGGA 242  
 Db 368 TACAGTGGCGGTCCCGCGCAGCTTCATTTGGTGTAGCTAACACCTCGCACTGGAGGA 427  
 Oy 243 GCGGGCGGCGCAGCGCGTAAACACCAACTTGTGAATGTGACCTCGAATCAGTAGGA 302  
 Db 428 GCGGGCGGCGCAGCGCGTAAACACCAACTTGTGAATGTGACCTCGAATCAGTAGGA 487  
 Oy 303 ATACCGCGTGAAT 316  
 Db 488 ATACCGCGTGAAT 501

RESULT 9

AF165874 509 bp DNA linear PLN 18-JUL-1999  
 LOCUS  
 DEFINITION Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
 ACCESSION AF165874  
 VERSION AF165874.1 GI:5524731  
 KEYWORDS  
 SOURCE Fusarium solani  
 ORGANISM Fusarium solani  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
 REFERENCE 1 (bases 1 to 509)  
 AUTHORS Iwen, P.C., Henry, T. and Hinrichs, S.H.  
 TITLE Sequence analysis of the internal transcribed spacer regions of Fusarium species most commonly associated with human invasive disease  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 509)  
 AUTHORS Iwen, P.C., Henry, T. and Hinrichs, S.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-JUL-1999) Pathology and Microbiology, University of Nebraska Medical Center, 986485 Nebraska Medical Center, Omaha, NE 68198-6495, USA  
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 Best Local Similarity 100.0%; Pred. No. 1.9e-76;  
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 Db 202 AAATGCATTAAGTAATGTAATGCAATTCAGATCATCGAATCTTTGAACGACCA 261  
 Oy 63 TTGGCGCCGCGCAGTAATTCGGCGGGCATGCTGTTGAGCGTCATTACAACCTCAGGCC 122  
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 Db 322 CCCGGGCTTGCGCTGGGGATTCGGGGAGAGCCCTGCGGGCACAAGCCGCTCCGCCAAA 381  
 Oy 183 TACAGTGGCGGTCCCGCGCAGCTTCATTTGGTGTAGCTAACACCTCGCACTGGAGGA 242  
 Db 382 TACAGTGGCGGTCCCGCGCAGCTTCATTTGGTGTAGCTAACACCTCGCACTGGAGGA 441  
 Oy 243 GCGGGCGGCGCAGCGCGTAAACACCAACTTGTGAATGTGACCTCGAATCAGTAGGA 302  
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 Oy 303 ATACCGCG 310  
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LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
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Mycol. 41 (2), 149-161 (2003)	<p>misc_RNA</p> <p>1 (bases 1 to 582)</p> <p>2 (bases 1 to 582)</p> <p>3 (bases 1 to 582)</p> <p>4 (bases 1 to 582)</p> <p>5 (bases 1 to 582)</p> <p>6 (bases 1 to 582)</p> <p>7 (bases 1 to 582)</p> <p>8 (bases 1 to 582)</p> <p>9 (bases 1 to 582)</p> <p>10 (bases 1 to 582)</p> <p>11 (bases 1 to 582)</p> <p>12 (bases 1 to 582)</p> <p>13 (bases 1 to 582)</p> <p>14 (bases 1 to 582)</p> <p>15 (bases 1 to 582)</p> <p>16 (bases 1 to 582)</p> <p>17 (bases 1 to 582)</p> <p>18 (bases 1 to 582)</p> <p>19 (bases 1 to 582)</p> <p>20 (bases 1 to 582)</p> <p>21 (bases 1 to 582)</p> <p>22 (bases 1 to 582)</p> <p>23 (bases 1 to 582)</p> <p>24 (bases 1 to 582)</p> <p>25 (bases 1 to 582)</p> <p>26 (bases 1 to 582)</p> <p>27 (bases 1 to 582)</p> <p>28 (bases 1 to 582)</p> <p>29 (bases 1 to 582)</p> <p>30 (bases 1 to 582)</p> <p>31 (bases 1 to 582)</p> <p>32 (bases 1 to 582)</p> <p>33 (bases 1 to 582)</p> <p>34 (bases 1 to 582)</p> <p>35 (bases 1 to 582)</p> <p>36 (bases 1 to 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LOCUS	AF178394	550 bp	DNA	linear	PLN 20-DEC-2001
DEFINITION	Nectria haematococca mpiv strain NRRL22163 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.				
ACCESSION	AF178394				
VERSION	AF178394.1				
KEYWORDS	GI:10180235				
SOURCE	Nectria haematococca mpiv (anamorph: Fusarium solani f. sp. xanthoxyli)				
ORGANISM	Nectria haematococca mpiv				
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.				
AUTHORS	1 (bases 1 to 550)				
TITLE	O'Donnell, K.				
REFERENCE	Molecular phylogeny of the Fusarium solani species complex				
JOURNAL	Unpublished				
AUTHORS	2 (bases 1 to 550)				
REFERENCE	O'Donnell, K.				
TITLE	Direct Submission				
JOURNAL	Submitted (18-AUG-1999) Microbial Properties Research, NCAUR, USDA, ARS, 1815 N. University St., Peoria, IL 61604, USA				
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misc_RNA					
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QY	63	TTGGCGCCGCGCAGATTTCTGGCGGGCATGCCCTGTTGAGCGCTATTAACAACCTTCAGGCC	122		
DB	295	TTGGCGCCGCGCAGATTTCTGGCGGGCATGCCCTGTTGAGCGCTATTAACAACCTTCAGGCC	354		
QY	123	CCCGGGCGCTGGCGTTGGGGAGTCGGCGGAAAGCCCTCGGGGCACAAGCGGCTCCGCCAAA	182		
DB	355	CCCGGGCGCTGGCGTTGGGGAGTCGGCGGAAAGCCCTCGGGGCACAAGCGGCTCCGCCAAA	413		
QY	183	TACAGTGGCGGTCCCGCGCAGCTTTCATTGCGTAGTAGTTAACACCTTCGCACTGAGAGA	242		
DB	414	TACAGTGGCGGTCCCGCGCAGCTTTCATTGCGTAGTAGTTAACACCTTCGCACTGAGAGA	473		
QY	243	GGCGCGGGCGCCAGCGCGTAAACACCCCACTTTCGAATGTTGACCTGGAATCAGGTAGGA	302		
DB	474	GGCGCGGGCGCCAGCGCGTAAACACCCCACTTTCGAATGTTGACCTGGAATCAGGTAGGA	533		
QY	303	ATACCGCGTGAACTTAA 319			
DB	534	ATACCGCGTGAACTTAA 550			
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LOCUS	AF178401				
DEFINITION	Nectria haematococca mpiv strain NRRL22277 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S				

REFERENCE	AUTHORS	TITLE	JOURNAL
1	Min,B.R.	Direct Submision	Submitted (17-FEB-1999) Biology, Sangmyung university, 7 Hong Ji Dong, Chong Ro-gu, Seoul 110-743, Korea
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Query Match	93.6%; Score 298.6; DB 8; Length 569;		
Best Local Similarity	98.4%; Pred. No. 8,9e-74;		
Matches 312; Conservative	0; Mismatches 4; Indels 1; Gaps 1;		
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DB	294	TTGGGCCCCGACGATTTCTGGCCGGGCAATGCTTTGAGAGCTCATTTCAACACCTCAGGCC	353
QY	123	CCCCGGGCGTGGCGTTGGGGGATCGGCGGGAAGCCCCCTCGGGCACAACGCGCGTCCCCCAA	182
DB	354	CCCCGGGCGTGGCGTTGGGGGATCGGCGGGAAGCCCCCTCGGGCACAACGCGCGTCCCCCAA	412
QY	183	TACAGTGGCGGTCCCGCGCAGCTTCATTCGTTAGTAGCTAACACCTCGCACTGAGGA	242
DB	413	TACAGTGGCGGTCCCGCGCAGCTTCATTCGTTAGTAGCTAACACCTCGCACTGAGGA	472
QY	243	GGGGCGGGGCGCAGCCCGTAAACACCCCACTTCGTGAATGTTGACCTCGAATCAGATGGA	302
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QY	303	ATACCGCGTGAACCTTA 319	
DB	533	ATACCGCGTGAACCTTA 549	
RESULT 14			
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LOCUS			
DEFINITION	Fusarium ambrosium strain NRRL20438 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.		
ACCESSION	AF178397		
KEYWORDS	AF178397.1 GI:10180238		
SOURCE	Fusarium ambrosium		
ORGANISM	Fusarium ambrosium		
REFERENCE	Hypocremycetidae; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocremycetidae; Hypocreales; Nectriaceae; Nectria.		
AUTHORS	Submitted (17-FEB-1999) Biology, Sangmyung university, 7 Hong Ji Dong, Chong Ro-gu, Seoul 110-743, Korea		
TITLE	Direct Submision		
JOURNAL	Submitted (17-FEB-1999) Biology, Sangmyung university, 7 Hong Ji Dong, Chong Ro-gu, Seoul 110-743, Korea		
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rRNA	/product="28S ribosomal RNA"		
ORIGIN			
Query Match	93.6%; Score 298.6; DB 8; Length 569;		
Best Local Similarity	98.4%; Pred. No. 8,9e-74;		
Matches 312; Conservative	0; Mismatches 4; Indels 1; Gaps 1;		
QY	3	AAATGCATTAAGTATGTAATTCAGATTCAGTGAATCATCGAATCTTTGAAGCACA	62
DB	234	AAATGCATTAAGTATGTAATTCAGATTCAGTGAATCATCGAATCTTTGAAGCACA	293
QY	63	TTGGGCCCCGACGATTTCTGGCCGGGCAATGCTTTGAGAGCTCATTTCAACACCTCAGGCC	122
DB	294	TTGGGCCCCGACGATTTCTGGCCGGGCAATGCTTTGAGAGCTCATTTCAACACCTCAGGCC	353
QY	123	CCCCGGGCGTGGCGTTGGGGGATCGGCGGGAAGCCCCCTCGGGCACAACGCGCGTCCCCCAA	182
DB	354	CCCCGGGCGTGGCGTTGGGGGATCGGCGGGAAGCCCCCTCGGGCACAACGCGCGTCCCCCAA	412
QY	183	TACAGTGGCGGTCCCGCGCAGCTTCATTCGTTAGTAGCTAACACCTCGCACTGAGGA	242
DB	413	TACAGTGGCGGTCCCGCGCAGCTTCATTCGTTAGTAGCTAACACCTCGCACTGAGGA	472
QY	243	GGGGCGGGGCGCAGCCCGTAAACACCCCACTTCGTGAATGTTGACCTCGAATCAGATGGA	302
DB	473	GGGGCGGGGCGCAGCCCGTAAACACCCCACTTCGTGAATGTTGACCTCGAATCAGATGGA	532
QY	303	ATACCGCGTGAACCTTA 319	
DB	533	ATACCGCGTGAACCTTA 549	
RESULT 14			
AF178397	548 bp	DNA	linear
LOCUS			
DEFINITION	Fusarium ambrosium strain NRRL20438 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.		
ACCESSION	AF178397		
KEYWORDS	AF178397.1 GI:10180238		
SOURCE	Fusarium ambrosium		
ORGANISM	Fusarium ambrosium		
REFERENCE	Hypocremycetidae; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocremycetidae; Hypocreales; Nectriaceae; Nectria.		
AUTHORS	Submitted (17-FEB-1999) Biology, Sangmyung university, 7 Hong Ji Dong, Chong Ro-gu, Seoul		

JOURNAL REFERENCE	Unpublished 2 (bases 1 to 548)
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**JOURNAL**  
Submitted (18-AUG-1999) Microbial Properties Research, NCAUR, USDA,  
ARS, 1815 N. University St., Peoria, IL 61604, USA

source	location/qualifiers
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/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA"

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ORIGIN

Query Match 297; DB 8; Length 548;  
Best Local Similarity 98.1%;  
Matches 311; Conservative 0; Mismatches 5; Indels 1; Gaps 1.

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QY	63	TTGCGCGCCCGCAGTATTTGCGGGGCGATGCTGTTGAGCGCTATTACAACCTTCAGGCG	122
Db	293	TTGCGCGCCCGCAGTATTTGCGGGGCGATGCTGTTGAGCGCTATTACAACCTTCAGGCG	352
QY	123	CCCGGGCCTGGCGTTGGGGATCGGCGGAAAGCCCTTCGCGGCGCAACGCGCTGCCCAA	182
Db	353	CCCGGGCCTGGCGTTGGGGATCGGCGGAAAGCCCTTCGAGGGAAC-ACGCGGTCCCCAAA	411
QY	183	TACAGTGGCGGTCCTCCCGCAGCTTTCATTTGCGTAAGCTAACACTCGGCACTGGAAG	242
Db	412	TACAGTGGCGGTCCTCCCGCAGCTTTCATTTGCGTAAGCTAACACTCGGCACTGGAAG	471
QY	243	GCGGCGCGGCGCAGCGCGTAAACACCCAACTTTCGATGTTGAACCTCGAATCAGGTAGGA	302
Db	472	GCGGCGCGGCGCAGCGCGTAAACACCCAACTTTCGATGTTGAACCTCGAATCAGGTAGGA	531
QY	303	ATAACCGCTGAACCTTAA	319
Db	532	ATAACCGCTGAACCTTAA	548

## RESULT 15

AF178398  
E40 bp  
DWA  
110000  
BIN 20-DEC-2001

LOCUS	Accession	Size (bp)	Gene	Product
DEFINITION	Neceria 1pomoeae strain NRRL2510	165	ribosomal RNA gene	partial
SEQUENCE	internal transcribed spacer 1, 5.8S ribosomal RNA gene 1, 5.8S ribosomal RNA gene 1, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.			

ACCESSION	AF178398
VERSION	AF178398.1
	GI:10180239

KEYWORDS	SOURCE	ORGANISM
	Nectria ipomoeae	
	Nectria ipomoeae	

REFERENCE  
1 (bases 1 to 549)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Dothideales; Dothiorales; Dothioraceae; Nectria  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria

O'Donnell, K.,  
 Molecular phylogeny of the *Fusarium solani* species complex  
 Unpublished  
 2 (bases 1 to 549)  
 O'Donnell, K.,  
 Direct Submission  
 Submitted (18-VUG-1999) Microbial Properties Research, NCAUR, USDA  
 JOURNAL  
 AUTHORS  
 TITLE  
 REFERENCE  
 JOURNAL  
 TITLE  
 JOURNAL

```

ARS, 1815 N. University St., Peoria,
FEATURES
source
1. .549
Location/Qualifiers
/organism="Nectria ipomoeae"

```

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misc_RNA
/molecule_type="genomic DNA"
/strain="NRRL22101"
/db_xref="taxon:57162"
<1..>549
/feature_location="185 rib"
```

/note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

Query Match	92.4%;	Score 294.6;	DB 8;	Length 549;
Best Local Similarity	95.6%;	Pred. No. 1.2e-72;		
Matches 303;	Conservative	0;	Mismatches 14;	Indels 0;
			Gaps	0
Qy	3	AAATCGATTAAGTAATGTGAATTGCAGAAATTCAGTGAATCATGAAATCTTTGAAGCCACA	62	
Db	233	AAATGCGAATAGTAATGTGAATTGCAGAAATTCAGTGAATCATGAAATCTTTGAAGCCACA	292	
Qy	63	TTGCGCGCCGCAATTTCTGGCGGGCATTCCTGTTGAGGCGTAAACACCTCAGGCC	122	
Db	293	TTGCGCGCCGCAATTTCTGGCGGGCATTCCTGTTGAGGCGTAAACACCTCAGGCC	352	
Qy	123	CCCGGGCCGTGGGAGTTCGGGGAAGCCCTCTCGGGCAACCGCCGTCCCCAA	182	
Db	353	CCCGGGCCGTGGGAGTTCGGGGAAGCCCTCTCGGGGAACGGCGGTCCCCAA	412	
Qy	183	TACAGTGGCGGTCCCGCCGACAGCTTCATTCGTAGTAGCTAACACCTCGCAACTGGAG	242	
Db	413	TACAGTGGCGGTCCCGCCGACAGCTTCATTCGTAGTAGCTAACACCTCGCAACTGGAG	472	
Qy	243	GCGGCGCGGCCACGCGCGTAACACCCCACTTCGTGAATGTGAACCTCGATCAGGTAGG	302	
Db	473	GCGGCGCGGCCACGCGCGTAACACCCCACTTCGTGAATGTGAACCTCGATCAGGTAGG	532	
Qy	303	ATACCGCGTGAACCTTAA	319	
Db	533	ATACCGCGTGAACCTTAA	549	

Search completed: October 1, 2004, 05:16:56  
Job time : 2606.72 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 23:11:57; Search time 565.953 Seconds  
(without alignments)  
2394.501 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319  
1 gaataatgataagtaagtc.....ggataaccgcctgaacttaa 319

Sequence: 1 gaataatgataagtaagtc.....ggataaccgcctgaacttaa 319

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	319	100.0	319	2	AAV70850 Internal
2	244.4	76.6	2293	4	AA616211 Fungus ge
3	241.8	75.8	502	3	AAA61893 Fusarium
4	240.8	75.5	659	6	ABV78724 C. sinens
5	240.4	75.4	534	7	ACC50001 Internal
6	240.2	75.3	310	2	AAV70851 Internal
7	240	75.2	561	2	AAV59009 F. avenac
8	213.2	66.8	647	6	ABV78700 C. crass
9	195.2	61.2	582	2	AA616100 T. harzia
10	190	59.6	661	6	ABV78721 C. sinens
11	184.8	57.9	569	2	AA616101 T. harzia
12	183.8	57.6	504	2	AAV62591 Fusarium
13	183.8	57.6	504	2	AAV62591 Fusarium
14	183.8	57.6	504	2	AAV62591 Fusarium
15	183.2	57.4	522	7	ACC49999 Internal
16	183.2	57.4	522	7	ACC49999 Internal
17	180.4	56.6	545	2	AAV62593 Fusarium
18	180.4	56.6	545	2	AAV62593 Fusarium
19	180	56.4	546	2	AAV62596 Fusarium
20	180	56.4	546	2	AAV62596 Fusarium
21	179.6	56.3	546	2	AAV62596 Fusarium
22	176.4	55.3	521	7	ACC50000 Internal
23	174.8	54.8	503	2	AA616211 Fungus ge

24	174.8	54.8	503	2	AAV62592 Fusarium
25	174.8	54.8	503	2	AAV59029 F. gramin
26	171.4	53.7	504	4	AA608426 Internal
27	166.8	52.3	659	6	ABV78715 C. sinens
28	165.2	51.8	625	6	ABV78718 C. sinens
29	165.2	51.8	632	6	ABV78709 C. sinens
30	165.2	51.8	632	6	ABV78706 C. sinens
31	165.2	51.8	664	6	ABV78703 C. sinens
32	165.2	51.8	667	6	ABV78712 C. sinens
33	163.6	51.3	615	5	AAV76260 Cortidiceps
34	156.8	49.2	610	2	AAV90111 Phomopsis
35	155	48.6	537	3	AAZ91725 Rosellini
36	154.8	48.5	545	2	AA605403 Microdoch
37	145.6	45.6	608	2	AAV90110 Phomopsis
38	138.8	43.5	549	3	AAZ91723 Rosellini
39	138.8	43.5	549	3	AAZ91724 Rosellini
40	134.2	42.1	382	3	AAA72783 5.8S rRNA
41	133.4	41.8	686	6	ABV78727 C. sinens
42	131.8	41.3	652	7	ABZ20765 Mucodora
43	128.4	40.3	605	2	AAV90108 Euryptella
44	127.8	40.1	553	3	AAZ91726 Rosellini
45	127.4	39.9	537	6	ABA01153 Deuteromy

## ALIGNMENTS

RESULT 1  
ID AAV70850 standard; DNA; 319 BP.  
XX  
XX AAV70850;  
XX  
XX 26-FEB-1999 (first entry)  
XX  
XX Internal transcribed spacer 2 (ITS2) and adjacent regions.  
DE  
XX Internal transcribed spacer 2 (ITS2) and adjacent regions.  
XX  
XX Internal transcribed spacer 2; ITS2; probe: Aspergillus flavus; A. niger;  
KW A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;  
KW M. racemosus; M. plumbeus; M. indicus; A. fumigatus;  
KW M. circinellioideus f. circinellioideus; Rhizopus oryzae; R. microsporus;  
KW R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;  
KW Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;  
KW Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.  
XX  
XX Fusarium solani.  
OS  
XX  
XX MO9850584-A2.  
XX  
XX 12-NOV-1998.  
XX  
XX 01-MAY-1998; 98WO-US008926.  
XX  
XX 02-MAY-1997; 97US-0045400P.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Morrison CJ, Reiss E, Aidorevich L, Choi JS;  
XX WPI, 1999-034737/03.  
XX  
XX New nucleic acid probes for filamentous fungi - for detecting e.g.  
XX Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,  
XX Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix  
XX species.  
XX  
XX Claim 1; Page 12; 45pp; English.  
XX  
XX The present sequence represents an internal transcribed spacer 2 (ITS2)  
XX and adjacent regions. Probes can be derived from the present sequence  
XX which are species-specific. The specification also describes ITS2  
XX sequence-derived probes for identifying a species selected from  
XX Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,



DT 14-NOV-2000 (first entry)  
 XX XX  
 DE Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.  
 XX  
 KW Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469;  
 KW HIV integrase inhibitor; steroid compound; human immunodeficiency virus;  
 KW acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;  
 KW symptomatic infection; asymptomatic infection; potential HIV exposure;  
 KW combination therapy; ds.  
 XX  
 OS Fusarium sp.; MF6381.  
 XX  
 PN WO200036132-A1.  
 XX  
 PD 22-JUN-2000.  
 XX  
 PF 09-DEC-1999; 99WO-US029356.  
 XX  
 PR 14-DEC-1998; 98US-0112168P.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;  
 PI Dombrowski AW;  
 XX  
 DR WPI; 2000-431606/37.  
 XX  
 FT New steroid compounds are HIV integrase inhibitors used for treating HIV  
 FT infection and AIDS.  
 XX  
 PS Disclosure; Page 14; 113pp; English.  
 XX  
 CC The invention relates to novel steroid compounds derived from the African  
 CC soil fungus Fusarium sp. MF6381 (ATCC 74469) which act as inhibitors of  
 CC HIV integrase. The invention encompasses cultures of Fusarium sp. MF6381.  
 CC The invention also relates to a composition comprising a compound of the  
 CC invention in combination with an AIDS antiviral agent, an immunomodulator  
 CC and an antileptic agent. The compounds of the invention may be used in  
 CC the inhibition of HIV integrase and in the prevention and treatment of  
 CC HIV infection. A wide range of state of HIV infection may be treated;  
 CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex);  
 CC both symptomatic and asymptomatic HIV infection; and actual or potential  
 CC exposure to HIV. The compounds may be used to isolate HIV integrase  
 CC mutants which are potentially useful as screening tools for antiviral  
 CC compounds. The compounds may also be used to establish or determine the  
 CC site at which other antivirals bind to HIV integrase (e.g., by  
 CC competitive inhibition). The present sequence represents the ribosomal  
 CC DNA (rDNA) internal transcribed spacer (ITS) region of Fusarium sp.  
 CC MF6381, which may be used to characterize MF6381. (Updated on 15-SEP-2003  
 CC to standardise OS field)  
 XX  
 SQ Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 U; 0 Other;  
 Query Match 75.8%; Score 241.8; DB 3; Length 502;  
 Best Local Similarity 88.2%; Pred. No. 1.6e-70;  
 Matches 276; Conservative 0; Mismatches 32; Indels 5; Gaps 1;  
 QY 2 AAAATGCGATGAATGTAATGCAATTCAGTAATCATGAACTTTGAACGAC 61  
 DB 195 AAAATGCGATGAATGTAATGCAATTCAGTAATCATGAACTTTGAACGAC 254  
 QY 62 ATTGCGCGCCGAGTATTCGCGGCGATGCTGTTCAGAGCTATTACAACCTTCAGGC 121  
 DB 255 ATTGCGCGCCGAGTATTCGCGGCGATGCTGTTCAGAGCTATTACAACCTTCAGGC 314  
 QY 122 CCGCGGCGCTGCGGTGGGATCGGCGGAGCCCTCGGGGCAACAAGCGTCCGCCAA 181  
 DB 315 CCGCGGCTTGTGTGGGATCGGCGGAGCTCGGCTTACCGCG-----TCCGCGCCCGAA 369  
 QY 182 ATACAGTGGCGGTCCCGCGAGCTTCATTGCGTAGTAAACACTTCGCACTGGAG 241  
 DB 370 ATTAGTGGCGGTCTCGCTGAGCGCTTCATTGCGTAGTAAACACTTCGCACTGGAA 429

QY 242 AGCGCGCGGCGACCGCTTAACACCACTTCTGAATGTGACCTCGAATCAGTAGG 301  
 DB 430 CGCGGCGCGGCGACCGCTTAAACCCCACTTCTGAATGTGACCTCGAATCAGTAGG 489  
 QY 302 AATACCGGCTGAA 314  
 DB 490 AATACCGGCTGAA 502  
 RESULT 4  
 ABV78724  
 ID ABV78724 standard; rRNA; 659 BP.  
 XX  
 AC ABV78724;  
 XX  
 DT 14-JAN-2003 (first entry)  
 XX  
 DE C. sinensis rRNA sequence #23.  
 XX  
 KW Ribosome ribonucleic acid; rRNA; Cordyceps crassisporea; classification;  
 KW Cordyceps sinensis; ss.  
 XX  
 OS Cordyceps sinensis.  
 XX  
 PN JP2002204696-A.  
 XX  
 PD 23-JUL-2002.  
 XX  
 PF 12-JAN-2001; 2001JP-00004805.  
 XX  
 PR 12-JAN-2001; 2001JP-00004805.  
 XX  
 PA (HEAL-) HEALTHWAY KK.  
 PA (KANE/) KANESHIRO N.  
 XX  
 DR WPI; 2002-639075/69.  
 XX  
 FT Ribosome RNA gene base sequence of Cordyceps sinensis for classification  
 FT of seeds of Cordyceps sinensis.  
 XX  
 PS 26; Page 25; 33pp; Japanese.  
 XX  
 CC The invention relates to a novel base sequence which is part of a fully  
 CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassisporea.  
 CC The base sequences can be used for the classification of Cordyceps  
 CC sinensis. The sequence represents a C. sinensis rRNA sequence of the  
 CC invention  
 XX  
 SQ Sequence 659 BP; 183 A; 173 C; 160 G; 143 T; 0 U; 0 Other;  
 Query Match 75.5%; Score 240.8; DB 6; Length 659;  
 Best Local Similarity 89.3%; Pred. No. 3.9e-70;  
 Matches 284; Conservative 0; Mismatches 27; Indels 7; Gaps 2;  
 QY 2 AAAATGCGATGAATGTAATGCAATTCAGTAATCATGAACTTTGAACGAC 61  
 DB 259 AAAATGCGATGAATGTAATGCAATTCAGTAATCATGAACTTTGAACGAC 318  
 QY 62 ATTGCGCGCCGAGTATTCGCGGCGATGCTGTTCAGAGCTATTACAACCTTCAGGC 121  
 DB 319 ATTGCGCGCCGAGTATTCGCGGCGATGCTGTTCAGAGCTATTACAACCTTCAGGC 378  
 QY 122 CCGCGGCGCTGCGGTGGGATCGGCGGAGCCCTCGGGGCAACAAGCGTCCGCCAA 181  
 DB 379 CCGCGGCTTGTGTGGGATCGGCGGAGCTCGCTCAAGCGG-----TGC CGCCCGGAA 432  
 QY 182 ATACAGTGGCGGTCCCGCGAGCTTCATTGCGTAGTAAACACTTCGCACTGGAG 241  
 DB 433 ATACAGTGGCGGTCTCGCTGAGCGCTTCATTGCGTAGTAAACACTTCGCACTGGAA 492  
 QY 242 AGCGCGCGGCGACCGCTTAACACCACTTCTGAATGTGACCTCGAATCAGTAGG 301  
 DB 493 CGCGGCGCGGCGACCGCTTAAAC-CCCACTTCTGAATGTGACCTCGAATCAGTAGG 551

QY 302 AATACCGCTGAACCTTAA 319  
 Db 552 AATACCGCTGAACCTTAA 569

## RESULT 5

ACC50001  
 ID ACC50001 standard; DNA; 534 BP.

AC ACC50001;

DT 14-JUL-2003 (first entry)

DE Internal transcribed spacer RNA encoding sequence #3.

KM Mitochondria; fungal pathogen; ds.

XX Paearium proliferatum.

XX WO2003027635-A2.

PD 03-APR-2003.

PF 19-SEP-2002; 2002WO-US030311.

PR 24-SEP-2001; 2001US-00961755.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

PI Beck JJ, Barnett CJ;

XX MPI; 2003-363229/34.

DR Detecting a fungal pathogen, useful for monitoring disease development,

PT comprises subjecting the DNA to PCR amplification using at least one

PT primer having sequence identity with at least 10 contiguous nucleotides

XX of *Fusarium* spp.

PS Claim 5; Page 38-39; 44pp; English.

XX This invention relates to the detection of a fungal pathogen comprising

CC isolating DNA from a plant leaf infected with a pathogen. The methods and

CC primers are useful for identifying fungal isolates of fungal pathogens

CC and monitoring of disease development in plant populations. The present

CC sequence represents an internal transcribed spacer RNA encoding sequence

XX

SO Sequence 534 BP; 135 A; 149 C; 130 G; 120 T; 0 U; 0 Other;

Query Match 75.4%; Score 240.4; DB 7; Length 534;

Best Local Similarity 87.9%; Pred. No. 4.9e-70;

Matches 276; Conservative 0; Mismatches 31; Indels 7; Gaps 1;

QY 2 AATATGGATGAAGTAATGTAATGCAATTCAGTAATCATCGAATCTTTGAACGCAC 61

Db 228 AATATGGATGAAGTAATGTAATGCAATTCAGTAATCATCGAATCTTTGAACGCAC 287

QY 62 ATTGCGCCCGCCAGTATTCGCGCGGCGATGCTGTTGAGCGTCATTAACCCCTGAGG 121

Db 288 ATTGCGCCCGCCAGTATTCGCGCGGCGATGCTGTTGAGCGTCATTAACCCCTGAGG 347

QY 122 CCCCAGGCTGGCGTTGGGATGCGCGAAGCCCTGCGGCGACAACGCCGCTCCCCCA 181

Db 348 CCCCAGGCTGGCGTTGGGATGCGCGAAGCCCTGCGGCGACAACGCCGCTCCCCCA 400

QY 182 ATACAGTGGGGTCCCGCCGACCTTCATTTGCTAGTACTTAACCTTCGCAACTGGAG 241

Db 401 ATCTAGTGGGGTCCCGCCGACCTTCATTTGCTAGTACTTAACCTTCGCAACTGGAG 460

QY 242 AGCGGCGCGGCGACGCGTAACCACTTCTGAATGTGACCTCGAATCAGGTAG 301

Db 461 CGGCGCGGCGGCAAGCGTTAAACCCCACTTCTGAATGTGACCTCGAATCAGGTAG 520

QY 302 AATACCGCTGAAC 315  
 Db 521 AATACCGCTGAAC 534

## RESULT 6

AAV70851  
 ID AAV70851 standard; DNA; 310 BP.

AC AAV70851;

DT 17-OCT-2003 (revised)

DT 26-FEB-1999 (first entry)

DE Internal transcribed spacer 2 (ITS2) and adjacent regions.

KM Internal transcribed spacer 2; ITS2; probe; *Aspergillus flavus*; *A. niger*;

KM *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*; *Mucor rouxii*;

KM *M. racemosus*; *M. plumbeus*; *M. indicus*; *A. fumigatus*;

KM *M. circinilloides* f. *circinelloides*; *Rhizopus oryzae*; *R. microsporus*;

KM *R. circinans*; *R. stolonifer*; *Rhizomucor pusillus*; *Absidia corymbifera*;

KM *Cunninghamella elegans*; *Pseudallescheria boydii*; *Scedosporium apiospermum*;

KM *Penicillium notatum*; *Sporothrix schenckii*; filamentous fungus; ss.

XX

OS *Gibberella fujikuroi*.

XX WO9850584-A2.

XX 12-NOV-1998.

XX 01-MAY-1998; 98WO-US008926.

XX 02-MAY-1997; 97US-0045400P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Morrison CJ, Reiss E, Aldorevich L, Choi JS;

XX MPI; 1999-034737/03.

XX New nucleic acid probes for filamentous fungi - for detecting e.g.

XX *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Absidia*.

XX *Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix*

XX species.

PS Claim 1; Page 12; 45pp; English.

XX The present sequence represents an internal transcribed spacer 2 (ITS2)

XX and adjacent regions. Probes can be derived from the present sequence

XX which are species-specific. The specification also describes ITS2

XX sequence-derived probes for identifying a species selected from

XX *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,

XX *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,

XX *M. indicus*, *M. circinilloides* f. *circinelloides*, *Rhizopus oryzae*, *R.*

XX *microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Absidia*

XX *corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph

XX *Schenckii*. The probes can be used for differentiating filamentous fungal

XX species from each other and from other medically important fungi.

XX (Updated on 17-OCT-2003 to standardise OS field)

SO Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 U; 0 Other;

Query Match 75.3%; Score 240.2; DB 2; Length 310;

Best Local Similarity 87.4%; Pred. No. 4.6e-70;

Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

QY 3 AATGCGATAGTATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAACGCACA 62

Db 1 AATGCGATAGTATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAACGCACA 60

QY 63 TTGGCGCCGCGAGTAATTCGCGGCGATGCTGTTGAGCGTCATTAACCCCTGAGGCC 122



```
Db      61 TTGCGCCGCCGACGATATTCTGGCGGCGATGCTGTTCGAGCGTCATTTCACACCTCAAGCC 120
Qy      123 CCGGCGCCCTGGGCGTGGGAGATGGCGGGAAGCCCCCTGCGGGGACAAAGCGCTCCCAAA 182
Db      121 CCGGCGGTTGGTGGTGGGATGGCAAGCCCTTGGCGG-----AAGCGGCGCCGAAA 173
Qy      183 TACAGTGGCGGTCCCGCCGACGCTTCATTTGGTGTAGTAAACACTTGCACTGGAGAGA 242
Db      174 TCTATGTGGCGGTCTCGCTGCAGCTTCATGTGCTGTAGTAAACCTTCGCAACTGTGAC 233
Qy      243 GCGGCGCGGCGCACGCGCTTAAACACCCAACTTGTGAATGTTGACCTCGAATCAGTAGGA 302
Db      234 GCGGCGCGGCGCAAGCGCTTAAACCCCAACTTGTGAATGTTGACCTCGAATCAGTAGGA 293
Qy      303 ATACCGGCTGAACCTTAA 319
Db      294 ATACCGGCTGAACCTTAA 310

RESULT 7
AAV59009 standard; DNA; 561 BP.
XX AC      AAV59009;
XX DT      17-OCT-2003 (revised)
XX DT      25-MAR-2003 (revised)
XX DT      06-JAN-1999 (first entry)
XX DE      F. avenaceum internal transcribed spacer.
XX XX      Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
XX KW      fungal pathogen identification; infection identification; ss.
XX OS      Gibberella avenacea.
XX XX      Key      Location/Qualifiers
XX FH      miec_feature      31.181
XX FT      /*tag= a
XX FT      /note= "ITS1"
XX FT      miec_feature      339..504
XX FT      /*tag= b
XX FT      /note= "ITS2"
XX PN      US5827695-A.
XX PD      27-OCT-1998.
XX PF      04-AUG-1997; 97US-00905314.
XX PR      04-AUG-1997; 97US-00905314.
XX PA      (NOVS ) NOVARTIS FINANCE CORP.
XX PI      Beck JT;
XX DR      WPI; 1998-593995/50.
XX PT      Wheat pathogen internal transcribed spacer sequences - used as a basis
XX PT      for primers for the species-specific polymerase chain reaction detection
XX PT      of the pathogens.
XX PS      Claim 1; Col 29-30; 20pp; English.
XX CC      This sequence represents an internal transcribed spacer (ITS) sequence of
XX CC      the invention. The primer pairs, based on the ITS sequences, are used for
XX CC      the PCR amplification detection of wheat Microdochium and Fusarium fungal
XX CC      pathogens, especially M. nivale, F. graminearum, F. culmorum, F.
XX CC      avenaceum, F. roseum, F. moniliforme or F. roseum. The two different
XX CC      strains of fungi show different symptoms during infection, which may or
XX CC      may not be due to infection. Early identification of the strain causing
XX CC      the infection allows early, and more specific fungicidal treatment.
XX CC      (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
```

```
CC correct PR field.) (updated on 17-OCT-2003 to standardise OS field)
XX SQ      Sequence 561 BP; 145 A; 152 C; 135 G; 126 T; 0 U; 3 Other;
XX      Query Match      75.2%; Score 240; DB 2; Length 561;
XX      Best Local Similarity 88.7%; Pred. No. 6,8e-70;
XX      Matches 282; Conservative 2; Mismatches 27; Indels 7; Gaps 2;

Qy      2 AAATGCGATTAAGTATGTGATATGCAAGATTCAGTGAATATGATCTTTGAACGAC 61
Db      231 AAATGCGATTAAGTATGTGATATGCAAGATTCAGTGAATATGATCTTTGAACGAC 290
Qy      62 ATTGGCGCGCGCAGATTCGCGGCGCATGCTGTGAGGCGTATTACACCTCAAGC 121
Db      291 ATTGGCGCGCGTGTATTCGCGGCGCATGCTGTGAGGCGTATTACACCTCAAGC 350
Qy      122 CCGCGGCGCTGCGTGGGAGATCGCGGAACCCCTGCGGCAACGCGCTCCCA 181
Db      351 CCGCGGCGTGTGTGGGAGATCGGCTGCTGCTTMYGCGG-----TGCGGCCCGGAA 404
Qy      182 ATACAGTGGCGGTCCCGCCGACGCTTCATTTGGTGTAGTAAACACTTGCAACTGGAG 241
Db      405 ATACATTTGGCGGTCTCGCTGCAGCCTTCATTTGGTGTAGTAAACACTTGCAACTGGAG 464
Qy      242 AGCGGCGCGCGCACGCGGTAACACCCAACTTGAATGTTGACCTCGAATCAGTAGG 301
Db      465 GCGGCGGCGGCAATGCGTAAAC-CCCAACTTGTGAATGTTGACCTCGAATCAGTAGG 523
Qy      302 AATACCGGCTGAACCTTAA 319
Db      524 AATACCGGCTGAACCTTAA 541
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RESULT 8
ABV78700 standard; rRNA; 647 BP.
XX ID      ABV78700
XX XX      ABV78700;
XX AC      14-JAN-2003 (first entry)
XX DT      14-JAN-2003 (first entry)
XX DE      C. crassispota rRNA sequence #2.
XX XX      Ribosome ribonucleic acid; rRNA; Cordyceps crassispota; classification;
XX KW      Cordyceps sinensis; ss.
XX OS      Cordyceps crassispota.
XX PN      JP2002204696-A.
XX PD      23-JUL-2002.
XX PF      12-JAN-2001; 2001JP-00004805.
XX PR      12-JAN-2001; 2001JP-00004805.
XX PA      (HEAL-) HEALTHWAY KK.
XX PA      (KANE/) KANESHIRO N.
XX DR      WPI; 2002-639075/69.
XX PT      Ribosome RNA gene base sequence of Cordyceps sinensis for classification
XX PT      of seeds of Cordyceps sinensis.
XX PS      2; Page 12; 33pp; Japanese.
XX CC      The invention relates to a novel base sequence which is part of a fully
XX CC      defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispota.
XX CC      The base sequences can be used for the classification of Cordyceps
XX CC      sinensis. The sequence represents a C. crassispota rRNA sequence of the
XX CC      invention.
XX SQ      Sequence 647 BP; 166 A; 178 C; 160 G; 143 T; 0 U; 0 Other;
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US-09-645-073-1

Sequence 1, Application US/09645073  
Patent No. 6287800  
GENERAL INFORMATION:  
APPLICANT: Lee, May  
APPLICANT: Galazzo, Jorge  
TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7  
FILE REFERENCE: L02-01NP  
CURRENT APPLICATION NUMBER: US/09/645,073  
CURRENT FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: US 60/151,770  
PRIOR FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 1  
LENGTH: 2293  
TYPE: DNA  
ORGANISM: Gibberella fujikuroi  
US-09-645-073-1

Query Match 76.6%; Score 244.4; DB 3; Length 2293;  
Best Local Similarity 88.1%; Pred. No. 1.1e-69;  
Matches 280; Conservative 0; Mismatches 31; Indels 7; Gaps 1;

QY 2 AAAATGGGATTAAGTAATGTAATTCAGAAATTCAGATCATCGAATCTTTGAACGAC 61  
DB 1971 AAAATGGGATTAAGTAATGTAATTCAGAAATTCAGATCATCGAATCTTTGAACGAC 2030  
QY 62 ATTGCGCGCCGCAATATTCGCGCGGCAATGCTTTGAGCGTCATTACAACCTCAGGC 121  
DB 2031 ATTGCGCGCCGCAATATTCGCGCGGCAATGCTTTGAGCGTCATTACAACCTCAGGC 2090  
QY 122 CCGCGGCGCTGCGCTTGGGAGATCGCGGAAAGCCCTCGCGGCAACAAGCGCTGCCCAA 181  
DB 2091 CCGCGGCGCTTGGGAGATCGCGGCAATGCTTTGAGCGTCATTACAACCTCAGGC 2143  
QY 182 ATACAGTGGCGGTCCCGCGGCAATTCATTGCGTAAGTAAACCTCGCAACTGGAG 241  
DB 2144 ATACAGTGGCGGTCCCGCGGCAATTCATTGCGTAAGTAAACCTCGCAACTGGAG 2203  
QY 242 AGCGGCGCGGCGCAACCGGTAACCACTCTGTAATTTGACCTCGCAATCAGGTAG 301  
DB 2204 CGCGGCGCGGCGCAACCGGTAACCACTCTGTAATTTGACCTCGCAATCAGGTAG 2263  
QY 302 AATACCGGCTGAACCTTA 319  
DB 2264 AATACCGGCTGAACCTTA 2281

RESULT 3  
US-09-423-233-7  
Sequence 7, Application US/09423233  
Patent No. 6372430  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America as  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
FILE REFERENCE: 03063-0341WP  
CURRENT APPLICATION NUMBER: US/09/423,233  
CURRENT FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 7  
LENGTH: 310  
TYPE: DNA  
ORGANISM: Fusarium moniliforme  
US-09-423-233-7

Query Match 75.3%; Score 240.2; DB 4; Length 310;  
Best Local Similarity 87.4%; Pred. No. 1.1e-68;  
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

QY 3 AATTCGATTAAGTAATGTAATTCAGAAATTCAGATCATCGAATCTTTGAACGAC 62  
|||||

DB 1 AAATGGGATTAAGTAATGTAATTCAGAAATTCAGATCATCGAATCTTTGAACGAC 60  
QY 63 TTGCGCGCGGCAATATTCGCGGCGGCAATGCTTTGAGCGTCATTACAACCTCAGGC 122  
DB 61 TTGCGCGCGGCAATATTCGCGGCGGCAATGCTTTGAGCGTCATTACAACCTCAGGC 120  
QY 123 CCGCGGCGCTGCGCTTGGGAGATCGCGGAAAGCCCTCGCGGCAACAAGCGCTGCCCAA 182  
DB 121 CCGCGGCGCTTGGGAGATCGCGGAAAGCCCTCGCGGCAACAAGCGCTGCCCAA 173  
QY 183 TACAGTGGCGGTCCCGCGGCAATTCATTGCGTAAGTAAACCTCGCAACTGAGA 242  
DB 174 TCAAGTGGCGGTCCCGCGGCAATTCATTGCGTAAGTAAACCTCGCAACTGAGTAC 233  
QY 243 GCGGCGCGGCGCAACCGGTAACCACTCTGTAATTTGACCTCGAATCAGGTAGA 302  
DB 234 GCGGCGCGGCGCAACCGGTAACCACTCTGTAATTTGACCTCGAATCAGGTAGA 293  
QY 303 AATACCGGCTGAACCTTA 319  
DB 294 AATACCGGCTGAACCTTA 310

RESULT 4  
US-08-905-314A-24  
Sequence 24, Application US/08905314A  
Patent No. 5827695  
GENERAL INFORMATION:  
APPLICANT: Beck, James J.  
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 5827695artis Corporation Patent Department  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 20779-2257  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,314A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1944  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 561 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: Fusarium avenaceum  
INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..30  
OTHER INFORMATION: /note="3' end of small subunit  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 31..181









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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..12
OTHER INFORMATION: /note= "3', end of small subunit"
FEATURE:
NAME/KEY: misc feature
LOCATION: 13..161
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc feature
LOCATION: 162..318
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 319..472
OTHER INFORMATION: /note= "ITS 2"
NAME/KEY: misc feature
LOCATION: 473..504
OTHER INFORMATION: /note= "5', end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-19

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Query Match 57.6%; Score 183.8; DB 1; Length 504;
Best Local Similarity 81.5%; Pred. No. 2.9e-50;
Matches 255; Conservative 1; Mismatches 38; Indels 19; Gaps 3;

QY 2 AAATGCGATGAATGTAATGCAATTCAGTGAATCAGTGAATCTTTGAACGAC 61
DB 211 AAATGCGATGAATGTAATGCAATTCAGTGAATCAGTGAATCTTTGAACGAC 270
QY 62 ATTGCGCCCGCAGTATTCTGCGGGGATGCTGTTGAGCGTCATTACAACCTTCAGGC 121
DB 271 ATTGCGCCCGCAGTATTCTGCGGGGATGCTGTTGAGCGTCATTACAACCTTCAGGC 330
QY 122 CCGCGGGCTGGCGTTGGGATCGGCGGAAGCCCTCGCGGCAACGCGTCCCCCA 181
DB 331 CC---AGCTTGTTGGAGAGCTG-----CAGTCTGTCGCACTCCCA 372
QY 182 ATACAGTGGGGTCCCGCCGACCTTCATGCTAGTACTAACCCTTCGCACTGAG 241
DB 373 ATACATTTGGGTCAGTCTGACCTTCATGCTAGTACTAACCCTTCGCACTGAG 432
QY 242 AGCGGCGCGGCAAGCGCTTAACCACTTGAATGTTGACCTGCAATCAGGTAG 301
DB 433 ATGCTGGCGGCAAGCGCTTAAC-CCCACTTGAATGTTGACCTGCAATCAGGTAG 491

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QY 302 AATACCCGCTGAA 314
DB 492 AATACCCGCTGAA 504

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## RESULT 11

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US-08-722-187-82
Sequence 82, Application US/08722187
Patent No. 5955274
GENERAL INFORMATION:
APPLICANT: Ligdon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:
CLASSIFICATION: 435
PRIORITY INFORMATION:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum"
OTHER INFORMATION: (fcuim.con)"
US-08-722-187-82

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Query Match 57.6%; Score 183.8; DB 2; Length 504;
Best Local Similarity 81.5%; Pred. No. 2.9e-50;
Matches 255; Conservative 1; Mismatches 38; Indels 19; Gaps 3;

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QY 2 AAATGCGATGAATGTAATGCAATTCAGTGAATCAGTGAATCTTTGAACGAC 61
DB 211 AAATGCGATGAATGTAATGCAATTCAGTGAATCAGTGAATCTTTGAACGAC 270
QY 62 ATTGCGCCCGCAGTATTCTGCGGGGATGCTGTTGAGCGTCATTACAACCTTCAGGC 121
DB 271 ATTGCGCCCGCAGTATTCTGCGGGGATGCTGTTGAGCGTCATTACAACCTTCAGGC 330
QY 122 CCGCGGGCTGGCGTTGGGATCGGCGGAAGCCCTTCGCGGCAACGCGTCCCCCA 181
DB 331 CC---AGCTTGTTGGAGAGCTG-----CAGTCTGTCGCACTCCCA 372

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NAME/KEY: misc feature  
LOCATION: 31..178  
OTHER INFORMATION: /note= "ITS 1"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 179..335  
OTHER INFORMATION: /note= "5.8S rRNA gene"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 336..488  
OTHER INFORMATION: /note= "ITS 2"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 489..545  
OTHER INFORMATION: /note= "5' end of large subunit"  
OTHER INFORMATION: rRNA gene"  
US-08-887-480-84

Query Match 56.6%; Score 180.4; DB 1; Length 545;  
Best Local Similarity 82.4%; Pred. No. 3.8e-49;  
Matches 262; Conservative 0; Mismatches 36; Indels 20; Gaps 4;

QY 2 AAAATGCGATAGTAATGTAATGCAAGATTGCAATGATCATGCAATCTTTGAGCGCAC 61  
DB 228 AAAATGCGATAGTAATGTAATGCAAGATTGCAATGATCATGCAATCTTTGAGCGCAC 287  
QY 62 ATTGGCGCCCGCAATATTTGCGCGGCGATGCTGTTGAGCGCTATTACACCTTCAGGC 121  
DB 288 ATTGGCGCCCGCAATATTTGCGCGGCGATGCTGTTGAGCGCTATTACACCTTCAGGC 347  
QY 122 CCGCGGCGCTGCGCTTGGGGATCGCGGGAAGCCCTCGCGGCGACAGCGCGTCCCCCA 181  
DB 348 CC---AGCTTGCTGTTGGAGCTG-----CAGTCTGCTGCACTCCCCCA 389  
QY 182 ATACAGTGGCGGCTCCCGCGAGCTTCATGTCGTAGTACCTGACCTGCACTGAG 241  
DB 390 ATACATTTGGCGGCTACCGTCG-AGCTTCATAGCGTAGTAATTACATGCTACTGTA 448  
QY 242 AGCGGCGCGGCGACGCGGTAAACACCAACTTCTGAATTTGACCTCGCAATGAGTAG 301  
DB 449 ATGCTCGCGGCGACGCGGTAAAC-CCCAACTTCTGAATTTGACCTCGGATGAGTAG 507  
QY 302 AATACCGCTGAACCTTAA 319  
DB 508 AATACCGCTGAACCTTAA 525

RESULT 14  
US-08-905-314A-21  
Sequence 21, Application US/08905314A  
Patent No. 5827695

GENERAL INFORMATION:  
APPLICANT: Beck, James J.  
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5827695artis Corporation Patent Department  
STREET: 3054 Cornwells Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 20779-2257  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,314A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1944  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ. ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 545 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORGANISM: Fusarium moniliforme  
INDIVIDUAL ISOLATE: 4551  
IMMEDIATE SOURCE:  
CLONE: pCRFMON1  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..30  
OTHER INFORMATION: /note= "3' end of small subunit"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 31..178  
OTHER INFORMATION: /note= "ITS 1"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 179..335  
OTHER INFORMATION: /note= "5.8S rRNA gene"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 336..488  
OTHER INFORMATION: /note= "ITS 2"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 489..545  
OTHER INFORMATION: /note= "5' end of large subunit"  
OTHER INFORMATION: rRNA gene"  
US-08-905-314A-21

Query Match 56.6%; Score 180.4; DB 1; Length 545;  
Best Local Similarity 82.4%; Pred. No. 3.8e-49;  
Matches 262; Conservative 0; Mismatches 36; Indels 20; Gaps 4;

QY 2 AAAATGCGATAGTAATGTAATGCAAGATTGCAATGATCATGCAATCTTTGAGCGCAC 61  
DB 228 AAAATGCGATAGTAATGTAATGCAAGATTGCAATGATCATGCAATCTTTGAGCGCAC 287  
QY 62 ATTGGCGCCCGCAATATTTGCGCGGCGATGCTGTTGAGCGCTATTACACCTTCAGGC 121  
DB 288 ATTGGCGCCCGCAATATTTGCGCGGCGATGCTGTTGAGCGCTATTACACCTTCAGGC 347  
QY 122 CCGCGGCGCTGCGCTTGGGGATCGCGGGAAGCCCTCGCGGCGACAGCGCGTCCCCCA 181  
DB 348 CC---AGCTTGCTGTTGGAGCTG-----CAGTCTGCTGCACTCCCCCA 389  
QY 182 ATACAGTGGCGGCTCCCGCGAGCTTCATGTCGTAGTACCTGACCTGCACTGAGTAG 241  
DB 390 ATACATTTGGCGGCTACCGTCG-AGCTTCATAGCGTAGTAATTACATGCTACTGTA 448  
QY 242 AGCGGCGCGGCGACGCGGTAAACACCAACTTCTGAATTTGACCTCGCAATGAGTAG 301  
DB 449 ATGCTCGCGGCGACGCGGTAAAC-CCCAACTTCTGAATTTGACCTCGGATGAGTAG 507  
QY 302 AATACCGCTGAACCTTAA 319  
DB 508 AATACCGCTGAACCTTAA 525

RESULT 15  
US-08-887-480-96

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Sequence 96, Application US/0887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artie Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Fusarium rose
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
INDIVIDUAL ISOLATE: sequence)
IMMEDIATE SOURCE:
CLONE: pCRFpoeat427(1-2), pCRFpoeat534(2-2), and
CLONE: pCRFpoeat756(3-1)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..180
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 181..337
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 338..489
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-887-480-96
Query Match 56.4%; Score 180; DB 1; Length 546;
Best Local Similarity 82.4%; Pred. No. 5.2e-49;

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Matches 262; Conservative 0; Mismatches 35; Indels 21; Gaps 4.
QY      2  AAAATGCGATAGTAATGTGAATTGCGAATTCAGTAATATCGAATCTTTGAAACGCAC 61
Db      230  AAAATGCGATAGTAATGTGAATTGCGAATTCAGTAATATCGAATCTTTGAAACGCAC 289
QY      62  ATTGCGCCCGCGAGATTTCTGGCGGAGCATGCTGTTGCGAGGTCATTACAACCCTCAGAC 121
Db      290  ATTGCGCCCGCGAGTATTTCTGGCGGAGCATGCTGTTGCGAGGTCATTACAACCCTCAGAC 349
QY      122  CCCCgggCCTTggCgTtggggATCGCGGAGCCCCCTGCGGgCAACAACCGCGTCCCCCA 181
Db      350  CC---AGCTTgGTtTggGg-----ATCTGTGTGAACACAGTCCCA 390
QY      182  ATACAGTGGCGGTCCTCCGCGCGAGCTTCCATTGCGTAGTAGTAACTCTCGCACTGGAG 241
Db      391  ATTATATGGCGCGTCAACGCG-AGCTTCCATAGCGTAGTAATTTACACATCGTTACTGTATA 449
QY      242  AGCGGCGCGCGCACGCGCGTAAACAACCCAACTTCTGTAATGTTGACCTCGATCAGTAGG 301
Db      450  ATCGTCGCGGCGCAAGCGCGTTAAAC-CCCAACTTCTGAATGTGACCTCGATCAGTAgG 508
QY      302  AATAACCGCGTGAAGTTAA 319
Db      509  AATAACCGCGTGAAGTTAA 526

Search completed: October 1, 2004, 08:05:39
Job time : 110.125 secs

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Search completed: October 1, 2004, 08:05:39  
Job time : 110.125 secs

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100

Db 1 GAAATGGATAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCA 60  
 QY 61 CATTGCGCCCGCAGTATTTCTGGCGGGGATGCTGTTGAGCGTCAATTAACAACCTCAGG 120  
 Db 61 CATTGCGCCCGCAGTATTTCTGGCGGGGATGCTGTTGAGCGTCAATTAACAACCTCAGG 120  
 QY 121 CCCCCGCGGCTGGGCTGGGGGATGGGGGAGCCCGCTGGGGGACAACCGCGTCCCCCA 180  
 Db 121 CCCCCGCGGCTGGGCTGGGGGATGGGGGAGCCCGCTGGGGGACAACCGCGTCCCCCA 180  
 QY 181 AATACAGTGGCGGTCCCGCGCAGCTTCATTTGGGTAGTACTAACAACCTGCAACTGGA 240  
 Db 181 AATACAGTGGCGGTCCCGCGCAGCTTCATTTGGGTAGTACTAACAACCTGCAACTGGA 240  
 QY 241 GAGGGCGCGGCGCCGCTGTAACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 300  
 Db 241 GAGGGCGCGGCGCCGCTGTAACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 300  
 QY 301 GAATACCGCTGAACCTTAA 319  
 Db 301 GAATACCGCTGAACCTTAA 319

RESULT 2  
 US-09-961-755A-7  
 ; Sequence 7, Application US/09961755A  
 ; Publication No. US20030113722A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beck, Jim  
 ; APPLICANT: Barnett, Jason  
 ; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the  
 ; FILE REFERENCE: 60055  
 ; CURRENT APPLICATION NUMBER: US/09/961,755A  
 ; CURRENT FILING DATE: 2001-09-24  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 534  
 ; TYPE: DNA  
 ; ORGANISM: Fusarium proliferatum  
 US-09-961-755A-7

Query Match 75.4%; Score 240.4; DB 10; Length 534;  
 Best Local Similarity 87.9%; Pred. No. 3.6e-76;  
 Matches 276; Conservative 0; Mismatches 31; Indels 7; Gaps 1;  
 QY 2 AAAATGCGATGATGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCA 61  
 Db 228 AAAATGCGATGATGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCA 287  
 QY 62 ATTGCGCGCGCAGTATTTCTGGCGGGGATGCTGTTGAGCGTCAATTAACAACCTCAGG 121  
 Db 288 ATTGCGCGCGCAGTATTTCTGGCGGGGATGCTGTTGAGCGTCAATTAACAACCTCAGG 347  
 QY 122 CCCCCGCGGCTGGGCTGGGGGATGGGGGAGCCCGCTGGGGGACAACCGCGTCCCCCA 181  
 Db 348 CCCCCGCGGCTGGGCTGGGGGATGGGGGAGCCCGCTGGGGGACAACCGCGTCCCCCA 400  
 QY 182 AATACAGTGGCGGTCCCGCGCAGCTTCATTTGGGTAGTACTAACAACCTGCAACTGGA 241  
 Db 401 AATACAGTGGCGGTCCCGCGCAGCTTCATTTGGGTAGTACTAACAACCTGCAACTGGA 460  
 QY 242 AGCGGCGCGGCGCCGCTGTAACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 301  
 Db 461 AGCGGCGCGGCGCCGCTGTAACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 520  
 QY 302 AATACCGCTGAAC 315  
 Db 521 AATACCGCTGAAC 534

RESULT 3

US-10-046-955-7  
 ; Sequence 7, Application US/10046955  
 ; Publication No. US20030129600A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Government of the United States of America, as Represented by the  
 ; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis  
 ; APPLICANT: Control and Prevention  
 ; APPLICANT: Morrison, Christine J.  
 ; APPLICANT: Reiss, Errol  
 ; APPLICANT: Aidorevich, Lilianna  
 ; APPLICANT: Choi, Jong Soo  
 ; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
 ; FILE REFERENCE: Other Filamentous Fungi  
 ; FILE REFERENCE: 6395-62064  
 ; CURRENT APPLICATION NUMBER: US/10/046,955  
 ; CURRENT FILING DATE: 2002-06-04  
 ; PRIOR APPLICATION NUMBER: US 09/423,233  
 ; PRIOR FILING DATE: 2000-06-27  
 ; PRIOR APPLICATION NUMBER: PCT/US98/08926  
 ; PRIOR FILING DATE: 1998-05-01  
 ; PRIOR APPLICATION NUMBER: US 60/045,400  
 ; PRIOR FILING DATE: 1997-05-02  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 310  
 ; TYPE: DNA  
 ; ORGANISM: Fusarium moniliforme  
 US-10-046-955-7

Query Match 75.3%; Score 240.2; DB 15; Length 310;  
 Best Local Similarity 87.4%; Pred. No. 3.3e-76;  
 Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;  
 QY 3 AAATGCGATGATGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCA 62  
 Db 1 AAATGCGATGATGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCA 60  
 QY 63 TTGCGCGCGCGCAGTATTTCTGGCGGGGATGCTGTTGAGCGTCAATTAACAACCTCAGG 122  
 Db 61 TTGCGCGCGCGCAGTATTTCTGGCGGGGATGCTGTTGAGCGTCAATTAACAACCTCAGG 120  
 QY 123 CCCCCGCGGCTGGGCTGGGGGATGGGGGAGCCCGCTGGGGGACAACCGCGTCCCCCA 182  
 Db 121 CCCCCGCGGCTGGGCTGGGGGATGGGGGAGCCCGCTGGGGGACAACCGCGTCCCCCA 173  
 QY 183 TACAGTGGCGGTCCCGCGCAGCTTCATTTGGGTAGTACTAACAACCTGCAACTGGA 242  
 Db 174 TACAGTGGCGGTCCCGCGCAGCTTCATTTGGGTAGTACTAACAACCTGCAACTGGA 233  
 QY 243 GCGGCGCGCGCAGCGCTGTAACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 302  
 Db 234 GCGGCGCGCGCAGCGCTGTAACCCCACTTCTGAATTTGACCTCGAATCAGGTAG 293  
 QY 303 AATACCGCTGAACCTTAA 319  
 Db 294 AATACCGCTGAACCTTAA 310

RESULT 4  
 US-09-961-755A-5  
 ; Sequence 5, Application US/09961755A  
 ; Publication No. US20030113722A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beck, Jim  
 ; APPLICANT: Barnett, Jason  
 ; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the  
 ; FILE REFERENCE: 60055  
 ; CURRENT APPLICATION NUMBER: US/09/961,755A  
 ; CURRENT FILING DATE: 2001-09-24  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.0

	Query Match	Best Local Similarity	Score	DB 10;	Length	522;
	Matches	Conservative	0;	Mismatches	33;	Indels 19; Gaps 4
Qy	2	AAATGCGATTAAGTATGTGATTTGAGCAATTCAGTGAATCATCGAATCTTTGAAGCGAC	61			
Db	228	AAATATGCGATTAAGTATGTGATTTGAGCAATTCAGTGAATCATCGAATCTTTGAAGCGAC	287			
Qy	62	ATTGCGCGCCGCGAGTATTCGCGCGGCGATGCTGTTCCAGGCTCATTAACAACCTCAGAC	121			
Db	288	ATTGCGCGCCGCGAGTATTCGCGCGGCGATGCTGTTCCAGGCTCATTAACAACCTCAGAC	347			
Qy	122	CCCCGGGCGTCCGCTTGGGGAGATCGCGGGAAGCCCCCTTCGGGCAACAAGCGCTCCCCCA	181			
Db	348	CC---AGCTTGTGTGGGACTC-----CGAGTCAAAATCGCGTTCGCCCA	390			
Qy	182	ATACAGTGGCGTCCCGCGAGCTTCCATTGCGTAAAGCTAACCTCCGCACTGGAG	241			

Query Match	55.3%;	Score 176.4;	DB 10;	Length 521;
Best Local Similarity	82.2%;	Pred. No. 5.2e-53;		
Matches 258;	Conservative	0;	Mismatches 36;	Indels 20;
				Gaps 4.
Qy	2	AAATGCGATAGTAATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC	61	
Db	228	AAATGCGATAGTAATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC	287	
Qy	62	ATTGCGCCCGCCAGTAATTTCTGGCGCGGCATGCTCTGTTGAGCGCTATTACAACTTCAGGC	121	
Db	288	ATTGCGCCCGCCAGTAATTTCTGGCGCGGCATGCTCTGTTGAGCGCTATTACAACTTCAGGC	347	
Qy	122	CCCCGGGCGCTGGCGCTTGGGGGATTCGGCGGAAGCCCCCTCGGGGCACAAAGCCGTCGCCCAA	181	
Db	348	CC---ACCTTGGTGTGTGGAGCTG-----CAGTCTGTGTGACTTCCCA	389	
Qy	182	ATTACAGTGGCGGTCCCGCCGAGCTTCCATTCGCTAGTAGCTAACACCTCCGCACTGGAG	241	
Db	390	ATTACATTGGCGGTACGCTCG-AGCTTTCATAGCTAGTAATTTACACATGCTTACTGTA	448	
Qy	242	AGCGGCGCGGCACCGCGTAAACAAACCAACCTTGTGAATGTTGAACCTTGAATCAGTAGG	301	
Db	449	ATCGTCCGCGGCACGCGTTAAAC-CCCAATTCTGAATGTTGAACCTTGCATCAGTAGG	507	
Qy	302	AATACCCGCTGTAAC	315	
Db	508	AATACCCGCTGTAAC	521	

```

RESULT 7
US-10-121-740-2
; Sequence 2, Application US/10121740
; Publication No. US20030186425A1
; GENERAL INFORMATION:
; APPLICANT: Strobel, Denise
; APPLICANT: Manker, Gary
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019, 40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902

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;; PRIOR FILING DATE: 2002-03-11  
;; PRIOR APPLICATION NUMBER: 60/363,072  
;; PRIOR FILING DATE: 2001-04-16  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 652  
;; TYPE: DNA  
;; ORGANISM: Muscodor albus  
US-10-121-740-2

Query Match 41.3%; Score 131.8; DB 15; Length 652;  
Best Local Similarity 72.6%; Pred. No. 7.9e-37;  
Matches 230; Conservative 0; Mismatches 72; Indels 15; Gaps 4;

QY 3 AAATGCGATTAAGTGAATTCGAGAAATTCAGTGAATTCGATCTTTGAACGACACA 62  
DB 329 AAATGCGATTAAGTGAATTCGAGAAATTCAGTGAATTCGATCTTTGAACGACACA 388  
QY 63 TTGCGCCCGCCAGTATTCGTGGCGGCATGCTGTTGAGGCTCAATTCAGCCCTCAGGCC 122  
DB 389 TTGCGCCCATTAAGTATTCAGTGGGATGCTGTTGAGGCTCAATTCAGCCCTCAGGCC 448  
QY 123 CCGGCGCTGGCGTTGGGGAATCGCGGAGGCCCTCGCGGACAGACGCCCTCCCAAA 182  
DB 449 CTGTTGCTTAAGCTGGGAGGCTACGGCAGCTGCC-----CGTAGCTCCCTAAA 496  
QY 183 TACAGTGGCGGTCCCGCCGAGCTTCATTCGAGTAACTAACCTCCGCAATCGAGACA 242  
DB 497 GTGATGGCGGAGTTGTTCTACTCTA-GGCGTAGTAAT-CTATCTCGCTCTGTAGT 554  
QY 243 GCGGCGCGCCAGCGCGTAAACCCCACTTGAATGTGAATCGTGAATCGAGTAGGA 302  
DB 555 GGTTCGGGCGCCCTGCGTAAACCCCTATATC-AAAGTTGACTCGATCAGTAGGA 613  
QY 303 ATACCGCTGAACCTTA 319  
DB 614 ATACCGCTGAACCTTA 630

RESULT 8  
US-10-623-432-2  
; Sequence 2, Application US/10623432  
; Publication No. US20040141955A1  
; GENERAL INFORMATION:  
; APPLICANT: Strobel, Gary  
; APPLICANT: Manke, Denise  
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF  
; FILE REFERENCE: AQ 2019, 40  
; CURRENT APPLICATION NUMBER: US/10/623,432  
; PRIOR FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: US/10/121,740  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: 60/283,902  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/363,072  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 652  
; TYPE: DNA  
; ORGANISM: Muscodor albus  
US-10-623-432-2

Query Match 41.3%; Score 131.8; DB 17; Length 652;  
Best Local Similarity 72.6%; Pred. No. 7.9e-37;  
Matches 230; Conservative 0; Mismatches 72; Indels 15; Gaps 4;

QY 3 AAATGCGATTAAGTGAATTCGAGAAATTCAGTGAATTCGATCTTTGAACGACACA 62  
DB 329 AAATGCGATTAAGTGAATTCGAGAAATTCAGTGAATTCGATCTTTGAACGACACA 388

QY 63 TTGCGCCCGCCAGTATTCGTGGCGGCATGCTTTCAGAGCTTACATTAACACCTCAGGCC 122  
DB 389 TTGCGCCCATTAAGTATTCAGTGGGATGCTGTTGAGGCTATTCACCACTTAAGCC 448  
QY 123 CCGGCGCTGGCGTTGGGGAATCGCGGAGGCCCTCGCGGACAGACGCCCTCCCAAA 182  
DB 449 CTGTTGCTTAAGCTGGGAGGCTACGGCAGCTGCC-----CGTAGCTCCCTAAA 496  
QY 183 TACAGTGGCGGTCCCGCCGAGCTTCATTCGAGTAACTAACCTCGCAACTGAGACA 242  
DB 497 GTGATGGCGGAGTTGTTCTACTCTA-GGCGTAGTAAT-CTATCTCGCTCTGTAGT 554  
QY 243 GCGGCGCGCCAGCGCGTAAACCCCACTTGAATGTGAATCGTGAATCGAGTAGGA 302  
DB 555 GGTTCGGGCGCCCTGCGTAAACCCCTATATC-AAAGTTGACTCGATCAGGTAGGA 613  
QY 303 ATACCGCTGAACCTTA 319  
DB 614 ATACCGCTGAACCTTA 630

RESULT 9  
US-10-046-955-3  
; Sequence 3, Application US/10046955  
; Publication No. US20030129600A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as Represented by the  
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease  
; APPLICANT: Control and Prevention  
; APPLICANT: Morison, Christine J.  
; APPLICANT: Reis, Etrol  
; APPLICANT: Ahdorovich, Lilliana  
; APPLICANT: Choi, Jong Soo  
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
; FILE REFERENCE: 6395-62064  
; CURRENT APPLICATION NUMBER: US/10/046,955  
; PRIOR FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 09/423,233  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: PCT/US98/08926  
; PRIOR FILING DATE: 1998-05-01  
; PRIOR APPLICATION NUMBER: US 60/045,400  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 365  
; TYPE: DNA  
; ORGANISM: Aspergillus niger  
US-10-046-955-3

Query Match 39.7%; Score 126.6; DB 15; Length 365;  
Best Local Similarity 64.7%; Pred. No. 4.7e-35;  
Matches 205; Conservative 0; Mismatches 109; Indels 3; Gaps 1;

QY 3 AAATGCGATTAAGTGAATTCGAGAAATTCAGTGAATTCGATCTTTGAACGACACA 62  
DB 52 AAATGCGATTAAGTGAATTCGAGAAATTCAGTGAATTCGATCTTTGAACGACACA 111  
QY 63 TTGCGCCCGCCAGTATTCGTGGCGGCATGCTGTTGAGGCTAATTCAGCCCTCAGGCC 122  
DB 112 TTGCGCCCGCCAGTATTCGTGGCGGCATGCTGTTGAGGCTAATTCAGCCCTCAGGCC 171  
QY 123 CCGGCGCTGGCGTTGGGGAATCGCGGAGGCCCTCGCGGACAGACGCCCTCCCAAA 182  
DB 172 C---GGCTTGTGTGTGGTGCCTGCTCCCGGGGAGCGGGCCGAAAGGACAG 228  
QY 183 TACAGTGGCGGTCCCGCGGAGCTTCATTCGAGTAACTAACCTCGCAACTGAGACA 242  
DB 229 GCGGCGACCGGCTCGATCTCGAGCGTATGGGGCTTTGTCACTCTCTGTAGGCCGG 288

Qy	Db	Qy	Db
243	289	303	349
GGGGCGGGGCGACGGCTGAAAACCCAACTTCTGAATGTTGACCTCGAATCAGGTGGA	CCGGCGGCTCCGACGTTATCCACCACTTTTTCAGAGTTGACCTCGGATCAGGTAGG	ATACCCGCTGAACCTTAA	ATACCGGCTGAACCTTAA
302	348	319	365

RESULT 10  
US-10-046

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? Sequence 5, Application US/10046955
? Publication No. US20030129600A1
?
? GENERAL INFORMATION:
? APPLICANT: The Government of the United States of America, as Represented by the
? APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
? APPLICANT: Control and Prevention
? APPLICANT: Morrison, Christine J.
? APPLICANT: Reiss, Errol
? APPLICANT: Aldorevich, Lilliana
? APPLICANT: Choi, Jong Soo
? TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
? TITLE OF INVENTION: Other Filamentous Fungi
? FILE REFERENCE: 6395-62064
? CURRENT APPLICATION NUMBER: US/10/046,955
? CURRENT FILING DATE: 2002-06-04
? PRIOR APPLICATION NUMBER: US 09/423,233
? PRIOR FILING DATE: 2000-06-27
? PRIOR APPLICATION NUMBER: PCT/US98/08926
? PRIOR FILING DATE: 1998-05-01
? PRIOR APPLICATION NUMBER: US 60/045,400
? PRIOR FILING DATE: 1997-05-02
? NUMBER OF SEQ ID NOS: 61
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 5
? LENGTH: 365
? TYPE: DNA
? ORGANISM: Aspergillus nidulans
? US-10-046-955-5

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Query Match	38.6%	Score 123.2;	DB 15;	Length 365;
Best Local Similarity	66.0%;	Pred. No. 7.9e-34;		
Matches 210; Conservative	0;	Mismatches 103;	Indels 5;	Gaps 2

[illegible]

RESULT 11  
US-10-046-955-2  
; Sequence 2, Application US/10046955  
; Publication No. US20030129600A1

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GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reis, Etrol
APPLICANT: Aldorevich, Liliانا
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 364
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-10-046-955-2

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Query Match	38.0%;	Score 121.2;	DB 15;	Length 364;
Best Local Similarity	65.9%;	Pred. No. 4.2e-33;		
Matches 211; Conservative	0;	Mismatches 98;	Indels 11;	Gaps 2

Oy	3	AAATGGGAATGAATATGTGAATTGAGAAATTCAGTAATCATCGAATCTTTGAACGACA	62
Db	52	AAATGGGAATGAATATGTGAATTGAGAAATTCAGTAATCATCGAATCTTTGAACGACA	111
Oy	63	TTGCGCGCCGACGATATTCTGGCGGCGATGCTGTTCGAGCTCATTAACAACCTCAGGCC	122
Db	112	TTGCGCGCCCTGGATATCCGGGGGGGACATGCTGTTCGAGCTCATTAAGCTCAGCAAGC	171
Oy	123	CCCGGGGCTGGCGTTGGGGATCGGGGGAAGCCCCCTGGGGGACAAAGCCGTCGCCAAA	182
Db	172	ACGGCTGTGTGTGTGGGCCCCCGTCCCTCTCCCGGGG-----GAGGGGCGGAAA	223
Oy	183	TACAGTGGCGGTCCTCCGCGGACGTTCCATTCGTAAGTAACTACACTCGCAACTGGAGA	242
Db	224	GGCAGCGGGGACACGCGTCCTCGATCGATGAGGGCTTGTCACTGCTCTGTAAG	283
Oy	243	GGGGCGCGGCCACGCGCTAAACACCC---AATCTTGAATGTTGACCTGGAATCAGGTA	299
Db	284	CCCGGCGCGGCGCACCGACACCCCACTTATTTTCTAAGGTGACCTGGATCAGGTA	343
Oy	300	GGAAATACCCGCTGAACCTTAA	319
Db	344	GGGATACCCGCTGAACCTTAA	363

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RESULT 12
US-10-121-740-4
: Sequence 4, Application US/10121740
: Publication No. US20030186425A1
: GENERAL INFORMATION:
: APPLICANT: Strobel, Gary
: APPLICANT: Manke, Denise
: TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
: TITLE OF INVENTION: USE
: FILE REFERENCE: AO 2019, 40
: CURRENT APPLICATION NUMBER: US/10/121,740
: CURRENT FILING DATE: 2002-04-11
: PRIOR APPLICATION NUMBER: 60/283,902
: PRIOR FILING DATE: 2002-03-11
: PRIOR APPLICATION NUMBER: 60/263,072
: PRIOR FILING DATE: 2001-04-16
: NUMBER OF SEQ ID NOS: 4

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SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 4  
 LENGTH: 650  
 TYPE: DNA  
 ORGANISM: Muscodor roseus  
 US-10-121-740-4

Query Match 37.6%; Score 119.8; DB 15; Length 650;  
 Best Local Similarity 72.2%; Pred. No. 1.7e-32;  
 Matches 229; Conservative 0; Mismatches 72; Indels 16; Gaps 5;

QY 3 AAATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 62  
 Db 329 AAATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 388  
 QY 63 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTCAATTAACAACCTTCAGGCC 122  
 Db 389 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTCAATTAACAACCTTCAGGCC 447  
 QY 123 CCGGCGCTGCGCTTGGGGATCGCGGAGCCCGCGCGGACCAAGCCGCTCCCAAA 182  
 Db 448 CTGTGCTTAGCGTTGGAGCGCTACGCGACTGCC-----CGTAGCTCCCTTAA 495  
 QY 183 TACAGTGGCGGTCCCGCGAGCTTCATTGCGTAGTACACCTCGAAGCTGAGAGA 242  
 Db 496 GTGATTGGCGAGTTGGTCTCACTCTA-GGCGTAGTAAT-CTATCGCTCTGTAGT 553  
 QY 243 GCGGCGCGCGCGCGCGTAAACACCCAACTTGAATTTGAGCTCGAATCAGGTAGA 302  
 Db 554 GGTTCGCGCGCGCGCGCGTAAACCCCTATATC-AAAGTTGAGCTCGAATCAGGTAGA 612  
 QY 303 ATACCGCGTGAACCTTAA 319  
 Db 613 ATACCGCGTGAACCTTAA 629

RESULT 13  
 US-10-623-432-4

Sequence 4, Application US/10623432  
 Publication No. US20040141955A1  
 GENERAL INFORMATION:

APPLICANT: Strobel, Gary  
 APPLICANT: Manker, Denise  
 TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF  
 FILE REFERENCE: USE

CURRENT APPLICATION NUMBER: US/10/623,432  
 CURRENT FILING DATE: 2003-07-17  
 PRIOR APPLICATION NUMBER: US/10/121,740  
 PRIOR FILING DATE: 2002-04-11  
 PRIOR APPLICATION NUMBER: 60/283,902  
 PRIOR FILING DATE: 2002-03-11  
 PRIOR APPLICATION NUMBER: 60/363,072  
 PRIOR FILING DATE: 2001-04-16  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 4  
 LENGTH: 650  
 TYPE: DNA  
 ORGANISM: Muscodor roseus  
 US-10-623-432-4

Query Match 37.6%; Score 119.8; DB 17; Length 650;  
 Best Local Similarity 72.2%; Pred. No. 1.7e-32;  
 Matches 229; Conservative 0; Mismatches 72; Indels 16; Gaps 5;

QY 3 AAATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 62  
 Db 329 AAATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 388  
 QY 63 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTCAATTAACAACCTTCAGGCC 122  
 Db 389 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTCAATTAACAACCTTCAGGCC 447

QY 123 CCGGCGCTGCGCTTGGGGATCGCGGAGCCCGCTGCGGAGCAACGCCGCTCCCAAA 182  
 Db 448 CTGTGCTTAGCGTTGGAGCGCTACGCGACTGCC-----CGTAGCTCCCTTAA 495  
 QY 183 TACAGTGGCGGTCCCGCGAGCTTCATTGCGTAGTACCAACCTTCGCAACTGAGAGA 242  
 Db 496 GTGATTGGCGAGTTGGTCTCACTCTA-GGCGTAGTAAT-CTATCTGCTCTGTAGT 553  
 QY 243 GCGGCGCGCGCGCGCGTAAACACCCAACTTGAATTTGAGCTCGAATCAGGTAGA 302  
 Db 554 GGTTCGCGCGCGCGCGTAAACCCCTATATC-AAAGTTGAGCTCGAATCAGGTAGA 612  
 QY 303 ATACCGCGTGAACCTTAA 319  
 Db 613 ATACCGCGTGAACCTTAA 629

RESULT 14  
 US-09-766-173C-4

Sequence 4, Application US/09766173C  
 Patent No. US20020172945A1  
 GENERAL INFORMATION:

APPLICANT: Cartoll, George C.  
 TITLE OF INVENTION: Materials and Methods For Detection of  
 TITLE OF INVENTION: Pathogenic Guignardia Citricarpa

FILE REFERENCE: Oregon 99-09  
 CURRENT APPLICATION NUMBER: US/09/766,173C  
 CURRENT FILING DATE: 2001-01-22  
 PRIOR APPLICATION NUMBER: PCT/US01/01735  
 PRIOR FILING DATE: 2001-01-19  
 PRIOR APPLICATION NUMBER: 60/177,013  
 PRIOR FILING DATE: 2000-01-19  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 4  
 LENGTH: 641  
 TYPE: DNA  
 ORGANISM: Guignardia Citricarpa  
 US-09-766-173C-4

Query Match 35.8%; Score 114.2; DB 9; Length 641;  
 Best Local Similarity 62.5%; Pred. No. 1.8e-30;  
 Matches 198; Conservative 0; Mismatches 113; Indels 6; Gaps 1;

QY 3 AAATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 62  
 Db 318 AAATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATCGAATCTTTGAAGCACA 377  
 QY 63 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTCAATTAACAACCTTCAGGCC 122  
 Db 378 TTGGGCGCGCGAGTATTCGCGCGGATGCGCTGTTGAGCGTCAATTAACAACCTTCAGGCC 437  
 QY 123 CCGGCGCTGCGCTTGGGGATCGCGGAGCCCGCTGCGGAGCAACGCCGTCGCCCAAA 182  
 Db 438 CTGTGCTTAGCGTTGGAGCGCTCCGCTGCGGAGCGCCCTCGAAGACTCGG-----CGA 491  
 QY 183 TACAGTGGCGGTCCCGCGAGCTTCATTGCGTAGTACCAACCTTCGCAACTGAGAGA 242  
 Db 492 CCGGCTTCAGCTTCAGCGTAGTAAATAATCTGCTTGGAGAGGGGGCGCTGG 551  
 QY 243 GCGGCGCGCGCGCGCGTAAACACCCAACTTGAATTTGAGCTCGAATCAGGTAGA 302  
 Db 552 CCGGCGCGCGCGCGCGTAAACACCCAACTTGAATTTGAGCTCGAATCAGGTAGA 611  
 QY 303 ATACCGCGTGAACCTTAA 319  
 Db 612 ATACCGCGTGAACCTTAA 628

RESULT 15  
 US-10-046-955-24  
 Sequence 24, Application US/10046955



***This Page Blank (uspto)***



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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 : Search time 4466 Seconds  
(without alignments)  
2133.013 Million cell updates/sec

Title: US-10-046-955-6  
Perfect score: 319  
Sequence: 1 gaaatgcgaagtaagtatgt.....sgaataccgcgtgaacttaa 319

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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2: em\_eesthum:\*  
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4: em\_eestmu:\*  
5: em\_eestov:\*  
6: em\_eestpl:\*  
7: em\_eestro:\*  
8: em\_hlc:\*  
9: gb\_eestl:\*  
10: gb\_eest2:\*  
11: gb\_hlc:\*  
12: gb\_eest3:\*  
13: gb\_eest4:\*  
14: gb\_eest5:\*  
15: em\_eestlum:\*  
16: em\_eestom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_rhg:\*  
27: em\_gss\_vrt1:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183	57.4	739	14	CF870552 tric024xb
2	183	57.4	755	14	CF870665 tric024xj
3	183	57.4	796	14	CB900742 tric024xb
4	183	57.4	808	14	CB900860 tric024xj

5	139.4	43.7	735	14	CF880267 tric081xc
6	139.4	43.7	840	14	CB907036 tric081xc
7	117.2	36.7	704	13	BQ751285
8	117.2	36.7	725	13	BQ752001
9	117.2	36.7	806	13	BQ751015
10	117.2	36.7	806	13	BQ751484
11	115.6	36.2	745	13	BQ751971
12	115.6	36.2	758	13	BQ751399
13	114.4	35.9	169	12	BM870292
14	110.6	34.7	774	13	BQ751236
15	109	34.2	743	13	BQ751027
16	105	32.9	225	18	BZ424439
17	102.8	32.2	214	10	BF251183
18	101.8	31.9	195	28	BZ425056
19	101.8	31.9	389	28	BZ424690
20	100.2	31.4	213	9	A1209736
21	100.2	31.4	318	9	A1213025
22	93.6	29.3	570	28	BZ293287
23	93.6	29.3	597	28	BZ293462
24	93.6	29.3	603	28	BZ296472
25	92.4	29.0	147	14	CF800463
26	92	28.8	120	9	A1327878
27	92	28.8	141	9	A1327879
28	92	28.8	384	28	BZ304161
29	92	28.8	458	28	BZ304060
30	92	28.8	497	28	BZ302024
31	92	28.8	498	28	BZ304069
32	92	28.8	549	28	BZ303682
33	92	28.8	556	28	BZ304433
34	92	28.8	870	29	CNS06K29
35	92	28.8	1004	29	CNS06KGP
36	92	28.8	1043	29	CNS06LUT
37	91.2	28.6	846	29	CNS0782Q
38	91.2	28.6	893	29	CNS079EG
39	91.2	28.6	939	29	CNS06K16
40	91.2	28.6	995	29	CNS07A08
41	91.2	28.6	999	29	CNS07730
42	91.2	28.6	1034	29	CNS0792Z
43	91.2	28.6	1094	29	CNS076RE
44	91.2	28.6	1098	29	CNS07812
45	90.8	28.5	981	29	CNS0769H

## ALIGNMENTS

RESULT 1  
LOCUS CF870552  
DEFINITION tric024xb14.b1 T.reesei mycelial culture, Version 6 October 2003  
ACCESSION CF870552  
VERSION CF870552.1 GI:38125234  
KEYWORDS  
SOURCE  
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
REFERENCE Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D., Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and Dean, R.A.  
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset  
Unpublished (2003)  
CONTACT: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: LR-F1 primer.





Query Match	43.7%	Score 139.4	DB 14	Length 735
Best Local Similarity	79.9%	Pred. No. 5.5e-27		
Matches 203, Conservative	0	Mismatches 42	Indels 9	Gaps 3

QY	3	AAATGCGAATGATGATGAAATTGCAGAAATCAGGAATCATCGAATCTTTGAACGCACA	62
Db	50	AAATGCGAATGATGATGAAATTGCAGAAATCAGGAATCATCGAATCTTTGAACGCACA	109
QY	63	TTGGGCCCCCAGATTCTGGGGGGCATGCTGTTGAGCGTCATTCAACCTCTAGGCC	122
Db	110	TTGGGCCCCCAGATTCTGGGGGGCATGCTGTTGAGCGTCATTCAACCTCTAGAAC	169
QY	123	CCCCGGCCTGCGTGGGGGATCGGGGAAAGCCCTCGGGGACAAAGCCCGTCCCCCAA	182
Db	170	CC---TCCGGGGGGTCCGTTTGGGGATCGGCGCT---CACCGGGCGCCCCCGAAA	221
QY	183	TACAGTGGCGGTCCCGCCGACGCTTCCATTGCGTAGTGAACAC-CTCGCAACTGGAG	241
Db	222	TACAGNAGCGGTCTCGCGCACCTTTTCTGCGAGGTACTTGGACACTTCAACCCGAG	281
QY	242	AGCGGCGCGGCCAC	255
Db	282	CGCGGCGGGCCAC	295

RESULT 6	CB907036	840 bp	mRNA	linear	EST 02-UTL-2003
LOCUS	CB907036				
DEFINITION	tricc081xc18 T. reesei mycelial culture, Version 3				april Hypocrea
ACCESSION	tricc081xc18				mRNA sequence.

SOURCE ORGANISM	Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina	

**DEPENDENCE**

REFERENCE	AUTHORS
1 (bases 1 to 840)	Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,

**TITLE** Transcriptional regulation of biomass-degrading enzymes in the  
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.

filamentous fungus *Trichoderma reesei*  
J. Biol. Chem. 278 (34), 31988-31997 (2003)  
MEDLINE 32803214

MEDLINE 22005514  
 PUBMED 12788920  
 COMMENT Contact: Pamela K. Foreman

Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 945 8800

Tel: (650) 846-7635  
 Fax: (650) 621-7817  
 Email: [pfloremang@genecor.com](mailto:pfloremang@genecor.com)  
 Seq primer: LT-F1 primer.

FEATURES	Location/Qualifiers
source	1. .840

Source

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"organism":"Hydrocrea jecorina"
"mol_type":"mRNA"
"/strain="Om6a"
"/db_xref="taxon:51453"
"/clone="tr1c081xc18"
"/dev_stage="mycelial"
"/clone_lib="T_rresel mycelial culture, Version 3 apr11"
"note="Vector: pREP4; Site_1: Not I/Sal I; Mycelial

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culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

Query Match	43.7%	Score 139.4	DB 14	Length 840
Best Local Similarity	79.9%	Pred. No. 5.8e-27		
Matches 203; Conservative	0	Mismatches 42	Indels 9	Gaps 3

QY	3	AAATGGCAATGAATGTGAATTTGCAGAAATTCAGTAATCATCGAATCTTTGAACGACA	62
Db	155	AAATGGCAATGAATGTGAATTTGCAGAAATTCAGTAATCATCGAATCTTTGAACGACA	214
QY	63	TTGCGCGCCGCAATTTCTGCGCGGACATCCTGTTTCAGAGCTCAATCAACCTTCAGGCC	122
Db	215	TTGCGCGCCGCAATTTCTGCGCGGACATCCTGTTTCAGAGCTCAATCAACCTTCAGACC	274
QY	123	CCCGGAGCTCGAGGTGAGGGATCGGCGGAAGCCCCCTCGGGGCACAACGCCGTCGCCCAAA	182
Db	275	CC---TCGGGGGGGTCGGTTTTTGGGGATCGGCCCCCT---CACGGGGCGGCCCCGAAA	326
QY	183	TACAGTGGCGGATCCGCGCGCAGCTTCCATTGCGTAGTAGCTAACAC-CTCGCAACTGGAG	241
Db	327	TACAGTGGCGGATCTCGCGCACCCCTTTCTTCGCGAGCTACTGTGCACACTCTCACCCGCGAG	386
QY	242	AGCGGCGCGGCGCAC	255
Db	387	CGGGGCGGCGCAC	400

RESULT 7	LOCUS	DEFINITION
BO751285	BO751285	704 bp mRNA linear EST 18-JUL-2007
BO751285	BO751285	DSCC Collectotrichum trifolii cDNA clone pDSCC74-17, mRNA sequence.

ORGANISM	COLLETOTRICHIUM TRICHOLOM
SOURCE	COLLETOTRICHIUM TRICHOLOM
KEYWORDS	EST
VERSION	B0751285.1
ACCESSION	B0751285
GI	21906690

REFERENCE  
1 (bases 1 to 704)  
Samadpour M, Dickman M, Town C D, Van Alen C  
1990. *Journal of Virology* 64: 1000-1004.

TITLE

JOURNAL Unpublished (2002)  
COMMENT Other ESTs: EST631847

CONTACT: Deborah A. Samac  
 Department of Plant Pathology  
 University of Minnesota  
 495 Portland Hall 1001 Tower Drive  
 St Paul, MN 55106

1200 BOLLING ROAD,  
TEL: 612 625 1243  
FAX: 651 649 5058  
1991 UPPER BULLOCK CIRCLE, ST. PAUL, MN 55108, USA

Email: [debbyspuccini.crl@umn.edu](mailto:debbyspuccini.crl@umn.edu)  
TIGR sequence name: MTSAD17TV More information is available at [www.medicare.gov](http://www.medicare.gov)

Seq primer: (gtA AtA CGA CTC ACT AtA ggg C)  
Location/Qualifiers

Source

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/organism="Colletotrichum trifolii"
/mol_type="mRNA"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSC7-17"
/tissue_type="mycelia"
/dev_strage="Young, actively growing mycelia (3 days after
inoculation), grown in liquid culture (cutin minimal, medium
containing 2%glucose)."
/lab_host="DH5alpha"
/clone_lib="DSC7"
/notes="vector: Bluescript SK+, Site_1: EcoRI, Site_2:
EcoRI; isolate: 2sp2 ; cDNA was prepared from polyA+
```

enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce *E. coli* Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform *E. coli* DH5alpha which were plated onto medium with X-gal for selection of recombinants."

## ORIGIN

Query Match 36.7%; Score 117.2; DB 13; Length 704;  
Best Local Similarity 77.6%; Pred. No. 5.5e-21;  
Matches 225; Conservative 0; Mismatches 43; Indels 22; Gaps 6;

QY 35 AGTGAATCATGAACTCTTTGAACGACATGGCGCCGCAATATTCTGGCGGCGATGCT 94  
DB 1 AGTGAATCATGAACTCTTTGAACGACATGGCGCCGCAATATTCTGGCGGCGATGCT 60  
QY 95 GTTGGAGGCTATTCACACCTCCAGGCGCGGCGCTGGGCGATGCGCGGAAAGCC 154  
DB 61 GTTGGAGGCTATTCACACCTCCAGGCGCGGCGCTGGGCGATGCGCGGAAAGCC 104  
QY 155 CCTGCGGGGCAACAAGCGCGTCCCAATATACAGTGGCGGTCGCCGCGCAGCTTCATG 213  
DB 105 -CTTCCAGCGGCTGACGTGGGCGCTCAAGACAGTGGCGGACCTTCGCGGAGCTCTTG 163  
QY 214 CGTAGTAGC-TACACCTCGCACTGGA-GAGCGCGCGGCGCAAGCCGCTAAACCCCA 271  
DB 164 CGTAGTAGCATACCACTCGCACCGGACCGCGGCACTCTCCCTAAACCCCA 223  
QY 272 CTCTT-GAATGTGACCTCGAATGAGTAGAATACCGCGTGAATTA 319  
DB 224 ATTTTTACAGGTGACCTCGAATGAGTAGAATACCGCGTGAATTA 273

RESULT 8  
B0752001 725 bp mRNA linear EST 18-JUL-2002  
LOCUS EST1632564 DSCT Colletotrichum trifolii cDNA clone pDSCT9-22, mRNA  
DEFINITION

ACCESSION B0752001  
VERSION B0752001  
KEYWORDS EST.  
SOURCE Colletotrichum trifolii  
ORGANISM Colletotrichum trifolii  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae;  
mitosporic Phyllochoraceae; Colletotrichum.

REFERENCE 1 (bases 1 to 725)  
Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,  
Cheung,F., and Fraser,C.M.  
ESTs from mycelia of Colletotrichum trifolii race 1  
Unpublished (2002)  
Other ESTs: EST632563  
Contact: Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debby@puccini.crl.umn.edu  
TIGR sequence name: MTSAB07TV More information is available at:  
www.medicago.org  
Seq primer: (gta ACA CGA CTC Act ACA 999 C) .  
Location/Qualifiers

FEATURES  
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/strain="race 1"  
/db\_xref="taxon:5466"  
/clone="pDSCT9-22"  
/tissue\_type="mycelia"

/dev stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."  
/lab\_host="DH5alpha"  
/clone\_id="DSCT"  
/note="Vector: pBluescript SK+, Site 1: EcoRI; Site 2: EcoRI; isolate: 26p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce *E. coli* Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform *E. coli* DH5alpha which were plated onto medium with X-gal for selection of recombinants."

## ORIGIN

Query Match 36.7%; Score 117.2; DB 13; Length 725;  
Best Local Similarity 77.6%; Pred. No. 5.6e-21;  
Matches 225; Conservative 0; Mismatches 43; Indels 22; Gaps 6;

QY 35 AGTGAATCATGAACTCTTTGAACGACATGGCGCCGCAATATTCTGGCGGCGATGCT 94  
DB 1 AGTGAATCATGAACTCTTTGAACGACATGGCGCCGCAATATTCTGGCGGCGATGCT 60  
QY 95 GTTGGAGGCTATTCACACCTCCAGGCGCGGCGCTGGGCGATGCGCGGAAAGCC 154  
DB 61 GTTGGAGGCTATTCACACCTCCAGGCGCGGCGCTGGGCGATGCGCGGAAAGCC 104  
QY 155 CCTGCGGGGCAACAAGCGCGTCCCAATATACAGTGGCGGTCGCCGCGCAGCTTCATG 213  
DB 105 -CTTCCAGCGGCTGACGTGGGCGCTCAAGACAGTGGCGGACCTTCGCGGAGCTCTTG 163  
QY 214 CGTAGTAGC-TACACCTCGCACTGGA-GAGCGCGCGGCGCAAGCCGCTAAACCCCA 271  
DB 164 CGTAGTAGCATACCACTCGCACCGGACCGCGGCACTCTCCCTAAACCCCA 223  
QY 272 CTCTT-GAATGTGACCTCGAATGAGTAGAATACCGCGTGAATTA 319  
DB 224 ATTTTTACAGGTGACCTCGAATGAGTAGAATACCGCGTGAATTA 273

RESULT 9  
B0751015 806 bp mRNA linear EST 18-JUL-2002  
LOCUS EST1631578 DSCT Colletotrichum trifolii cDNA clone pDSCT2-7, mRNA  
DEFINITION

ACCESSION B0751015  
VERSION B0751015  
KEYWORDS EST.  
SOURCE Colletotrichum trifolii  
ORGANISM Colletotrichum trifolii  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae;  
mitosporic Phyllochoraceae; Colletotrichum.

REFERENCE 1 (bases 1 to 806)  
Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,  
Cheung,F., and Fraser,C.M.  
ESTs from mycelia of Colletotrichum trifolii race 1  
Unpublished (2002)  
Other ESTs: EST631577  
Contact: Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debby@puccini.crl.umn.edu  
TIGR sequence name: MTSAB07TV More information is available at:  
www.medicago.org  
Seq primer: (gta ACA CGA CTC Act ACA 999 C) .  
Location/Qualifiers

## FEATURES

source

1. 806  
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 /strain="race 1"  
 /db\_xref="taxon:5466"  
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 /lab\_host="DH5alpha"  
 /clone\_1ib="DSC2"  
 /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

## ORIGIN

Query Match 36.7%; Score 117.2; DB 13; Length 806;  
 Best Local Similarity 77.6%; Pred. No. 5.9e-21;  
 Matches 225; Conservative 0; Mismatches 43; Indels 22; Gaps 6;

QY 35 AGTGAATCATGAAATCTTTGAAGCAGCATTTGGCGGCGATGCT 94  
 DB 1 AGTGAATCATGAAATCTTTGAAGCAGCATTTGGCGGCGATGCT 60

QY 95 GTTGAAGCGTATTTCACACCTTCAGGCCCCCGGCGCTGGGGATGCGCGAAGCC 154  
 DB 61 GTTGAAGCGTATTTCACACCTTCAGGCCCCCGGCGCTGGGGATGCGCGAAGCC 104

QY 155 CCTGCGGGGCAACAGCGCGTCCCAATACAGTGGCGGTCCGC-CCGACCTTCATTG 213  
 DB 105 -CTTCAAGCGGTGACGTGGGCGCTCAAGACAGTGGCGGACCTCGGGAGCTCTTTG 163

QY 214 CGTAGTAGC-TAACACCTTCGCACTGGA-GAGCGGCGCGGCGACCGCTTAACACCCAA 271  
 DB 164 CGTAGTAGCATACCACTTCGACCGGAGCCGCGGCGACCTCTGCGCTTAACACCCCA 223

QY 272 CTCTT-GAATGTTGACCTCGAATCAGTAGAATATACCGCTGAATTAA 319  
 DB 224 ATTTTACAGGTTGACCTCGAATCAGTAGAATATACCGCTGAATTAA 273

RESULT 10 806 bp mRNA linear EST 18-JUL-2002  
 LOCUS B0751484  
 DEFINITION EST632047 DSC2 Colletotrichum trifolii cDNA clone pDSC2-48, mRNA  
 ACCESSION B0751484  
 VERSION B0751484.1 GI:21906889  
 SOURCE EST.  
 ORGANISM Colletotrichum trifolii  
 Colletotrichum trifolii  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae;  
 mitosporic Phyllochoraceae; Colletotrichum.  
 1 (bases 1 to 806)  
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,  
 Cheung,F., and Fraser,C.M.  
 ESTs from mycelia of Colletotrichum trifolii race 1  
 Unpublished (2002)  
 Other\_ESTs: EST632046  
 Contact: Deborah A. Samac  
 Department of Plant Pathology  
 University of Minnesota  
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

FEATURES

source

1. 806  
 /organism="Colletotrichum trifolii"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:5466"  
 /clone="pDSC2-48"  
 /tissue\_type="mycelia"  
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 /lab\_host="DH5alpha"  
 /clone\_1ib="DSC2"  
 /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

## ORIGIN

Query Match 36.7%; Score 117.2; DB 13; Length 806;  
 Best Local Similarity 77.6%; Pred. No. 5.9e-21;  
 Matches 225; Conservative 0; Mismatches 43; Indels 22; Gaps 6;

QY 35 AGTGAATCATGAAATCTTTGAAGCAGCATTTGGCGGCGATGCT 94  
 DB 1 AGTGAATCATGAAATCTTTGAAGCAGCATTTGGCGGCGATGCT 60

QY 95 GTTGAAGCGTATTTCACACCTTCAGGCCCCCGGCGCTGGGGATGCGCGAAGCC 154  
 DB 61 GTTGAAGCGTATTTCACACCTTCAGGCCCCCGGCGCTGGGGATGCGCGAAGCC 104

QY 155 CCTGCGGGGCAACAGCGCGTCCCAATACAGTGGCGGTCCGC-CCGACCTTCATTG 213  
 DB 105 -CTTCAAGCGGTGACGTGGGCGCTCAAGACAGTGGCGGACCTCGGGAGCTCTTTG 163

QY 214 CGTAGTAGC-TAACACCTTCGCACTGGA-GAGCGGCGCGGCGACCGCTTAACACCCAA 271  
 DB 164 CGTAGTAGCATACCACTTCGACCGGAGCCGCGGCGACCTCTGCGCTTAACACCCCA 223

QY 272 CTCTT-GAATGTTGACCTCGAATCAGTAGAATATACCGCTGAATTAA 319  
 DB 224 ATTTTACAGGTTGACCTCGAATCAGTAGAATATACCGCTGAATTAA 273

RESULT 11 745 bp mRNA linear EST 18-JUL-2002  
 LOCUS B0751971  
 DEFINITION EST632534 DSC2 Colletotrichum trifolii cDNA clone pDSC2-3, mRNA  
 ACCESSION B0751971  
 VERSION B0751971.1 GI:21907376  
 SOURCE EST.  
 ORGANISM Colletotrichum trifolii  
 Colletotrichum trifolii  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae;  
 mitosporic Phyllochoraceae; Colletotrichum.  
 1 (bases 1 to 745)  
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,  
 Cheung,F., and Fraser,C.M.



	DEFINITION	mgnm009xkj23f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgnm009xkj23 5', mRNA sequence.
	ACCESSION	BM870292
	VERSION	BM870292.2
	KEYWORDS	GI:30404719
	SOURCE ORGANISM	Magnaporthe grisea (anamorph: Pyricularia grisea) Magnaporthe grisea Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 169)
	REFERENCE AUTHORS	Ebbole,D.U., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhattacharj,K. and Dean,R.A.
	TITLE	Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
	JOURNAL COMMENT	Unpublished (2002) On Mar 7, 2002 this sequence version replaced gi:19237974. Contact: Ebbole DJ Department of Plant Pathology & Microbiology Texas A&M University Peterson Bldg, MS2132, College Station, TX 77843-2132, USA Tel.: 979 845 4831 Fax: 979 845 6483 Email: d-ebbole@tamu.edu Chromatogram file of this sequence is available, see contact person.Best nr hit (April. 22, 2003) gb AAU79278.1  unknown [Saccharomyces cerevisiae] 79 le-14
	FEATURES	PCR Primers FORWARD: T3 primer BACKWARD: T7 primer Plate: mgnm009 row: J column: 23 Seq primer: T3.
	Source	Location/Qualifiers 1..169 /organism="Magnaporthe grisea" /mol_type="mRNA" /strain="Guy11" /db_xref="taxon:148305" /clone="mgnm009xkj23" /sex="Mat1-2 hermaphrodite" /cell_type="mycelium" /clone_lhb="Magnaporthe grisea NS Uni-Zap XR library" /note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI site has 13 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Nitrogen starvation library. Cells were inoculated into minimal medium and grown for two days with shaking (150 rpm) at room temperature. Culture was harvested, blended, inoculated into minimal medium as above for 24 h. Cells were harvested, washed with water and inoculated into minimal medium base lacking nitrogen source for 6 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPrap version 991019 and trimmed according to phd files (0.05) and for vector segs."
	ORIGIN	
	Query Match	35.9%; Score 114.4; DB 12; Length 169;
	Best Local Similarity	95.2%; Pred. No.1.ee-20;
	Matches 118; Conservative	0; Mismatches 6; Indels 0; Gaps 0;
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Db	39	AAATGCATAGAATGTGAATTGCGAATTCAGTGTAATCATGGATCTTTGAAGCACA 98
Oy	63	TTGCGCCGCCAGTATCTTGCGCGGCATGCTCTTGAGCGGTCAATCAACCTCAGGCC 122
Db	99	TTGCGCCCCCGGATATCCGGCGGCATGCTCTTGAGCGGTCAATCAACCTCAGGCC 158
Oy	123	CCCG 126
Db	159	TCGG 162

<b>RESULT 14</b>	
<b>LOCUS</b>	B0752136 774 bp mRNA linear EST 18-JUL-2002
<b>DEFINITION</b>	EST63269 DScT Colletotrichum trifolii cDNA clone pDSCtt10-23, mRNA sequence.
<b>ACCESSION</b>	B0752136
<b>VERSION</b>	B0752136.1 GI:21907541
<b>KEYWORDS</b>	EST.
<b>SOURCE</b>	Colletotrichum trifolii Colletotrichum trifolii
<b>ORGANISM</b>	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllostachyales; Phyllostachyceae; mitosporic Phyllachoraceae; Colletotrichum. 1 (bases 1 to 774)
<b>REFERENCE</b>	Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T., Cheng,F. and Fraiser,C.M. ESTs from mycelia of Colletotrichum trifolii race 1 Unpublished (2002) Other ESTs: EST632698
<b>AUTHORS</b>	Contact: Deborah A. Samac Department of Plant Pathology University of Minnesota 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA Tel.: 612 625 1243 Fax: 651 649 5058 Email: debbye@puccini.crl.umn.edu TISSR sequence name: MTSBJ23TV More information is available at: <a href="http://www.medicago.org">www.medicago.org</a> Seq primer: (GLA ACA CGA CTC ACT ACA ggg C).
<b>TITLE</b>	
<b>JOURNAL</b>	
<b>COMMENT</b>	
<b>FEATURES</b>	
<b>source</b>	Location/Qualifiers 1..774 /organism="Colletotrichum trifolii" /mol_type="mRNA" /strain="race 1" /db_xref="taxon:5466" /clone="pDSCtt10-23" /tissue_type="mycelia" /dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)." /lab_host="DH5alpha" /clone_id="DSCt" /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 2sp2 ; CDNA was prepared from polyA+ enriched RNA The cDNA was ligated into lambda gt10 from Stratagene and packaged using Gistapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."
<b>ORIGIN</b>	
<b>Query Match</b>	34.7%; Score 110.6; DB 13; Length 774;
<b>Best Local Similarity</b>	76.8%; Pred. No. 3,6e-19;
<b>Matches 219; Conservative</b>	0; Mismatches 44; Indels 22; Gaps 6;
<b>OY</b>	40 ATCATGCAATCTTTGAACGCACATTGGCGCCAGTAATTCGGCGGCGATGCTGTTCG 99
<b>Db</b>	5 ATTATCGAAACTTTTGAAACGCACATTCGCCGCCACACATTCGTGGCGGGCATGCTTTTCG 64
<b>OY</b>	100 AGCGTCAATTCACACCTCAGAGCCCCCGGGCGCTGGCGTGGGGATCGCGGGAAGCCCCCTG 159
<b>Db</b>	65 AGCGTATTTCAACCTCTCAGACACC---GCTTGGCCTTTGGG-----CTTC 107
<b>OY</b>	160 CGGGACAACGCCGCTCCCCCAAATAACAGTGGCGGTCCGC-CGACGCTTCATTGGGTAG 218
<b>Db</b>	108 CAGGGCTGACGTGGGCCCTCAAGAAGACGTGGGGAGCCCTCGGGAGAGCTCTTTGGGTAG 167



[illegible]

RESULT 15  
BQ751027

LOCUS	BO751027	743 bp	mRNA	linear	EST 18-JUL-2002
DEFINITION	EST61590	DGCT	Colletotrichum trifolii	CDNA clone	pDSCT2-20, mRNA
REFERENCE					

ACCESSION	BQ751027
VERSION	BQ751027.1
	GI:21906432

**SOURCE ORGANISM**

REFERENCE  
1 (bases 1 to 743)  
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T.,

TITLE	JOURNAL	COMMENT
ESTs from mycelia of <i>Colletotrichum trifolii</i> race 1	Unpublished (2002)	Other_ESTs: EST631589

**CONTACT:** Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel.: 612 625 1243  
Fax: 651 649 5058  
Email: debby@puccini.crl.umn.edu  
TIR sequence name: MTSAB2TV More information is available at:  
[www.medicgo.org](http://www.medicgo.org)  
Seq primer: (gta ACA CCA ACT ATA ggg C).  
Location/Qualifiers  
1..743

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/db_xref="taxon:5466"
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/tissue_type="mycelia"
/dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="DH5alpha"
/clone_id="pDSC17"
/notes="vector: plasmascript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 25p2 ; cDNA was prepared from polyA+ enriched RNA The cDNA was ligated into lambda gfil from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli V1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into plasmascript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

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## ORIGIN

Query Match	34.2%	Score 109;	DB 13;	Length 743;
Best Local Similarity	76.5%;	Pred. No. 9.5e-19;		
Matches 218;	Conservative 0;	Mismatches 45;	Indels 22;	Gaps 6;

QY 40 ATATCATGAACTTTGAACCCACATTTGGCGCCGACAGTATTTCTGGCGGGGACATGCTGTGTC 99  
 Db 5 ATTTTGAACCTTTGAACCCACATTTGGCGCCGACAGTATTTCTGGCGGGGACATGCTGTGTC 64  
 QY 100 AGCGTCATTACAACCTCTAGGCCCCCGGCGCTGGCGTTGGAGATCGGCGGGAAGCCCTCTG 159

Db	65	AGCGTATTTCAACCTCAAGCAC	--GCTTGGGTTGGGG	-----CTTC	107
Qy	160	CGGGCAACAAGCGGCTCCCCCA	ATACAGTGGGCGGTCGGC	-CGAGCTTCATTTGCGTAG	218
Db	108	CACGGCTGACGTGGGCTTC	CAAGACAGTGGGGAAGCTTCGGGAGGCTCTTTTGCTAG		167
Qy	219	TAGC-TAAGACCTCGCAACTGGA	-SAGCGGCGCGGCGCAGCGTAAACAACCCAACTTCT		276
Db	168	TAACTATACACTTCGCA	CCGGGAGCCGAGGGCACTCTGCGGTAAACCCCCCAATTTT		227
Qy	277	--GATGTTGACCTCGAATCAGT	AGATACCCGCTGAATCTTA		319
Db	228	TACAGGTTGACCTCGATCAGT	ATGGAAATACCGCTGAATCTTA		272

Search completed: October 1, 2004, 08:01:33  
Job time : 4475.33 secs

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GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 05:20:41 ; Search time 1621.37 Seconds  
(without alignments)  
8527.610 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319

Sequence: 1 gaatatgcataagtaatgt.....ggataaccgcctgaactraa 319

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1166728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_ey:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: gb\_pa:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pac:\*  
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25: em\_pl:\*  
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27: em\_scs:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rtd:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_ey:\*  
39: em\_hcg\_hum:\*  
40: em\_hcg\_mus:\*  
41: em\_hcg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	319	100.0	319	6 AF117921	AF117921 Nectria h
4	317	99.4	559	8 AY429048	AY429048 Chaetomiu
5	317	99.4	561	8 AY429053	AY429053 Chaetomiu
6	317	99.4	576	8 AY310442	AY310442 Nectria h
7	308	96.6	509	8 AF165874	AF165874 Nectria h
8	292	91.5	298	8 AY226096	AY226096 Nectria h
9	279	87.5	480	8 AF150466	AF150466 Nectria h
10	279	87.5	480	8 AF150467	AF150467 Nectria h
11	279	87.5	480	8 AF440567	AF440567 Nectria h
12	266	83.4	569	8 AY429049	AY429049 Chaetomiu
13	181	56.7	501	8 AY273332	AY273332 Unculture
14	157	49.2	478	8 AF132801	AF132801 Nectria h
15	157	49.2	478	8 AF150459	AF150459 Nectria h
16	157	49.2	478	8 AF150460	AF150460 Nectria h
17	157	49.2	478	8 AF150461	AF150461 Nectria h
18	157	49.2	478	8 AF150462	AF150462 Nectria h
19	157	49.2	478	8 AF150463	AF150463 Nectria h
20	157	49.2	478	8 AF150464	AF150464 Nectria h
21	157	49.2	582	8 AF455451	AF455451 Nectria h
22	152	47.6	546	8 AF178413	AF178413 Neocosmos
23	152	47.6	548	8 AF178397	AF178397 Fusarium
24	149	46.7	544	8 NEXITS	L36627 Neocosmospo
25	148	46.4	411	8 AF111061	AF111061 Fusarium
26	148	46.4	418	8 AY243054	AY243054 Ascomycet
27	148	46.4	471	8 AF150476	AF150476 Nectria h
28	148	46.4	478	8 AF150449	AF150449 Nectria h
29	148	46.4	478	8 AF150450	AF150450 Nectria h
30	148	46.4	478	8 AF150451	AF150451 Nectria h
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32	148	46.4	478	8 AF150454	AF150454 Nectria h
33	148	46.4	478	8 AF150455	AF150455 Nectria h
34	148	46.4	478	8 AF150456	AF150456 Nectria h
35	148	46.4	478	8 AF150457	AF150457 Nectria h
36	148	46.4	479	8 AF058207	AF058207 Nectria h
37	148	46.4	479	8 AF150453	AF150453 Nectria h
38	148	46.4	479	8 AF150469	AF150469 Nectria h
39	148	46.4	479	8 AF150470	AF150470 Nectria h
40	148	46.4	479	8 AF150475	AF150475 Nectria h
41	148	46.4	480	8 AF058206	AF058206 Nectria h
42	148	46.4	480	8 AF150477	AF150477 Nectria h
43	148	46.4	480	8 AF150478	AF150478 Nectria h
44	148	46.4	480	8 AF150479	AF150479 Nectria h
45	148	46.4	480	8 AF150480	AF150480 Nectria h

## ALIGNMENTS

RESULT 1  
LOCUS AR206400  
DEFINITION Sequence 6 from patent US 6372430.  
ACCESSION AR206400  
VERSION AR206400.1 GI:21504990  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 319)  
AUTHORS Morrison,C.U., Reiss,E., Aidorevich,L. and Choi,J.Soo.  
TITLE Nucleic acids for detecting Aspergillus species and other filamentous fungi  
JOURNML Patent: US 6372430-A 6 16-APR-2002

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Location/Qualifiers  
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/organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 2e-165;  
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATGCGATAGTATGTAATGCAAAATTCAGATCAATCAATCTTTGAACGA 60  
DB 1 GAAATGCGATAGTATGTAATGCAAAATTCAGATCAATCAATCTTTGAACGA 60  
QY 61 CATTGGCCCCCGCAATTTCTGGCGGCGATGCTTTGAGCGTCAATCAACCTTCAAG 120  
DB 61 CATTGGCCCCCGCAATTTCTGGCGGCGATGCTTTGAGCGTCAATCAACCTTCAAG 120  
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QY 181 AATACAGTGGCGGTCCCGCGAGCTTCATTGCGTAGTACCTGAACCTCGAATCGGA 240  
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DB 241 GAGCGGCGGCGCGACCGCTAAACACCCACTTCTGAATGTTGACCTCGAATCGGTAG 300  
QY 301 GAATACCCGCTGAACCTTAA 319  
DB 301 GAATACCCGCTGAACCTTAA 319

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BD083591  
LOCUS  
DEFINITION  
Nucleic acids for detecting *Aspergillus* species and other filamentous fungi.  
ACCESSION  
BD083591 GI:22629201  
VERSION  
JP 2001525665-A/6.  
KEYWORDS  
Fusarium solani  
SOURCE  
Fusarium solani  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
REFERENCE  
Morrison,C.U., Reiss,E., Aidorevich,L. and Choi,J.S.  
Nucleic acids for detecting *Aspergillus* species and other filamentous fungi  
Patent: JP 2001525665-A 6 11-DEC-2001;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES  
CENTERS FOR DISEASE PREVENTION AND CONTROL  
PREVENTION TECHNOLOGY TRANSFER OFFICE  
COMMENT  
OS Fusarium solani  
PN JP 2001525665-A/6  
PD 11-DEC-2001  
PF 01-MAY-1998 JP 1998548275  
PR 02-MAY-1997 US 60/045400  
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO  
PC CHOI  
CI 1201/68  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.

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FEATURES  
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DB 61 CATTGGCCCCCGCAATTTCTGGCGGCGATGCTTTGAGCGTCAATCAACCTTCAAG 120  
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DB 121 CCCCCGCGCTGGCGTGGGAGTCGAGGAGCCCTCGCGGACAAACCGCGTCCCCCA 180  
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DB 181 AATACAGTGGCGGTCCCGCGAGCTTCATTGCGTAGTACCTGAACCTCGAATCGGA 240  
QY 241 GAGCGGCGGCGCGACCGCTAAACACCCACTTCTGAATGTTGACCTCGAATCGGTAG 300  
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QY 301 GAATACCCGCTGAACCTTAA 319  
DB 301 GAATACCCGCTGAACCTTAA 319

RESULT 3  
AF117921  
LOCUS  
DEFINITION  
Nectria haematococca 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
ACCESSION  
AF117921 GI:8570107  
VERSION  
AF117921  
KEYWORDS  
Fusarium solani  
SOURCE  
Fusarium solani  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
REFERENCE  
Choi,J.S., Westerman,J.M. and Morrison,C.J.  
Rapid differentiation of filamentous fungi using species-specific DNA probes  
Abst. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)  
JOURNAL  
2 (bases 1 to 319)  
AUTHORS  
Choi,J.S., Westerman,J.M. and Morrison,C.J.  
TITLE  
Direct submission  
JOURNAL  
Submitted (09-SEP-1998) DEWD, CDC, 1600 Clifton Rd., Atlanta, GA 30333, USA

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Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2e-165;  
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAAAAATGGGATAGTAATGTGAATTGCAGAAATTCAGTAATCATGGAATCTTTGAACGA 60

QY 61 CATTCGCGCCCGCCAGTAATCTGTGCGGGGCAATGCTGTTGAGGGTCATTACAAACCTTCAGG 120

Db 61 CATTCGCGCCCGCCAGTAATCTGTGCGGGGCAATGCTGTTGAGGGTCATTACAAACCTTCAGG 120

QY 121 CCCCCGGGCGTTGCGCTTTGGGGATCGGCGGAACCCCTTGCGGGCAACAAGCCGTCGCCCA 180

Db 121 CCCCCGGGCGTTGCGCTTTGGGGATCGGCGGAACCCCTTGCGGGCAACAAGCCGTCGCCCA 180

QY 181 AATACAGTGGCGGCTCCCGCCGAGCTTCCATTGTCGTAGTACTTAACAACCTTGCGAACTGGA 240

Db 181 AATACAGTGGCGGCTCCCGCCGAGCTTCCATTGTCGTAGTACTTAACAACCTTGCGAACTGGA 240

QY 241 GAGCGGCGCGGCGCCACGCGCGGTAAACAACCAACTTCTGAATGTTGACCTTGAATTCAGTNG 300

Db 241 GAGCGGCGCGGCGCCACGCGCGGTAAACAACCAACTTCTGAATGTTGACCTTGAATTCAGTNG 300

QY 301 GAATACCGGCTGAACCTTAA 319

Db 301 GAATACCGGCTGAACCTTAA 319

RESULT 4			
AY429048			
LOCUS			
DEFINITION	AY429048	559 bp	DNA
	Chetoniom glabrosum isolate Cgl 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence.		linear
ACCESSION	AY429048		PLN 30-NOV-2003
VERSION	AY429048.1	GI:38503524	

ACCESSION	AY429048
VERSION	AY429048.1
KEYWORDS	GI:38503524
SOURCE	
ORGANISM	Chaetomium globosum
REFERENCE	Chaetomium globosum Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomaceae; Chaetomium. 1 (bases 1 to 559)
AUTHORS	Aggarwal, R., Renu, S. and Singh, D.V.
TITLE	Nucleotide sequence of full length ITS region of Cgl isolate of Chaetomium globosum
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 559)
AUTHORS	Aggarwal, R., Renu, S. and Singh, D.V.
TITLE	Direct Submission
JOURNAL	Submitted (07-OCT-2003) Division of Plant Pathology, IARI, Pusa Road, New Delhi, Delhi 110012, India
FEATURES	Location/Qualifiers

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spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA"

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DB	201	AAATGCGTAAGTATNGTGAATTGCGAATTGAGTAATCATCGAATCTTTGAAGCACA	260	
QY	63	TTGGCCCGCCGCAATTCGGGGGGGCGATCCGTTGCGAGTCATTAACAACCTCAGGCC	122	
DB	261	TTGGCCCGCCGCAATTCGGGGGGGCGATCCGTTGCGAGTCATTAACAACCTCAGGCC	320	

QY 123 CCGCGGCGCTGGGCGTTGGGGATCGGGGAAAGCCCCCTGGGGGACAAACGGCGTCCCCCAA 182

Db 321 CCGGCGCCTGGGCTGGGGGATCGGCGAAAGCCCCCTGGCGGSCAAACGCGTCCCCCAA 380

QY 183 TACAATGGCGGTCGCCCGCAGCTTCCATTGGCGTAGTCAACACTTGCACCTTGAGA 242

Db 381 TACAATGGCGGTCGCCCGCAGCTTCCATTGGCGTAGTCAACACTTGCACCTTGAGA 440

QY 243 GGGGCGGCGCCACGCGCTTAAAAACCCCACTTCTGAATTTGACTTCGAATCAGGTAGGA 302

Db 441 GGGGCGGCGCCACGCGCTTAAAAACCCCACTTCTGAATTTGACTTCGAATCAGGTAGGA 500

QY 303 ATACCGCGCTGAACCTTAA 319

Db 501 ATACCGCGCTGAACCTTAA 517

RESULT 5	561 bp	linear	PLN 30-NOV-2003
AY429053			
LOCUS			
DEFINITION	Chetomium globosum isolate Cg6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence.		
ACCESSION	AY429053		
VERSION	AY429053.1	GI:38503529	

SOURCE ORGANISM	Chaetomium globosum Chaetomium globosum Bakariote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomaceae; Chaetomium.
REFERENCE TITLE	1 (bases 1 to 561) Aggarwal, R., Renu, S. and Singh, D. V. Nucleotide sequence of full length ITS region of Cg6 isolate of Chaetomium globosum
JOURNAL REFERENCE	Unpublished 2 (bases 1 to 561)
AUTHORS	Aggarwal, R., Renu, S. and Singh, D. V.
TITLE	Direct Submission
JOURNAL	Submitted (07-OCT-2003) Division of Plant Pathology, IARI, Pusa
FEATURES	Road, New Delhi, Delhi 110012, India Location/Qualifiers

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source
1. .561
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/mol_type="genomic DNA"
/isolate="CG6"
/db_xref="taxon:38033"
misc_RNA
<1..>551
/note="contains 1S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA"

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ORIGIN	Query Match	99.4%	Score 317;	DB 8;	Length 561;
	Best Local Similarity	100.0%	Pred. No. 2.5e-164;		
	Matches 317;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps	0;
QY	3	AAATGCGATAGTATGATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCACA	62		
DB	203	AAATGCGATAGTATGATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCACA	262		
QY	63	TTGGCGCCCGCAGATTTCTGGCGGGGCATGCTGTTCCAGGCTCATTTACAAACCTTCAGGCC	122		
DB	263	TTGGCGCCCGCAGATTTCTGGCGGGGCATGCTGTTCCAGGCTCATTTACAAACCTTCAGGCC	322		
QY	123	CCCGGGCGCTGGCGTTGGGGAATCGCGCGAAGCCCCCTCGGGGCACAAAGCCGTCGCCCAAA	182		
DB	323	CCCGGGCGCTGGCGTTGGGGAATCGCGCGAAGCCCCCTCGGGGCACAAAGCCGTCGCCCAAA	382		
QY	183	TACAGTGGCGGTCCTCCCGCGCAGCTTCCATTGCGTAGTAGCTAACACCTTCGAACTGGAGA	242		
DB	383	TACAGTGGCGGTCCTCCCGCGCAGCTTCCATTGCGTAGTAGCTAACACCTTCGAACTGGAGA	442		

QY	243	GGGGGGGGCCAGCGCGTAAACACCACTTCTGATGTTGACTCGATCAGTAGAGA	302
Db	443	GGGGGGGGCCAGCGCGTAAACACCACTTCTGATGTTGACTCGATCAGTAGAGA	502
QY	303	ATACCGCTGGAATTAA 319	
Db	503	ATACCGCTGGAATTAA 519	
RESULT 6	AY310442		
LOCUS	AY310442	576 bp DNA linear	PLN 01-JUL-2003
DEFINITION	Nectria haematococca 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.		
ACCESSION	AY310442		
VERSION	AY310442.1	GI:32264972	
KEYWORDS			
SOURCE	Nectria haematococca		
ORGANISM	Nectria haematococca		
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocnemycetidae; Hypocreales; Nectriaceae; Nectria.		
AUTHORS	1 (bases 1 to 576)		
TITLE	Scott, P.T., Martin, H.L., Borel, S.M., Wearing, A.H. and Maclean, D.J.		
JOURNAL	Isolation and characterization of Nectria haematococca from table		
REFERENCE	beet grown in the Lockyer Valley, Queensland, Australia		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 576)		
JOURNAL	Scott, P.T.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (02-JUN-2003) Agronomy and Horticulture, The University		
TITLE	of Queensland, Warrego Highway, Gatton, QLD 4343, Australia		
JOURNAL	Location/Qualifiers		
FEATURES	1..576		
SOURCE	/organism="Nectria haematococca"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:140110"		
	/country="Australia: Lockyer Valley, Queensland"		
	<1..38		
rRNA	/product="18S ribosomal RNA"		
	39..188		
misc_RNA	/product="internal transcribed spacer 1"		
	189..345		
rRNA	/product="5.8S ribosomal RNA"		
	346..518		
misc_RNA	/product="internal transcribed spacer 2"		
	519..>576		
rRNA	/product="28S ribosomal RNA"		
ORIGIN			
Query Match	99.4%	Score 317, DB 8, Length 576;	
Best Local Similarity	100.0%;	Pred. No. 2.5e-164;	
Matches 317;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	3	AAATGCGATAGTATGATGTAATTCAGAAATTCAGTACATGCAATCTTTGAAGCACA	62
Db	240	AAATGCGATAGTATGATGTAATTCAGAAATTCAGTACATGCAATCTTTGAAGCACA	299
QY	63	TTGGCGCCGCGCAATATTTCTGGCGGCAATGCTTTGAGCGTCATTAAACCTCAGGCC	122
Db	300	TTGGCGCCGCGCAATATTTCTGGCGGCAATGCTTTGAGCGTCATTAAACCTCAGGCC	359
QY	123	CCCGGCGCTGGCGCTTTGGGAGTCGGCGGAAGCCCCCGCGGGGCAACAGCGCTCCCCCAA	182
Db	360	CCCGGCGCTGGCGCTTTGGGAGTCGGCGGAAGCCCCCGCGGGGCAACAGCGCTCCCCCAA	419
QY	183	TACAGTGGCGGTCCTCGCGCAGCTTCCATTCGTGCTAGTACATCAACCTCGCAACTGAGAG	242
Db	420	TACAGTGGCGGTCCTCGCGCAGCTTCCATTCGTGCTAGTACATCAACCTCGCAACTGAGAG	479
QY	243	GGGGGGGGCCAGCGCGTAAACACCACTTCTGATGTTGACTCGATCAGTAGAGA	302

Db	480	GGCGCGCGGCACGCCGTAAAAACCCCACTTGTGATGTTGACTCGAATCAGGTAGGA	539
Qy	303	ATAACCGGTGAACCTTA	319
Db	540	ATACCGCGTGAACCTTA	556
RESULT 7			
LOCUS	AF165874	509 bp	DNA
DEFINITION	Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.		
ACCESSION	AF165874		
VERSION	AF165874.1	GI:5524731	
KEYWORDS			
SOURCE	Fusarium solani		
ORGANISM	Fusarium solani Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocryomycetidae; Hypocreales; Nectriaceae; Nectria.		
REFERENCE	1 (bases 1 to 509) Iwen, P.C., Henry, T. and Hinrichs, S.H. Sequence analysis of the internal transcribed spacer regions of Fusarium species most commonly associated with human invasive disease		
AUTHORS	Iwen, P.C., Henry, T. and Hinrichs, S.H.		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 509) Iwen, P.C., Henry, T. and Hinrichs, S.H.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (07-JUL-1999) Pathology and Microbiology, University of Nebraska Medical Center, 986485 Nebraska Medical Center, Omaha, NE 68198-6499, USA		
JOURNAL	Location/Qualifiers		
FEATURES	1..509 /organism="Fusarium solani" /mol_type="genomic DNA" /strain="ATCC62877" /db_xref="ATCC:62877" /db_xref="taxon:169388" /note="anamorph: Fusarium solani"		
source	1..150 /product="internal transcribed spacer 1" /note="ITS1" 151..307 /product="5.8S ribosomal RNA" 308..480 /product="internal transcribed spacer 2" /note="ITS2" 481..>509 /product="28S ribosomal RNA"		
misc_RNA			
rRNA			
misc_RNA			
rRNA			
ORIGIN			
Query Match	96.6%;	Score 308;	DB 8; Length 509;
Best Local Similarity	100.0%;	Pred. No. 2.5e-159;	
Matches 308;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;
Qy	3	AAATGCATTAAGTAATGTAATTCGAGATTGAGTATCATGATCATGAAATCTTTTAAAGCACA	62
Db	202	AAATGCGATTAAGTAATGTAATTCGAGAAATTGAGTAATCATCGAATCTTTTAAAGCACA	261
Qy	63	TTGCGCCCGGCATATTTCTGCGCGGAGATCGTGTGAGCGCATTTAACAACCTGAGGCC	122
Db	262	TTGCGCCCGGCAGTATTTCTGCGCGGAGATCGTGTGAGCGCATTTAACAACCTGAGGCC	321
Qy	123	CCCGGCGCTTGCGGTTGGGATCGGCGGAAGCCCTCGCGGACAAAGCGCTCCCAAA	182
Db	322	CCCGGCGCTTGCGGTTGGGATCGGCGGAAGCCCTCGCGGACAAAGCGCTCCCAAA	381
Qy	183	TACAGTGGGAGTCCCGCGGACGCTTCATTTGGTGTAGCTTAACGCTTCGCAATCGGAGA	242
Db	382	TACAGTGGGAGTCCCGCGGACGCTTCATTTGGTGTAGCTTAACGCTTCGCAATCGGAGA	441
Qy	243	GGCGCGCGGCACGCCGTAAAAACCCCACTTGTGATGTTGACTCGAATCAGGTAGGA	302

Db	442	GGGGGGGGCCACGGCGTTAAACACCCAACTTGTAAATGTTGACTTCGAATAGATTAGCA	501
Qy	303	ATATCCGC 310	
Db	502	ATATCCGC 509	
RESULT 8			
LOCUS	AY226096	298 bp	linear
DEFINITION	Nectria haematococca 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.		
ACCESSION	AY226096		
VERSION	AY226096.1	GI:29293692	
KEYWORDS			
SOURCE			
ORGANISM	Nectria haematococca Nectria haematococca Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocnemycetidae; Hypocreales; Nectriaceae; Nectria.		
REFERENCE	1 (bases 1 to 298) Miller,B.C., Xu,J. and Moore,J.E.		
AUTHORS	Direct Submission		
TITLE	Submitted (28-JAN-2003) Department of Bacteriology, Northern Ireland Public Health Laboratory, Belfast City Hospital, Lisburn Road, Belfast, Co. Antrim BT9 7AD, Northern Ireland, UK		
JOURNAL	Location/Qualifiers		
FEATURES	1..298		
source	/organism="Nectria haematococca" /mol_type="genomic DNA" /strain="260499/24" /db_xref="taxon:140110" <1..132 /product="5.8S ribosomal RNA" 133..245 /product="internal transcribed spacer 2" 246..>298 /product="28S ribosomal RNA"		
ORIGIN			
Query Match	91.5%;	Score 292;	DB 8; Length 298;
Best Local Similarity	100.0%;	Pred. No. 1.9e-150;	
Matches	292;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	28	AGAAATTCAGTGAATCATCGAATCTTTGAACGCAATTCGGCCCGCAGATTTGGGGGG	87
Db	1	AGAAATTCAGTGAATCATCGAATCTTTGAACGCAATTCGGCCCGCAGATTTGGGGGG	60
Qy	88	CATGCTGTTCGAGCGGTGATTACAACCTCAGGCCCCCGGGCTTGGCTGGGATCGGC	147
Db	61	CATGCTGTTCGAGCGGTGATTACAACCTCAGGCCCCCGGGCTTGGGATCGGC	120
Qy	148	GGAAGCCCCCTTCGGGCGACAACGCGGTCCCCCAATATACATGTCGCGTCCCGCGCAGCTT	207
Db	121	GGAAGCCCCCTTCGGGCGACAACGCGGTCCCCCAATATACATGTCGCGTCCCGCGCAGCTT	180
Qy	208	CCATTGCGTAGTAGCTTAACACTCGCACTGGAGAGCGCGCGGCGACGCGTAAACAC	267
Db	181	CCATTGCGTAGTAGCTTAACACTCGCACTGGAGAGCGCGCGGCGACGCGTAAACAC	240
Qy	268	CCAACTTGTGAATGTTGACCTCGAATCAGTAGAATACCGCGTGAACCTTAA	319
Db	241	CCAACTTGTGAATGTTGACCTCGAATCAGTAGAATACCGCGTGAACCTTAA	292
RESULT 9			
LOCUS	AF150466	480 bp	DNA linear
DEFINITION	Nectria haematococca strain SJF209 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.		
ACCESSION	AF150466		

VERSION	AF150466.1	GI:7650164
KEYWORDS	Nectria haematococca	
SOURCE	Nectria haematococca	
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.	
REFERENCE	1 (bases 1 to 480)	
AUTHORS	Suga,H., Hasegawa,T., Mitsu,H., Kageyama,K. and Hyakumachi,M.	
TITLE	Phylogenetic analysis of phytopathogenic fungus, Fusarium solani based on the rDNA-ITS region	
JOURNAL	Mycol. Res. 104 (10), 1175-1183 (2000)	
REFERENCE	2 (bases 1 to 480)	
AUTHORS	Suga,H., Hyakumachi,M. and Kageyama,K.	
TITLE	Direct Submission	
JOURNAL	Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu University, Gifu 501-1112, Japan	
FEATURES	Location/Qualifiers	
source	1. 480	
	/organism="Nectria haematococca"	
	/mol_type="genomic DNA"	
	/strain="SUF209"	
	/db_xref="taxon:140110"	
	/note="anamorph: Fusarium solani f. sp. radiclecola"	
misc_RNA	1. 150	
	/product="internal transcribed spacer 1"	
rRNA	151. 308	
	/product="5.8S ribosomal RNA"	
misc_RNA	309. 480	
	/product="internal transcribed spacer 2"	
ORIGIN		
Query Match	87.5%;	Score 279; DB 8; Length 480;
Best Local Similarity	100.0%;	Pred. No. 3.1e-143;
Matches 279; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	3	AAATGCGTAAGTATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGACA 62
DB	202	AAATGCGTAAGTATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAACGACA 261
QY	63	TTGGCGCCCGCAGTAATCTGGCGGGGCAATGCGTGTTCGAGCGTCATTCAACCCCTCAGAGCC 122
DB	262	TTGGCGCCCGCAGTAATCTGGCGGGGCAATGCGTGTTCGAGCGTCATTCAACCCCTCAGAGCC 321
QY	123	CCCGGCGCTGCGCTGTGGGGAATCGCGGGAAGCCCTCTCGGGCAACAAGCGCGTCCGCCAA 182
DB	322	CCCGGCGCTGCGCTGTGGGGAATCGCGGGAAGCCCTCTCGGGCAACAAGCGCGTCCGCCAA 381
QY	183	TACAGTGGCGGTCCCGCGCGAGCTTCCATTGCGTAGTACTAACAACCTCGCACTGGAGA 242
DB	382	TACAGTGGCGGTCCCGCGCGAGCTTCCATTGCGTAGTACTAACAACCTCGCACTGGAGA 441
QY	243	GCGGCGGGCGGCGGCGGCGGTAACCAACCAACTTCGATG 281
DB	442	GCGGCGGGCGGCGGCGGCGGTAACCAACCAACTTCGATG 480
RESULT 10		
AF150467	480 bp	DNA linear PLN 05-JAN-2001
LOCUS	Nectria haematococca stratum SUF210 internal transcribed spacer 1,	
DEFINITION	5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.	
ACCESSION	AF150467	
VERSION	AF150467.1 GI:7650165	
KEYWORDS	Nectria haematococca	
SOURCE	Nectria haematococca	
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.	
REFERENCE	1 (bases 1 to 480)	
AUTHORS	Suga,H., Hasegawa,T., Mitsu,H., Kageyama,K. and Hyakumachi,M.	
TITLE	Phylogenetic analysis of phytopathogenic fungus, Fusarium solani based on the rDNA-ITS region	





Best Local Similarity 99.7%; Pred. No. 5.1e-136;  
Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTATGTAATGCAATTCAGTAATCATGATCTTTGAACGACA 62  
DB 212 AATGCGATTAAGTATGTAATGCAATTCAGTAATCATGATCTTTGAACGACA 271  
QY 63 TTGGCCCGGCGCATTTGCGCGGCGATGCGCTTTCAGGCGCATTAACCTTCAGGCC 122  
DB 272 TTGGCCCGGCGCATTTGCGCGGCGATGCGCTTTCAGGCGCATTAACCTTCAGGCC 331  
QY 123 CCGGGGCTGGCGGTGGGGATCGGCGAAGCCCTCGGGGACAAAGCCGTCGCCAAA 182  
DB 332 CCGGGGCTGGGGGTGGGGATCGGCGAAGCCCTCGGGGACAAAGCCGTCGCCAAA 391  
QY 183 TACAGTGGCGGTCCCGCGGAGCTTCATTTGGGTGATGCTAACCTTCGCACTGGAGA 242  
DB 392 TACAGTGGCGGTCCCGCGGAGCTTCATTTGGGTGATGCTAACCTTCGCACTGGAGA 451  
QY 243 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 302  
DB 452 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 511  
QY 303 ATACCGCTGAACCTTAA 319  
DB 512 ATACCGCTGAACCTTAA 528

RESULT 13  
LOCUS AY273332 501 bp DNA linear PLN 30-OCT-2003  
DEFINITION Uncultured ascomycete clone 77A6 18S ribosomal RNA gene, partial  
sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene,  
and internal transcribed spacer 2, complete sequence; and 28S  
ribosomal RNA gene, partial sequence.  
AY273332  
AY273332.1 GI:34420179

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Uncultured ascomycete  
uncultured ascomycete  
Eukaryota; Fungi; Ascomycota; environmental samples.  
1 (bases 1 to 501)  
Roose-Amaaleg,C., Brygoo,Y. and Harry,M.  
Marked discrepancy between fungal diversity in soil-feeding  
termitaries and tropical soils  
Unpublished  
2 (bases 1 to 501)  
Roose-Amaaleg,C., Brygoo,Y. and Harry,M.  
Direct Submission  
Submitted (09-APR-2003) UFR Sciences Universite Paris 12,  
UMR137-LBSE, Avenue du General de Gaulle, Creteil cedex 94010,  
France

FEATURES  
source  
Location/Qualifiers

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rRNA 142..292  
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misc\_RNA 293..501  
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ribosomal RNA"

ORIGIN  
Query Match 56.7%; Score 181; DB 8; Length 501;

Best Local Similarity 99.3%; Pred. No. 7.8e-89;  
Matches 281; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTATGTAATGCAATTCAGTAATCATGATCTTTGAACGACA 62  
DB 188 AATGCGATTAAGTATGTAATGCAATTCAGTAATCATGATCTTTGAACGACA 247  
QY 63 TTGGCCCGGCGCATTTGCGCGGCGATGCGCTTTCAGGCGCATTAACCTTCAGGCC 122  
DB 248 TTGGCCCGGCGCATTTGCGCGGCGATGCGCTTTCAGGCGCATTAACCTTCAGGCC 307  
QY 123 CCGGGGCTGGCGGTGGGGATCGGCGAAGCCCTCGGGGACAAAGCCGTCGCCAAA 182  
DB 308 CCGGGGCTGGCGGTGGGGATCGGCGAAGCCCTCGGGGACAAAGCCGTCGCCAAA 367  
QY 183 TACAGTGGCGGTCCCGCGGAGCTTCATTTGGGTGATGCTAACCTTCGCACTGGAGA 242  
DB 368 TACAGTGGCGGTCCCGCGGAGCTTCATTTGGGTGATGCTAACCTTCGCACTGGAGA 427  
QY 243 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 285  
DB 428 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 470

RESULT 14  
LOCUS AF132801 478 bp DNA linear PLN 20-JAN-2000  
DEFINITION Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal  
RNA, and internal transcribed spacer 2, complete sequence.  
AF132801  
AF132801.1 GI:4809015

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Fusarium solani  
Fusarium solani  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
1 (bases 1 to 478)  
Harrington,T.C., Steimel,J.P., Workneh,F. and Yang,X.B.  
Molecular identification of Fungi Associated with Vascular  
Discoloration of Soybean in the North Central United States  
Plant Dis. 84 (1), 83-89 (2000)  
2 (bases 1 to 478)  
Harrington,T.C., Steimel,J.P., Workneh,F. and Yang,X.B.  
Direct Submission  
Submitted (03-MAR-1999) Plant Pathology, Iowa State University,  
Room 351 Bessey Hall, Ames, IA 50011, USA

FEATURES  
source  
Location/Qualifiers

1..478  
/organism="Fusarium solani"  
/mol\_type="genomic DNA"  
/isolate="P185"  
/specific\_host="Glycine max"  
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1..149  
/product="internal transcribed spacer 1"  
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rRNA 150..306  
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misc\_RNA 307..478  
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ORIGIN

Query Match 49.2%; Score 157; DB 8; Length 478;

Best Local Similarity 100.0%; Pred. No. 1.7e-75;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTATGTAATGCAATTCAGTAATCATGATCTTTGAACGACA 62  
DB 201 AATGCGATTAAGTATGTAATGCAATTCAGTAATCATGATCTTTGAACGACA 260

QY 63 TTGCGCCCGCCAGATTTCTGCGCGGCGATGCTTTCAGAGTCATTACAACTCTCAGGCC 122  
 |||||  
 Db 261 TTGCGCCCGCCAGATTTCTGCGCGGCGATGCTTTCAGAGTCATTACAACTCTCAGGCC 320  
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QY 123 CCCGGGCTTGCGTTGGGGATCGCGGAAAGCCCCCTG 159  
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 Db 321 CCCGGGCTTGCGTTGGGGATCGCGGAAAGCCCCCTG 357  
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## RESULT 15

AF150459

LOCUS

## DEFINITION

478 bp DNA linear PLN 05-JAN-2001  
 Nectria haematococca strain K-1 internal transcribed spacer 1, 5.8S  
 ribosomal RNA gene, and internal transcribed spacer 2, complete  
 sequence.

ACCESSION AF150459.1 GI:7650157  
 VERSION AF150459

## KEYWORDS

SOURCE

ORGANISM

## REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

## FEATURES

source

1..478  
 /organism="Nectria haematococca"  
 /mol\_type="genomic DNA"  
 /strain="K-1"  
 /db\_xref="taxon:140110"  
 /note="anamorph: Fusarium solani"  
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 150..307  
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 308..478  
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## ORIGIN

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 Best local similarity 100.0%; Pred. No. 1,7e-75;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTAATGTAATGCAATTCAGTAATCATGAAATCTTTGAAGCACA 62  
 |||||  
 Db 201 AATGCGATTAAGTAATGTAATGCAATTCAGTAATCATGAAATCTTTGAAGCACA 260  
 |||||

QY 63 TTGCGCCCGCCAGATTTCTGCGCGGCGATGCTTTCAGAGTCATTACAACTCTCAGGCC 122  
 |||||  
 Db 261 TTGCGCCCGCCAGATTTCTGCGCGGCGATGCTTTCAGAGTCATTACAACTCTCAGGCC 320  
 |||||

QY 123 CCCGGGCTTGCGTTGGGGATCGCGGAAAGCCCCCTG 159  
 |||||  
 Db 321 CCCGGGCTTGCGTTGGGGATCGCGGAAAGCCCCCTG 357  
 |||||

Search completed: October 1, 2004, 09:56:21

Job time : 1626.37 secs

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:41:36 ; Search time 267.27 Seconds

(without alignments)  
5070.430 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319  
Sequence: 1 gaatacgcatgaagtaatgt.....sgaataccgcgtgaactaa 319Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373663 seqs, 212409041 residues

Word size : 10

Total number of hits satisfying chosen parameters: 606458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 29Jan04:\*

1: geneseqn1980s:\*\n2: geneseqn1990s:\*\n3: geneseqn2000s:\*\n4: geneseqn2001as:\*\n5: geneseqn2001bs:\*\n6: geneseqn2002s:\*\n7: geneseqn2003as:\*\n8: geneseqn2003bs:\*\n9: geneseqn2003cs:\*\n10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	319	100.0	319	2 AAV70850	Internal
2	107	33.5	382	3 AAA72783	5.8s rRNA
3	107	33.5	502	3 AAA61893	Fusarium
4	107	33.5	504	2 AAT05400	Fusarium
5	107	33.5	504	2 AAV62591	Fusarium
6	107	33.5	504	2 AAV59028	F. culmorum
7	107	33.5	504	4 AAS08426	Internal
8	107	33.5	521	7 ACC50000	Internal
9	107	33.5	522	7 ACC49999	Internal
10	107	33.5	534	7 ACC50002	Internal
11	107	33.5	545	2 AAC50001	Internal
12	107	33.5	545	2 AAV62593	Fusarium
13	107	33.5	545	2 AAV59030	F. moniliforme
14	107	33.5	546	2 AAV62596	Fusarium
15	107	33.5	546	2 AAV59007	F. poae
16	107	33.5	2293	4 AAS16211	Fungus
17	106	33.2	647	6 AAV78700	C. crassii
18	106	33.2	661	6 AAV78721	C. sinensis
19	94	29.5	389	3 AAV292490	Rhizoctonia
20	94	29.5	569	2 AAT65101	T. harzia
21	94	29.5	569	2 AAT65099	T. harzia
22	94	29.5	582	2 AAT65100	T. harzia
23	79	24.8	310	2 AAV70851	Internal

24	73	22.9	545	2 AAT05403	AAT05403 Microdoch
25	71	22.3	561	2 AAV59009	AAV59009 F. avenae
26	71	22.3	659	2 AAV78724	AAV78724 C. sinensis
27	70	21.9	537	3 AAZ91725	AAZ91725 Roseillini
28	69	21.6	343	2 AAV70871	AAV70871 Internal
29	69	21.6	344	2 AAV70870	AAV70870 Internal
30	68	21.3	377	6 ABA94559	ABA94559 Truncated
31	68	21.3	377	6 ABA94564	ABA94564 Consensus
32	68	21.3	377	6 ABA94561	ABA94561 Truncated
33	68	21.3	377	6 ABA94560	ABA94560 Truncated
34	68	21.3	415	4 AAF75169	AAF75169 Consensus
35	68	21.3	415	4 AAF75170	AAF75170 Consensus
36	68	21.3	451	2 AAZ22436	AAZ22436 Internal
37	68	21.3	466	8 ADA27321	ADA27321 P. micro
38	68	21.3	534	2 AAT05398	AAT05398 Mycosphae
39	68	21.3	534	2 AAV62505	AAV62505 Mycosphae
40	68	21.3	534	6 ABA94562	ABA94562 DNA seqe
41	68	21.3	537	6 ABA01153	ABA01153 Deuteromy
42	68	21.3	540	2 AAT05399	AAT05399 Mycosphae
43	68	21.3	540	2 AAV62506	AAV62506 Mycosphae
44	68	21.3	540	6 ABA94563	ABA94563 DNA seqe
45	68	21.3	548	2 AAT05394	AAT05394 Septoria

## ALIGNMENTS

RESULT 1  
AAV70850  
ID AAV70850 standard; DNA, 319 BP.  
XX  
AC AAV70850;  
XX  
DT 26-FEB-1999 (first entry)  
XX  
DE Internal transcribed spacer 2 (ITS2) and adjacent regions.  
XX  
KW Internal transcribed spacer 2; ITS2; probe: Aspergillus flavus; A. niger;  
KW A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;  
KW M. racemosus; M. plumbeus; M. indicus; A. fumigatus;  
KW R. circinellioideus F. circinellioideus; Rhizopus oryzae; R. microsporus;  
KW R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;  
KW Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;  
KW Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.  
XX  
XX Fusarium solani.  
XX OS  
XX  
XX MO9850584-A2.  
XX  
XX 12-NOV-1998.  
XX  
XX 01-MAY-1998; 98WC-US008926.  
XX  
XX 02-MAY-1997; 97US-0045400P.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Morrison CJ, Reiss E, Aidorevich L, Choi JS;  
XX  
XX WPI, 1999-034737/03.  
XX  
XX New nucleic acid probes for filamentous fungi - for detecting e.g.  
XX Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia.  
XX Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix  
XX species.  
XX  
XX Claim 1; Page 12; 45pp; English.  
XX  
XX The present sequence represents an internal transcribed spacer 2 (ITS2)  
XX and adjacent regions. Probes can be derived from the present sequence  
XX which are species-specific. The specification also describes ITS2  
XX sequence-derived probes for identifying a species selected from  
XX Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,



CC	these fungi (AA05394-705404 and AAQ94398) and are strain specific. The
CC	amplification products of the reactions using these primers can be used
CC	with the capture primers AAT05378-93 in colourimetric assays. The primers
CC	and ITS DNAs can be used for the detection of specific fungal pathogen
CC	isolates and in monitoring disease development in plant populations
XX	
SQ	Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
Query Match	33.5%; Score 107; DB 2; Length 504;
Best Local Similarity	100.0%; Pred. No. 1.9e-46;
Matches 107,	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	2 AAAATGGCAATGACGTGAATTGCAGCAATTCGATCGTGAATCATCTTTGAACGAC 61
Dd	211 AAAATGGCAATGACGTGAATGTAATTCGACAAATTCAGTAATCATCTTTGAACGAC 270
Oy	62 ATTGCGCCGCCAGTATTTGCGCGGAGATGCGCTTTGAGCGTCATT 108
Dd	271 ATTGCGCCGCCAGTATTTGCGCGGAGATGCGCTTTGAGCGTCATT 317
RESULT 5	
AAV62591	
ID	AAV62591 standard; DNA; 504 BP.
XX	
AC	AAV62591;
OS	
DT	17-DEC-1998 (first entry)
XX	
DE	Fusarium culmorum PCR amplified ITS region consensus DNA sequence.
XX	
KX	Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
KM	Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
KW	Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
KW	PCR; nucleic acid detection; ss.
XX	
XX	Fusarium culmorum.
XX	
Key	Location/Qualifiers
FT	misc_feature 1..12
FT	/tag= a
FT	/note= "3' end of small subunit rRNA gene"
FT	13..161
FT	/tag= b
FT	/note= "ITS 1"
FT	162..318
FT	/tag= c
FT	/note= "5.8S rRNA gene"
FT	319..472
FT	/tag= d
FT	/note= "ITS 2"
FT	473..504
FT	/tag= e
FT	/note= "5' end of large subunit rRNA gene"
XX	
XX	US5814453-A.
XX	
PD	29-SEP-1998.
XX	
XX	02-JUL-1997; 97US-00887480.
XX	
XX	19-APR-1995; 95WO-US004712.
PR	15-OCT-1996; 96US-00722187.
XX	
PA	(NOVS ) NOVARTIS FINANCE CORP.
XX	
PJ	Beck JI;
XX	
DR	WPI; 1998-541745/46.
XX	
FT	DNA isolated from fungal RNA, and its internal transcribed spacer
XX	sequence - used for detecting fungal pathogens in plant tissue.
XX	

PS Claim 2; Fig 3; 56bp; English.

XX This represents the consensus DNA sequence of the internal transcribed  
CC spacer (ITS) region that was PCR amplified from *Fusarium culmorum*  
CC isolates, R-5106, R-5126 and R-5146. The invention provides a DNA  
CC molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal  
CC pathogen, where the DNA molecule consists of an ITS sequence selected  
CC from ITS1 and ITS2 of *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium*  
CC moniliforme, *Septoria avenae* or *Microdochium nivale*. A method for  
CC detecting *F. graminearum*, *F. culmorum*, *F. moniliforme*, *F. poae*, *F.*  
CC *avenaceum* and *M. nivale* isolates is also provided. The method comprises  
CC isolating DNA from a plant leaf infected with at least one of the above  
CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by  
CC PCR using specific primers from within these sequences. The pathogen(s)  
CC are detected by visualising the amplified part of the ITS sequence

XX  
SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;

Query Match 33.5%; Score 107; DB 2; Length 504;  
Best Local Similarity 100.0%; Pred. No. 1.9e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAATGCGATAGTATGTAATTCAGAAATTCAGTATCATCGAATCTTTGAAGCGAC 61  
DB 211 AAAATGCGATAGTATGTAATTCAGAAATTCAGTATCATCGAATCTTTGAAGCGAC 270

QY 62 ATTCGCGCGCGCGAGTATCTTGGCGGCGATGCGCTGTTGAGCGTCATT 108  
DB 271 ATTCGCGCGCGCGAGTATCTTGGCGGCGATGCGCTGTTGAGCGTCATT 317

RESULT 6  
AAVS9028  
ID AAVS9028 standard; DNA; 504 BP.  
XX  
AC AAVS9028;  
XX  
DT 25-MAR-2003 (revised)  
DT 06-JAN-1999 (first entry)

XX F. *culmorum* internal transcribed spacer.  
XX  
XX Internal transcribed spacer; ITS; *Microdochium*; *Fusarium*; wheat pathogen;  
KM fungal pathogen identification; infection identification; ss.  
XX  
OS *Fusarium culmorum*.  
XX  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 13..161  
FT /\*tag= a  
FT /note= "ITS1"  
FT misc\_feature 319..472  
FT /\*tag= b  
FT /note= "ITS2"

XX US5827695-A.  
XX  
PD 27-OCT-1998.  
XX  
PF 04-AUG-1997; 97US-00905314.  
XX  
PR 04-AUG-1997; 97US-00905314.  
XX  
PA (NOVS ) NOVARTIS FINANCE CORP.  
XX  
PI Beck JJ;  
XX  
XX WPI; 1998-593995/50.  
XX  
XX Wheat pathogen internal transcribed spacer sequences - used as a basis  
PT for primers for the species-specific polymerase chain reaction detection  
PT of the pathogens.  
XX

PS Disclosure; Col 21-22; 20pp; English.

XX This sequence represents an internal transcribed spacer (ITS) sequence of  
CC the invention. The primer pairs, based on the ITS sequences, are used for  
CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal  
CC pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*, *F.*  
CC *avenaceum*, *F. poae*, *F. moniliforme* or *F. roseum*. The two different  
CC strains of fungi show different symptoms during infection, which may or  
CC may not be due to infection. Early identification of the strain causing  
CC the infection allows early, and more specific fungicidal treatment.  
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to  
CC correct PR field.)

XX  
SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;

Query Match 33.5%; Score 107; DB 2; Length 504;  
Best Local Similarity 100.0%; Pred. No. 1.9e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAATGCGATAGTATGTAATTCAGAAATTCAGTATCATCGAATCTTTGAAGCGAC 61  
DB 211 AAAATGCGATAGTATGTAATTCAGAAATTCAGTATCATCGAATCTTTGAAGCGAC 270

QY 62 ATTCGCGCGCGCGAGTATCTTGGCGGCGATGCGCTGTTGAGCGTCATT 108  
DB 271 ATTCGCGCGCGCGAGTATCTTGGCGGCGATGCGCTGTTGAGCGTCATT 317

RESULT 7  
AAS08426  
ID AAS08426 standard; DNA; 504 BP.  
XX  
AC AAS08426;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DE Internal transcribed spacer, ITS, region #16.  
XX  
XX Internal transcribed spacer; ITS; fungal pathogen; ss; wheat disease;  
KM Sharp eyespot; fungal pathotype identification; isolate 62215.  
XX  
XX *Fusarium culmorum*.  
XX  
XX WO200151653-A1.  
XX  
PD 19-JUL-2001.  
XX  
XX 09-JAN-2001; 2001WO-EP000172.  
XX  
PF 11-JAN-2000; 2000US-00481293.  
XX  
PR (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PA Beck JJ, Barnett CJ;  
XX  
PI WPI; 2001-442154/47.  
XX  
DR New internal transcribed spacer DNA sequences, useful for identifying  
PT fungal pathogen, particularly *Rhizoctonia cerealis*, and for monitoring  
PT disease development in plant population.  
XX  
XX  
PS Disclosure; Page 31; 35pp; English.  
XX  
XX The sequence is an internal transcribed spacer (ITS) region from *Fusarium*  
CC *culmorum*, isolate 62215. The ITS DNA sequences are useful for detecting  
CC *Rhizoctonia cerealis*, a fungal pathogen of wheat causing Sharp eyespot,  
CC for monitoring disease development in plant population, and for providing  
CC detailed information on the development and spread of specific pathogen  
CC races over extended geographical areas. The DNA sequences are  
CC specifically used as primers in PCR-based analysis for the identification  
CC of fungal pathotypes  
XX  
SQ Sequence 504 BP; 132 A; 133 C; 114 G; 123 T; 0 U; 2 Other;

Query Match 33.5%; Score 107; DB 4; Length 504;  
Best Local Similarity 100.0%; Pred. No. 1.9e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAAATGCGATGAATGATGCAATTCAGATTCATCGAATCTTTGAACGAC 61  
DB 214 AAAATGCGATGAATGATGCAATTCAGATTCATCGAATCTTTGAACGAC 273  
OY 62 ATTGGCCCCGCGAGTATCTGGCGGCATGCTGTTGAGCGTCATT 108  
DB 274 ATTGGCCCCGCGAGTATCTGGCGGCATGCTGTTGAGCGTCATT 320

RESULT 8  
ACCS0000  
ID ACC50000 standard; DNA; 521 BP.  
AC ACC50000;  
XX  
XX 14-JUL-2003 (first entry)  
XX  
XX Internal transcribed spacer RNA encoding sequence #2.  
XX  
XX Mitochondria; fungal pathogen; ds.  
XX  
XX Gibberella zeae.  
XX OS  
XX WO2003027635-A2.  
XX  
XX 03-APR-2003.  
XX  
XX 19-SEP-2002; 2002WO-US030311.  
XX  
XX 24-SEP-2001; 2001US-00961755.  
XX  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Beck JI, Barnett CJ;  
XX  
XX WPI; 2003-363229/34.  
XX  
XX Detecting a fungal pathogen, useful for monitoring disease development,  
XX PT comprises subjecting the DNA to PCR amplification using at least one  
XX PT primer having sequence identity with at least 10 contiguous nucleotides  
XX PT of Fusarium spp.  
XX  
XX Claim 5; Page 38; 44pp; English.  
XX  
XX This invention relates to the detection of a fungal pathogen comprising  
XX CC isolating DNA from a plant leaf infected with a pathogen. The methods and  
XX CC primers are useful for identifying fungal isolates of fungal pathogens  
XX CC and monitoring of disease development in plant populations. The present  
XX CC sequence represents an internal transcribed spacer RNA encoding sequence  
XX  
XX Sequence 521 BP; 138 A; 140 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 33.5%; Score 107; DB 7; Length 521;  
Best Local Similarity 100.0%; Pred. No. 1.9e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAAATGCGATGAATGATGCAATTCAGATTCATCGAATCTTTGAACGAC 61  
DB 228 AAAATGCGATGAATGATGCAATTCAGATTCATCGAATCTTTGAACGAC 287  
OY 62 ATTGGCCCCGCGAGTATCTGGCGGCATGCTGTTGAGCGTCATT 108  
DB 288 ATTGGCCCCGCGAGTATCTGGCGGCATGCTGTTGAGCGTCATT 334

RESULT 9  
ACCS0000  
ID ACC49999 standard; DNA; 522 BP.

XX  
AC ACC49999;  
XX  
XX 14-JUL-2003 (first entry)  
XX  
XX Internal transcribed spacer RNA encoding sequence.  
XX  
XX Mitochondria; fungal pathogen; ds.  
XX  
XX Fusarium subglutinans.  
XX  
XX WO2003027635-A2.  
XX  
XX 03-APR-2003.  
XX  
XX 19-SEP-2002; 2002WO-US030311.  
XX  
XX 24-SEP-2001; 2001US-00961755.  
XX  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Beck JI, Barnett CJ;  
XX  
XX WPI; 2003-363229/34.  
XX  
XX Detecting a fungal pathogen, useful for monitoring disease development,  
XX PT comprises subjecting the DNA to PCR amplification using at least one  
XX PT primer having sequence identity with at least 10 contiguous nucleotides  
XX PT of Fusarium spp.  
XX  
XX Claim 5; Page 38; 44pp; English.  
XX  
XX This invention relates to the detection of a fungal pathogen comprising  
XX CC isolating DNA from a plant leaf infected with a pathogen. The methods and  
XX CC primers are useful for identifying fungal isolates of fungal pathogens  
XX CC and monitoring of disease development in plant populations. The present  
XX CC sequence represents an internal transcribed spacer RNA encoding sequence  
XX  
XX Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 33.5%; Score 107; DB 7; Length 522;  
Best Local Similarity 100.0%; Pred. No. 1.9e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAAATGCGATGAATGATGCAATTCAGATTCATCGAATCTTTGAACGAC 61  
DB 228 AAAATGCGATGAATGATGCAATTCAGATTCATCGAATCTTTGAACGAC 287  
OY 62 ATTGGCCCCGCGAGTATCTGGCGGCATGCTGTTGAGCGTCATT 108  
DB 288 ATTGGCCCCGCGAGTATCTGGCGGCATGCTGTTGAGCGTCATT 334

RESULT 10  
ACCS0002  
ID ACC50002 standard; DNA; 522 BP.  
AC ACC50002;  
XX  
XX 27-OCT-2003 (revised)  
XX  
XX 14-JUL-2003 (first entry)  
XX  
XX Internal transcribed spacer RNA encoding sequence #4.  
XX  
XX Mitochondria; fungal pathogen; ds.  
XX  
XX Gibberella moniliformis.  
XX OS  
XX WO2003027635-A2.  
XX  
XX 03-APR-2003.  
XX  
XX 19-SEP-2002; 2002WO-US030311.

```

XX 24-SEP-2001; 2001US-00961755.
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX Beck JT, Barnett CJ;
XX WPI; 2003-363229/34.
XX
XX Detecting a fungal pathogen, useful for monitoring disease development,
XX comprises subjecting the DNA to PCR amplification using at least one
XX primer having sequence identity with at least 10 contiguous nucleotides
XX of Fusarium spp.
XX
XX Claim 5; Page 39; 44pp; English.
XX
XX This invention relates to the detection of a fungal pathogen comprising
XX isolating DNA from a plant leaf infected with a pathogen. The methods and
XX primers are useful for identifying fungal isolates of fungal pathogens
XX and monitoring of disease development in plant populations. The present
XX sequence represents an internal transcribed spacer RNA encoding sequence.
XX (Updated on 27-OCT-2003 to standardise OS field)
XX
XX Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;
XX
XX Query Match 33.5%; Score 107; DB 7; Length 522;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-46;
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 2 AAAATGCGATTAAGTAATGTAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC 61
XX 228 AAAATGCGATTAAGTAATGTAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC 287
XX
XX 62 ATTTGGCCCGCCAGCATTTCTGGCGGGCAGTGCCTGTTTCAGAGCTCATTT 108
XX 288 ATTTGGCCCGCCAGCATTTCTGGCGGGCAGTGCCTGTTTCAGAGCTCATTT 334
XX
XX RESULT 11
XX ACC50001
XX ACC50001 standard; DNA; 534 BP.
XX
XX ACC50001;
XX
XX 14-JUN-2003 (first entry)
XX
XX Internal transcribed spacer RNA encoding sequence #3.
XX
XX Mitochondria; fungal pathogen; ds.
XX
XX Fusaarium proliferatum.
XX
XX WO2003027635-A2.
XX
XX 03-APR-2003.
XX
XX 19-SEP-2002; 2002WO-US030311.
XX
XX 24-SEP-2001; 2001US-00961755.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Beck JT, Barnett CJ;
XX WPI; 2003-363229/34.
XX
XX Detecting a fungal pathogen, useful for monitoring disease development,
XX comprises subjecting the DNA to PCR amplification using at least one
XX primer having sequence identity with at least 10 contiguous nucleotides
XX of Fusarium spp.
XX
XX Claim 5; Page 38-39; 44pp; English.

```

CC	This invention relates to the detection of a fungal pathogen comprising
CC	isolating DNA from a plant leaf infected with a pathogen. The methods and
CC	primers are useful for identifying fungal isolates of fungal pathogens
CC	and monitoring of disease development in plant populations. The present
CC	sequence represents an internal transcribed spacer RNA encoding sequence
XX	
SQ	Sequence 534 BP; 135 A; 149 C; 130 G; 120 T; 0 U; 0 Other;
Query Match	33.5%; Score 107; DB 7; Length 534;
Best Local Similarity	100.0%; Pred. No. 1.9e-46;
Matches 107; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	2 AAAATGCATTAAGTATGTGAATTGCAAAATTCAGTGATCATGAACTTTGAACGCAC 61
Dd	228 AAATGGCATAAGTATGTGAATTGCGAATTCAGTGATCATGAACTTTGAACGCAC 287
Oy	62 ATTGGCGCCGCCGAGTATTCTGGCGGGCAGTCCTTTGAGCGTCATT 108
Dd	288 ATTGCGCCGCCGAGTATTCTGGCGGGCAGTCCTTTGAGCGTCATT 334
RESULT 12	
AAV62593	
ID	AAV62593 standard; DNA; 545 BP.
XX	
AC	AAV62593;
XX	
DT	17-OCT--2003 (revised)
DT	17-DEC-1998 (first entry)
DE	Fusarium moniliforme PCR amplified ITS region DNA sequence.
XX	
KW	Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
KM	Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
KX	Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
KW	PCR; nucleic acid detection; ss.
XX	
OS	Gibberella fujikuroi.
XX	
FH	Key Location/Qualifiers
FT	misc_feature 1..30
FT	/tag= a
FT	/note= "3' end of small subunit rRNA gene"
FT	31..178
FT	/tag= b
FT	/note= "ITS 1"
FT	179..335
FT	/tag= c
FT	/note= "5.8S rRNA gene"
FT	336..488
FT	/tag= d
FT	/note= "ITS 2"
FT	489..545
FT	/tag= e
FT	/note= "5' end of large subunit rRNA gene"
XX	
RN	US5814453-A.
XX	
PD	29-SEP-1998.
XX	
PF	02-JUL-1997; 97US-00887480.
XX	
PR	19-APR-1995; 95MO-US004712.
PR	15-OCT-1996; 96US-00722187.
XX	
PA	(NOVS ) NOVARTIS FINANCE CORP.
XX	
Beck JF;	
PI	WIPI; 1998-541745/46.
DR	
XX	
XX	DNA isolated from fungal RNA, and its internal transcribed spacer
XX	sequence - used for detecting fungal pathogens in plant tissue.



XX Claim 2; Fig 3; 56pp; English.

PS

XX This represents the DNA sequence of the internal transcribed spacer (ITS)

CC region that was PCR amplified from *Fusarium moniliforme*. The invention

CC provides a DNA molecule isolated from the ribosomal RNA gene region of a

CC fungal pathogen, where the DNA molecule consists of an ITS sequence

CC selected from ITS1 and ITS2 of *Fusarium culmorum*, *Fusarium graminearum*,

CC *Fusarium moniliforme*, *Septoria avenae* or *Microdochium nivale*. A method

CC for detecting *F. graminearum*, *F. culmorum*, *F. moniliforme*, *F. poae*, *F.*

CC *avenaceum* and *M. nivale* isolates is also provided. The method comprises

CC isolating DNA from a plant leaf infected with at least one of the above

CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by

CC PCR using specific primers from within these sequences. The pathogen(s)

CC are detected by visualizing the amplified part of the ITS sequence.

CC (Updated on 17-OCT-2003 to standardise OS field)

CC

XX

XX Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;

XX

XX Query Match 33.5%; Score 107; DB 2; Length 545;

XX Best Local Similarity 100.0%; Pred. No. 1.9e-46;

XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 2 AAAATGCATTAAGTAATGTAATTCAGATTCAGTGAATCATGAACTTTGAACGCAC 61

DB 228 AAAATGCATTAAGTAATGTAATTCAGATTCAGTGAATCATGAACTTTGAACGCAC 287

QY 62 ATTGGCCCCCGCAGTATTCTGGCGGGCATGCTGTTGAGCGTCATT 108

DB 288 ATTGGCCCCCGCAGTATTCTGGCGGGCATGCTGTTGAGCGTCATT 334

DB

RESULT 13

AAVS9030

ID AAVS9030 standard; DNA; 545 BP.

XX

XX AAVS9030;

XX

XX 17-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 06-JAN-1999 (first entry)

XX

DE F. moniliforme internal transcribed spacer.

XX

XX Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;

KW fungal pathogen identification; infection identification; ss.

KX

XX Gibberella fujikuroi.

OS

XX

XX Key Location/Qualifiers

XX Key misc\_feature 31..178

FT /\*tag= a

FT /note= "ITS1"

FT 336..488

FT /\*tag= b

FT /note= "ITS2"

FT

XX

XX US5827695-A.

XX

XX 27-OCT-1998.

PD

XX

XX 04-AUG-1997; 97US-00905314.

PF

XX

XX 04-AUG-1997; 97US-00905314.

PR

XX

XX (NOVS ) NOVARTIS FINANCE CORP.

PA

XX

XX Beck JU;

PI

XX

XX WPI; 1998-593995/50.

DR

XX

XX Wheat pathogen internal transcribed spacer sequences - used as a basis

PT for primers for the species-specific polymerase chain reaction detection

PT

PT of the pathogens.

PS

XX Disclosure; Col 23-26; 20pp; English.

XX

XX This sequence represents an internal transcribed spacer (ITS) sequence of

CC the invention. The primer pairs, based on the ITS sequences, are used for

CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal

CC pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*, *F.*

CC *avenaceum*, *F. poae*, *F. moniliforme* or *F. roseum*. The two different

CC strains of fungi show different symptoms during infection, which may or

CC may not be due to infection. Early identification of the strain causing

CC the infection allows early, and more specific fungicidal treatment.

CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to

CC correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)

CC

XX

XX Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;

XX

XX Query Match 33.5%; Score 107; DB 2; Length 545;

XX Best Local Similarity 100.0%; Pred. No. 1.9e-46;

XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 2 AAAATGCATTAAGTAATGTAATTCAGATTCAGTGAATCATGAACTTTGAACGCAC 61

DB 228 AAAATGCATTAAGTAATGTAATTCAGATTCAGTGAATCATGAACTTTGAACGCAC 287

QY 62 ATTGGCCCCCGCAGTATTCTGGCGGGCATGCTGTTGAGCGTCATT 108

DB 288 ATTGGCCCCCGCAGTATTCTGGCGGGCATGCTGTTGAGCGTCATT 334

DB

RESULT 14

AAV62596

ID AAV62596 standard; DNA; 546 BP.

XX

XX AAV62596;

XX

XX 17-DEC-1998 (first entry)

DT

XX

XX *Fusarium poae* PCR amplified ITS region consensus DNA sequence.

DE

XX

XX Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;

KW *Fusarium culmorum*; *Fusarium graminearum*; *Fusarium moniliforme*; plant;

KW *Septoria avenae*; *Microdochium nivale*; *Fusarium poae*; *Fusarium avenaceum*;

KX PCR; nucleic acid detection; ss.

KX

XX *Fusarium poae*.

OS

XX

XX Key Location/Qualifiers

XX Key misc\_feature 1..30

FT /\*tag= a

FT /note= "3' end of small subunit rRNA gene"

FT 31..180

FT /\*tag= b

FT /note= "ITS 1"

FT 181..337

FT /\*tag= c

FT /note= "5.8S rRNA gene"

FT 338..489

FT /\*tag= d

FT /note= "ITS 2"

FT 490..546

FT /\*tag= e

FT /note= "5' end of large subunit rRNA gene"

FT

XX

XX US5814453-A.

XX

XX 29-SEP-1998.

PD

XX

XX 02-JUN-1997; 97US-00887480.

PF

XX

XX 19-APR-1995; 95MO-US004712.

PR 15-OCT-1996; 96US-00722187.

XX

PA (NOVS ) NOVARTIS FINANCE CORP.  
 XX Beck JJ;  
 PI WPI; 1998-541745/46.  
 DR DNA isolated from fungal RNA, and its internal transcribed spacer  
 PT sequence - used for detecting fungal pathogens in plant tissue.  
 XX Example; Col 87-88; 56pp; English.  
 PS  
 CC This represents the consensus DNA sequence of the internal transcribed  
 CC spacer (ITS) region that was PCR amplified from *Fusarium poae* isolates, T  
 CC -427, T-534 and T-756. The invention provides a DNA molecule isolated  
 CC from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the  
 CC DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of  
 CC *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium moniliforme*, *Septoria*  
 CC *avenae* or *Microdochium nivale*. A method for detecting *F. graminearum*, *F.*  
 CC *culmorum*, *F. moniliforme*, *F. poae*, *F. avenaceum* and *M. nivale* isolates is  
 CC also provided. The method comprises isolating DNA from a plant leaf  
 CC infected with at least one of the above pathogens and amplifying parts of  
 CC the ITS sequence of the pathogen(s) by PCR using specific primers from  
 CC within these sequences. The pathogen(s) are detected by visualising the  
 CC amplified part of the ITS sequence  
 SQ Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;  
 Query Match 33.5%; Score 107; DB 2; Length 546;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 AAAATGCGATGATGATGATGATGATGCGAATTCGTAATCATCGAATCTTTGAACGAC 61  
 Db 230 AAAATGCGATGATGATGATGATGATGCGAATTCGTAATCATCGAATCTTTGAACGAC 289  
 QY 62 ATTGGCGCCGCCAGTATTCGTGGCGGCGATGCGCTGTTGAGCGTCATT 108  
 Db 290 ATTGGCGCCGCCAGTATTCGTGGCGGCGATGCGCTGTTGAGCGTCATT 336

RESULT 15  
 AAVS9007  
 ID AAVS9007 standard; DNA; 546 BP.  
 AC AAVS9007;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 06-JAN-1999 (first entry)  
 XX  
 DE F. poae internal transcribed spacer.  
 XX  
 XX Internal transcribed spacer; ITS; *Microdochium*, *Fusarium*, wheat pathogen;  
 KW fungal pathogen identification; infection identification; ss.  
 XX  
 XX *Fusarium poae*.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH misc\_feature 31..180  
 FT /\*tag= a  
 FT /note= "ITS1"  
 FT misc\_feature 338..489  
 FT /\*tag= b  
 FT /note= "ITS2"  
 FT  
 FT  
 PN US5827695-A.  
 XX  
 XX 27-OCT-1998.  
 PD  
 XX 04-AUG-1997; 97US-00905314.  
 PF  
 XX 04-AUG-1997; 97US-00905314.  
 PR  
 XX (NOVS ) NOVARTIS FINANCE CORP.  
 PA

XX Beck JJ;  
 PI WPI; 1998-593995/50.  
 DR Wheat pathogen internal transcribed spacer sequences - used as a basis  
 PT for primers for the species-specific polymerase chain reaction detection  
 PT of the pathogens.  
 XX Claim 1; Col 25-26; 20pp; English.  
 PS  
 CC This sequence represents an internal transcribed spacer (ITS) sequence of  
 CC the invention. The primer pairs, based on the ITS sequences, are used for  
 CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal  
 CC pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*, *F.*  
 CC *avenaceum*, *F. poae*, *F. moniliforme* or *F. roseum*. The two different  
 CC strains of fungi show different symptoms during infection, which may or  
 CC may not be due to infection. Early identification of the strain causing  
 CC the infection allows early, and more specific fungicidal treatment.  
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to  
 CC correct PR field.)  
 SQ Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;  
 Query Match 33.5%; Score 107; DB 2; Length 546;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 AAAATGCGATGATGATGATGATGCGAATTCGTAATCATCGAATCTTTGAACGAC 61  
 Db 230 AAAATGCGATGATGATGATGATGCGAATTCGTAATCATCGAATCTTTGAACGAC 289  
 QY 62 ATTGGCGCCGCCAGTATTCGTGGCGGCGATGCGCTGTTGAGCGTCATT 108  
 Db 290 ATTGGCGCCGCCAGTATTCGTGGCGGCGATGCGCTGTTGAGCGTCATT 336

Search completed: October 1, 2004, 09:02:48  
 Job time : 274.27 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: October 1, 2004, 08:06:18 : Search time 52.744 Seconds  
(without alignment)  
3356.386 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319

Sequence: 1 gaaatcgatgaagtaagtgt.....ggaatacccgctgaacttaa 319

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 10

Total number of hits satisfying chosen parameters: 87318

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : Issued Patents, NA:\*

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319	100.0	319	4	US-09-423-233-6
2	107	33.5	504	1	US-08-887-480-82
3	107	33.5	504	1	US-08-905-314A-19
4	107	33.5	504	2	US-08-722-187-82
5	107	33.5	504	4	US-09-481-293-32
6	107	33.5	504	5	PCT-US95-04712-82
7	107	33.5	545	1	US-08-887-480-84
8	107	33.5	545	1	US-08-905-314A-21
9	107	33.5	546	1	US-08-887-480-96
10	107	33.5	546	1	US-08-905-314A-22
11	107	33.5	2293	3	US-09-645-073-1
12	106	33.2	531	1	US-08-652-127C-7
13	106	33.2	581	1	US-08-652-127C-5
14	106	33.2	594	1	US-08-652-127C-5
15	79	24.8	310	4	US-09-423-233-7
16	73	22.9	545	2	US-08-722-187-85
17	73	22.9	545	5	PCT-US95-04712-85
18	71	22.3	561	1	US-08-905-314A-24
19	70	21.9	583	4	US-08-652-127C-8
20	69	21.6	343	4	US-09-423-233-27
21	69	21.6	344	4	US-09-423-233-26
22	68	21.3	415	4	US-09-635-747-39
23	68	21.3	415	4	US-09-635-747-40
24	68	21.3	451	3	US-09-037-990B-5
25	68	21.3	534	1	US-08-233-608-5
26	68	21.3	534	1	US-08-887-480-5
27	68	21.3	534	2	US-08-722-187-5

28	68	21.3	534	5	PCT-US95-04712-5	Sequence 5, Appli
29	68	21.3	540	1	US-08-233-608-6	Sequence 6, Appli
30	68	21.3	540	1	US-08-887-480-6	Sequence 6, Appli
31	68	21.3	540	2	US-08-722-187-6	Sequence 6, Appli
32	68	21.3	540	5	PCT-US95-04712-6	Sequence 6, Appli
33	68	21.3	548	1	US-08-233-608-1	Sequence 1, Appli
34	68	21.3	548	1	US-08-887-480-1	Sequence 1, Appli
35	68	21.3	548	2	US-08-722-187-1	Sequence 1, Appli
36	68	21.3	548	4	US-09-481-293-30	Sequence 30, Appli
37	68	21.3	548	5	PCT-US95-04712-1	Sequence 85, Appli
38	68	21.3	556	1	US-08-887-480-85	Sequence 23, Appli
39	68	21.3	556	3	US-08-905-314A-23	Sequence 5, Appli
40	68	21.3	568	3	US-08-986-727-5	Sequence 3, Appli
41	68	21.3	597	1	US-08-742-023-3	Sequence 1, Appli
42	68	21.3	597	3	US-08-968-505-3	Sequence 3, Appli
43	68	21.3	605	3	US-08-968-727-1	Sequence 1, Appli
44	68	21.3	608	3	US-08-986-727-3	Sequence 3, Appli
45	68	21.3	611	3	US-08-986-727-4	Sequence 4, Appli

## ALIGNMENTS

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RESULT 1
US-09-423-233-6
; Sequence 6, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-423-233-6

Query Match      100.0%; Score 319; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 2.5e-167;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAATGCGATGAATGAATGGAATTCGAGATTCGATCATCGAATCTTTGAACGCA 60
      |||||||
DB      1 GAAATGCGATGAATGAATGGAATTCGAGATTCGATCATCGAATCTTTGAACGCA 60

QY      61 CATTGCGCGCGCGCAGATTTCTGCGCGGATGCTGTTGAGCGTCAATTAACACCTTAGG 120
      |||||||
DB      61 CATTGCGCGCGCGCAGATTTCTGCGCGGATGCTGTTGAGCGTCAATTAACACCTTAGG 120

QY      121 CCCCCGCGCGCGCGGATTCGCGGAGACCCCTGCGGCGCAACCGCGTCCGCCA 180
      |||||||
DB      121 CCCCCGCGCGCGCGGATTCGCGGAGACCCCTGCGGCGCAACCGCGTCCGCCA 180

QY      181 AATACAGTGGCGTCCCGCGCAGCTTCATTGCGTAGTACTAACAACCTGCAACTGGA 240
      |||||||
DB      181 AATACAGTGGCGTCCCGCGCAGCTTCATTGCGTAGTACTAACAACCTGCAACTGGA 240

QY      241 GAGCGGCGCGCGCGCAGCGCGTAAACCCCACTTGTGATGTTGACTCGAATGAGTAG 300
      |||||||
DB      241 GAGCGGCGCGCGCGCAGCGCGTAAACCCCACTTGTGATGTTGACTCGAATGAGTAG 300

QY      301 GAATACCGCGTGAATCTTAA 319
      |||||||
DB      301 GAATACCGCGTGAATCTTAA 319

RESULT 2
US-08-887-480-82
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Sequence 82, Application US/08887480  
Patent No. 5814453  
GENERAL INFORMATION:  
APPLICANT: Beck, James J  
TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
TITLE OF INVENTION: Polymerase Chain Reaction  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5814453artis Corporation  
STREET: 520 White Plains Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,480  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/722,187  
FILING DATE: 15-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Fusarium culmorum  
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146  
INDIVIDUAL ISOLATE: (consensus sequence)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..12  
OTHER INFORMATION: /note= "3' end of small subunit  
OTHER INFORMATION: rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 13..161  
OTHER INFORMATION: /note= "ITS 1"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 162..318  
OTHER INFORMATION: /note= "5.8S rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 319..472  
OTHER INFORMATION: /note= "ITS 2"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 473..504  
OTHER INFORMATION: /note= "5' end of large subunit  
OTHER INFORMATION: rRNA gene"  
US-08-887-480-82

Query Match 33.5%; Score 107; DB 1; Length 504;  
Best Local Similarity 100.0%; Pred. No. 9.9e-50;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2 AATATGGATTAATGATGATTCGAGATTCATGATTCATCTTTGAACGAC 61

Db 211 AATATGGATTAATGATGATTCGAGATTCATGATTCATCTTTGAACGAC 270  
Qy 62 ATTGCCCGCCGAGATTCGCGGCATGCCGTTCGAGCGTCATT 108  
Db 271 ATTGCCCGCCGAGATTCGCGGCATGCCGTTCGAGCGTCATT 317  
RESULT 3  
US-08-905-314A-19  
Sequence 19, Application US/08905314A  
Patent No. 5827695  
GENERAL INFORMATION:  
APPLICANT: Beck, James J.  
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5827695artis Corporation Patent Department  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 20779-2257  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,314A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1944  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Fusarium culmorum  
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146  
INDIVIDUAL ISOLATE: (consensus sequence)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..12  
OTHER INFORMATION: /note= "3' end of small subunit  
OTHER INFORMATION: rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 13..161  
OTHER INFORMATION: /note= "ITS 1"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 162..318  
OTHER INFORMATION: /note= "5.8S rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 319..472  
OTHER INFORMATION: /note= "ITS 2"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 473..504  
OTHER INFORMATION: /note= "5' end of large subunit  
OTHER INFORMATION: rRNA gene"

US-08-905-314A-19

Query Match	33.5%	Score 107;	DB 1;	Length 504;
Best Local Similarity	100.0%	Pred. No. 9.9e-50;		
Matches 107; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      2 AAAATCGAATAAGTAAATGTGAATTGCAAGATTCAAGTAATCATTCGAATCTTTGAACGCAC   61
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Db      211 AAAATCGAATAAGTAAATGTGAATTGCAAGATTCAAGTAATCATTCGAATCTTTGAACGCAC   270
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QY      62 ATGGCGCCGCGCAGTATTCTGCGGGATGCCTGTTCAGCGTCATT 108
        |||||
db       271 ATGCGCCGCGCAGTATTCTGCGGGATGCCTGTTCAGCGTCATT 317

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RESULT 4  
US-08-722-187-82

1 GENERAL INFORMATION:  
2 APPLICANT: Ligon, James M  
3 APPLICANT: Beck, James J  
4 TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
5 TITLE OF INVENTION: Polymeraase Chain Reaction  
6 NUMBER OF SEQUENCES: 86  
7 CORRESPONDENCE ADDRESS: 8

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Query Match      33.5%: Score 107; DB 2; length 504;
Best Local Similarity 100.0%: Pred. NC. 9.9e-50;
Matches 107; Conservative 0; Mismatches 0; Gaps 0;

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2 AAAATCGATAAGTAATGTGAATTGCAGAAATTCAGTGAATCATCGAATCTTTGAAAGCAC 61

Db 211 AAATGCGATAAGTAATGTGAATTGCAGAA TTCAGTGAATCATCGAATCTTGAACGCAC 270

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QY      62 ATGGCGCCGCGCAGTATTCTGGCGGCATGCCGTTCGAGCGTCATT 108
        |||||
Db     271 ATTGGCGCCGCGCAGTATTCTGGCGGCATGCTGTTGAGCGTCATT 317
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RESULT 5  
US-09-481-293-32

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; APPLICANT: Beck, James
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: PCR-Based Detection of Rhizoctonia cerealis
; FILE REFERENCE: PB/5-31135PI
; CURRENT APPLICATION NUMBER: US/09/481,293
; CURRENT FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Fusarium culmorum
; US-09-481-293-32

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Query Match	33.5%	Score 107;	DB 4;	Length 504;
Best Local Similarity	100.0%;	Pred. No. 9.9e-50;		
Matches 107; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 2 AAAATGCCGATAGTAATGTCGAATTCAGGAATCATCGAATCTTTGAACGCAC 61  
|||||  
Db 214 AAAATGCCGATAGTAATGTCGAATTCAGGAATCATCGAATCTTTGAACGCAC 273

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QY      62 ATTGCGCCGCAGTATTCTGGCGGCATGCCCTGTTCAGCGCTATT   108
        |||||
Db     274 ATTTGCGCCGCAGTATTCTGGCGGCATGCTGTTCGAGCGCTATT   320
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RESULT 6  
PCT-US95-04712-82

1 APPLICANT: Ligon, James M  
2 APPLICANT: Beck, James J  
3 TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
4 TITLE OF INVENTION: Polymerase Chain Reaction  
5 NUMBER OF SEQUENCES: 86  
6 CORRESPONDENCE ADDRESS:  
7

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? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US95/04712
? FILING DATE:
?

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APPLICATION NUMBER: US 08/233,608  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Walish, Andrea C.  
REGISTRATION NUMBER: 34,988  
REFERENCE/DOCKET NUMBER: CGC 1739  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8666

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8666

```

TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 82:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 504 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
: OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
: OTHER INFORMATION: (fcuim.con)"
PCT-US95-04712-82

Query Match 33.5%; Score 107; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AAATGCGATTAAGTAATGTAATGCAGAAATTCAGTGAATCATGATCTTTGAAGCCAC 61
Db 211 AAATGCGATTAAGTAATGTAATGCAGAAATTCAGTGAATCATGATCTTTGAAGCCAC 270
Oy 62 ATTGCGCCCGCCAGTATCTTGCGCGGCAATGCTCTTGAGCGTCATT 108
Db 271 ATTGCGCCCGCCAGTATCTTGCGCGGCAATGCTCTTGAGCGTCATT 317

RESULT 7
US-08-867-480-84
: Sequence 84, Application US/08867480
: Patent No. 5814453
: GENERAL INFORMATION:
: APPLICANT: Beck, James J
: TITLE OF INVENTION: Detection of Fungal Pathogens Using the
: TITLE OF INVENTION: Polymerase Chain Reaction
: NUMBER OF SEQUENCES: 96
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: No. 5814453artis Corporation
: STREET: 520 White Plains Road
: CITY: Tarrytown
: STATE: NY
: COUNTRY: USA
: ZIP: 10591
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/867,480
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/722,187
: FILING DATE: 15-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8587
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 84:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 545 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:

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: ORGANISM: Fusarium moniliforme
: INDIVIDUAL ISOLATE: 4551
: IMMEDIATE SOURCE:
: CLONE: PCRPM01
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..30
: OTHER INFORMATION: /note= "3' end of small subunit
: OTHER INFORMATION: rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 31..178
: OTHER INFORMATION: /note= "ITS 1"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 179..335
: OTHER INFORMATION: /note= "5.8S rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 336..488
: OTHER INFORMATION: /note= "ITS 2"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 489..545
: OTHER INFORMATION: /note= "5' end of large subunit
: OTHER INFORMATION: rRNA gene"
US-08-887-480-84

Query Match          33.5%; Score 107; DB 1; Length 545;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  AAAATGCGATAGTAATGTGAATTGAGAAATTCAGTGAATCATGAACTTTGAACGCAC 61
Db       228  AAAATGCGATAGTAATGTGAATTGAGAAATTCAGTGAATCATGAACTTTGAACGCAC 287
QY      62  ATTGCGCGCCGCGCATTTCTGCGCGGCGATGCGCTTTCGAGCGTCATT 108
Db      288  ATTGCGCGCCGCGCATTTCTGCGCGGCGATGCGCTTTCGAGCGTCATT 334

RESULT 8
US-08-905-314A-21
: Sequence 21. Application US/08905314A
: Patent No. 5827695
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
: TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 5827695artis Corporation Patent Department
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 20779-2257
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/905,314A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC 1944
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689

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; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 545 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium moniliforme
; INDIVIDUAL ISOLATE: 4551
; IMMEDIATE SOURCE:
; CLONE: pCRFpoet756(3-1)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..330
; OTHER INFORMATION: /note="3' end of small subunit"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..178
; OTHER INFORMATION: /note="ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 179..335
; OTHER INFORMATION: /note="5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 336..488
; OTHER INFORMATION: /note="ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 489..545
; OTHER INFORMATION: /note="5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
; US-08-905-314A-21

Query Match 33.5%; Score 107; DB 1; Length 545;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAATGCGATAGTAATGTAATTCAGATTCAGATTCATCGAATCTTTGAACGCAC 61
Db 228 AAAATGCGATAGTAATGTAATTCAGATTCAGATTCATCGAATCTTTGAACGCAC 287
Qy 62 ATTGGCCCCCGCAGTATTCCTGGCGGCATGCTGTTCGAGCGTCATT 108
Db 288 ATTGGCCCCCGCAGTATTCCTGGCGGCATGCTGTTCGAGCGTCATT 334

RESULT 9
US-08-887-480-96
; Sequence 96, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; NUMBER OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium poae
; INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus
; INDIVIDUAL ISOLATE: sequence)
; IMMEDIATE SOURCE:
; CLONE: pCRFpoet427(1-2), pCRFpoet534(2-2), and
; CLONE: pCRFpoet756(3-1)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note="3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..180
; OTHER INFORMATION: /note="ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 181..337
; OTHER INFORMATION: /note="5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 338..489
; OTHER INFORMATION: /note="ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 490..546
; OTHER INFORMATION: /note="5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
; US-08-887-480-96

Query Match 33.5%; Score 107; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAATGCGATAGTAATGTAATTCAGATTCAGATTCATCGAATCTTTGAACGCAC 61
Db 230 AAAATGCGATAGTAATGTAATTCAGATTCAGATTCATCGAATCTTTGAACGCAC 289
Qy 62 ATTGGCCCCCGCAGTATTCCTGGCGGCATGCTGTTCGAGCGTCATT 108
Db 290 ATTGGCCCCCGCAGTATTCCTGGCGGCATGCTGTTCGAGCGTCATT 336

RESULT 10
US-08-905-314A-22
; Sequence 22, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; NUMBER OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Fusarium poae
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
IMMEDIATE SOURCE:
CLONE: pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and
pCRFpoaeT756(3-1)
FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..180
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 181..337
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 338..489
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-22

Query Match 33.5%; Score 107; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. 9.9e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAATGCGATTAAGTAATGTAATTCAGATTCAGTGAATCATCGAATCTTTGAAGCAC 61
DB 230 AAAATGCGATTAAGTAATGTAATTCAGATTCAGTGAATCATCGAATCTTTGAAGCAC 289

QY 62 ATTGCGCCCGCCAGATATTCTGCGCGGCATGCTGTTGAGCGTCATT 108
DB 290 ATTGCGCCCGCCAGATATTCTGCGCGGCATGCTGTTGAGCGTCATT 336

RESULT 11
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US-09-645-073-1
Sequence 1, Application US/09645073
Patent No. 6287800
GENERAL INFORMATION:
APPLICANT: Lee, May
APPLICANT: Galazzo, Jorge
TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7
FILE REFERENCE: L02-01NP
CURRENT APPLICATION NUMBER: US/09/645,073
CURRENT FILING DATE: 2000-08-25
PRIORITY APPLICATION NUMBER: US 60/151,770
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2293
TYPE: DNA
ORGANISM: Gibberella fujikuroi
US-09-645-073-1
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Query Match 33.5%; Score 107; DB 3; Length 2293;
Best Local Similarity 100.0%; Pred. No. 9.6e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 AAAATGCGATTAAGTAATGTAATTCAGATTCAGTGAATCATCGAATCTTTGAAGCAC 61
DB 1971 AAAATGCGATTAAGTAATGTAATTCAGATTCAGTGAATCATCGAATCTTTGAAGCAC 2030

QY 62 ATTGCGCCCGCCAGATATTCTGCGCGGCATGCTGTTGAGCGTCATT 108
DB 2031 ATTGCGCCCGCCAGATATTCTGCGCGGCATGCTGTTGAGCGTCATT 2077
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RESULT 12
US-08-652-127C-7
Sequence 7, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: George A. Seaby
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 531
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-7
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; GENERAL INFORMATION:
;
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT

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Db 28 AATTGAGTATCATCGAATCTTGAACGACATTCGCCCGCCAGTATTCGGCGG66CA 87

Qy 90 TGCCTGTTGAGCGTCATT 108  
|||  
Db 88 TGCCTGTTGAGCGTCATT 106  
|||

Search completed: October 1, 2004, 11:12:56  
Job time : 53.744 secs

us-10-046-955-6.01ig10.rnpb

16  
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seconds	22
minutes/sec	23
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[illegible]

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PRIOR FILLS

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      15, Appl
      16, Appl
      19, Appl
      e 1, Appl
      17, Appl

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e 6, Appl
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e 5, Appl
e 8, Appl
e 7, Appl
e 27, Appl
e 26, Appl
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16, Appl
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17, Appl

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41	C	
42		
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44		
45		

[illegible]

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Db      1  GAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCA 60
QY      61  CATTGCGCCCGCCGATATTCCTGGCGGGGATGCTCTGTTGAGCGTCATTAACACCTTGAAG 120
Db      61  CATTGCGCCCGCCGATATTCCTGGCGGGGATGCTCTGTTGAGCGTCATTAACACCTTGAAG 120
QY      121  CCCCCGGGAGCTGGGCTGGGGGATCGGCGGAAGCCCCCTGGCGGGGACAAACGCGTCCCCCA 180
Db      121  CCCCCGGGAGCTGGGCTGGGGGATCGGCGGAAGCCCCCTGGCGGGGACAAACGCGTCCCCCA 180
QY      181  AATACAGTGGGCGATCCCGCGCAGCTTCCATTTGGGTAAGCTTAACAACCTCGCAACTGGA 240
Db      181  AATACAGTGGGCGATCCCGCGCAGCTTCCATTTGGGTAAGCTTAACAACCTCGCAACTGGA 240
QY      241  GAGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db      241  GAGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY      301  GAATACCCCGCTGAACCTTAA 319
Db      301  GAATACCCCGCTGAACCTTAA 319

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## RESULT 2

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US-09-961-755A-6
; Sequence 6, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Gibberella zeae
US-09-961-755A-6

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Query Match      33.5%; Score 107; DB 10; Length 521;
Best Local Similarity 100.0%; Pred. No. 2,8e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCAC 61
Db      228  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCAC 287
QY      62  ATTGCGCCCGCCGATATTCCTGGCGGGGATGCTCTGTTGAGCGTCATT 108
Db      288  ATTGCGCCCGCCGATATTCCTGGCGGGGATGCTCTGTTGAGCGTCATT 334

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## RESULT 3

```

US-09-961-755A-5
; Sequence 5, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA

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; ORGANISM: Fusarium subglutinans
US-09-961-755A-5

```

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Query Match      33.5%; Score 107; DB 10; Length 522;
Best Local Similarity 100.0%; Pred. No. 2,8e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCAC 61
Db      228  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCAC 287
QY      62  ATTGCGCCCGCCGATATTCCTGGCGGGGATGCTCTGTTGAGCGTCATT 108
Db      288  ATTGCGCCCGCCGATATTCCTGGCGGGGATGCTCTGTTGAGCGTCATT 334

```

## RESULT 4

```

US-09-961-755A-8
; Sequence 8, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
US-09-961-755A-8

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Query Match      33.5%; Score 107; DB 10; Length 522;
Best Local Similarity 100.0%; Pred. No. 2,8e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      2  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCAC 61
Db      228  AAAATGCGATTAAGTAATGTAATTCGAGAAATTCAGTAATTCATCGAATCTTTGAAGCAC 287
QY      62  ATTGCGCCCGCCGATATTCCTGGCGGGGATGCTCTGTTGAGCGTCATT 108
Db      288  ATTGCGCCCGCCGATATTCCTGGCGGGGATGCTCTGTTGAGCGTCATT 334

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## RESULT 5

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US-09-961-755A-7
; Sequence 7, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

```

```

Query Match      33.5%; Score 107; DB 10; Length 534;
Best Local Similarity 100.0%; Pred. No. 2,8e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	2	AAATGCGAATATGAAATTTGAGAAATTCAGGAATATCGAATCTTTGAACGAC	61
Db	228	AAATGCGAATATGAAATTTGAGAAATTCAGGAATATCGAATCTTTGAACGAC	28
Qy	62	ATTGCGCGCGCGATATCTGGCGGCGAAGCCCTGTTGAGCGTCAAT	108
Db	288	ATTGCGCGCGCGAATATCTGGCGGCGAAGCCCTGTTGAGCGTCAAT	334

RESULT 6  
US-10-04

```

Sequence 7, application US/10046955
Publication No. US20030123600A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aldorevich, Lilliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIORITY APPLICATION NUMBER: US 09/423,233
PRIORITY FILING DATE: 2000-06-27
PRIORITY APPLICATION NUMBER: PCT/US98/08926
PRIORITY FILING DATE: 1998-05-01
PRIORITY APPLICATION NUMBER: US 60/045,400
PRIORITY FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 310
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-10-046-955-7

```

## RESULT 7

US-10-046-955-27  
Sequence 27, Application US/10046955  
Publication No. US20030123600A1  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America, as Represented by the  
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis  
APPLICANT: Control and Prevention  
APPLICANT: Morrison, Christine J.  
APPLICANT: Reiss, Errol  
APPLICANT: Aidorevich, Liliana  
APPLICANT: Choi, Jong Soo  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
TITLE OF INVENTION: Other Filamentous Fungi  
FILE REFERENCE: 6395-62064  
CURRENT APPLICATION NUMBER: US/10/046,955  
CURRENT FILING DATE: 2002-06-04  
PRIOR APPLICATION NUMBER: US 09/423,233  
PRIOR FILING DATE: 2000-06-27  
PRIOR APPLICATION NUMBER: PCT/US98/08926

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; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 27
; LENGTH: 343
; TYPE: DNA
; ORGANISM: Scedosporium apiospermum
US-10-046-955-27

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**RESULT 8**  
ME-10-04

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US-10-046-955-26
; Sequence 26, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; Secretary of the Department of Health and Human Services, Centers for Disease
; Control and Prevention
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reles, Errol
; APPLICANT: Aidorevich, Lilianna
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 344
; TYPE: DNA
; ORGANISM: Scedosporium apiospermum
US-10-046-955-26

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## RESULT 9

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US-09-961-663-14
; Sequence 14, Application US/09961663
; Patent No. US20020115084A1
; GENERAL INFORMATION:
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Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTATGATGATTCAGAAATTCAGTATCATCGAATCTTTGAACGCACA 62  
|||||  
Db 91 AATGCGATTAAGTATGATGATTCAGAAATTCAGTATCATCGAATCTTTGAACGCACA 150  
|||||

QY 63 TTGGCCCC 70  
|||||  
Db 151 TTGGCCCC 158

RESULT 13  
US-10-356-320-1  
; Sequence 1, Application US/10356320  
; Publication No. US20040009573A1  
; GENERAL INFORMATION:  
; APPLICANT: Strobel, Gary  
; APPLICANT: Ford, Eugene  
; APPLICANT: James, Harper K.  
; TITLE OF INVENTION: Pestalotiopsis Microsporia Isolates and Compounds Derived  
; TITLE OF INVENTION: Therefrom  
; FILE REFERENCE: A-72093 (470425-4)  
; CURRENT APPLICATION NUMBER: US/10/356,320  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US 60/352,254  
; PRIOR FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 466  
; TYPE: DNA  
; ORGANISM: Pestalotiopsis sp. NG12-30  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank Acc. No. US20040009573A1 AF377301  
; DATABASE ENTRY DATE: 2002-06-02  
; RELEVANT RESIDUES: (1)..(466)  
US-10-356-320-1

Query Match 21.3%; Score 68; DB 16; Length 466;  
Best Local Similarity 100.0%; Pred. No. 1.1e-28;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTATGATGATTCAGAAATTCAGTATCATCGAATCTTTGAACGCACA 62  
|||||  
Db 194 AATGCGATTAAGTATGATGATTCAGAAATTCAGTATCATCGAATCTTTGAACGCACA 253  
|||||

QY 63 TTGGCCCC 70  
|||||  
Db 254 TTGGCCCC 261

RESULT 14  
US-09-961-663-17  
; Sequence 17, Application US/09961663  
; Patent No. US20020115084A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnett, Jason  
; APPLICANT: Beck, James  
; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain  
; TITLE OF INVENTION: Reaction  
; FILE REFERENCE: PB/5-31382A  
; CURRENT APPLICATION NUMBER: US/09/961,663  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/211902  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 534  
; TYPE: DNA  
; ORGANISM: Mycosphaerella fijiensis  
US-09-961-663-17

Query Match 21.3%; Score 68; DB 9; Length 534;  
Best Local Similarity 100.0%; Pred. No. 1.1e-28;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTATGATGATTCAGAAATTCAGTATCATCGAATCTTTGAACGCACA 62  
|||||  
Db 222 AATGCGATTAAGTATGATGATTCAGAAATTCAGTATCATCGAATCTTTGAACGCACA 281  
|||||

QY 63 TTGGCCCC 70  
|||||  
Db 282 TTGGCCCC 289

RESULT 15  
US-09-961-663-18  
; Sequence 18, Application US/09961663  
; Patent No. US20020115084A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnett, Jason  
; APPLICANT: Beck, James  
; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain  
; TITLE OF INVENTION: Reaction  
; FILE REFERENCE: PB/5-31382A  
; CURRENT APPLICATION NUMBER: US/09/961,663  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/211902  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 540  
; TYPE: DNA  
; ORGANISM: Mycosphaerella musicola  
US-09-961-663-18

Query Match 21.3%; Score 68; DB 9; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.1e-28;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATTAAGTATGATGATTCAGAAATTCAGTATCATCGAATCTTTGAACGCACA 62  
|||||  
Db 231 AATGCGATTAAGTATGATGATTCAGAAATTCAGTATCATCGAATCTTTGAACGCACA 290  
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QY 63 TTGGCCCC 70  
|||||  
Db 291 TTGGCCCC 298

Search completed: October 1, 2004, 11:22:42  
Job time : 295.049 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 08:04:24 : Search time 2163.01 Seconds  
(without alignments)  
4404.059 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319  
Sequence: 1 gaaatgcgtaagtaatgc.....ggaataccgcgtgacttaa 319

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 10

Total number of hits satisfying chosen parameters: 5727071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
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19: em\_gss\_pln:\*  
20: em\_gss\_vrc:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	94	29.5	739	14	CF870552 tric024xb
3	94	29.5	755	14	CF870665 tric024xj
4	94	29.5	796	14	CB900742 tric024xb

5	94	29.5	808	14	CB900860	CB900860 tric024xj
6 <td>94</td> <td>29.5</td> <td>840</td> <td>14</td> <td>CB907036</td> <td>CB907036 tric081xc</td>	94	29.5	840	14	CB907036	CB907036 tric081xc
7 <td>71</td> <td>22.3</td> <td>169</td> <td>12</td> <td>BM870292</td> <td>BM870292 mgm009xu</td>	71	22.3	169	12	BM870292	BM870292 mgm009xu
8 <td>59</td> <td>18.5</td> <td>147</td> <td>14</td> <td>CF800463</td> <td>CF800463 ghrm31 6</td>	59	18.5	147	14	CF800463	CF800463 ghrm31 6
9 <td>59</td> <td>18.5</td> <td>190</td> <td>12</td> <td>BM347000</td> <td>BM347000 A1_3D11 h</td>	59	18.5	190	12	BM347000	BM347000 A1_3D11 h
10 <td>59</td> <td>18.5</td> <td>374</td> <td>14</td> <td>CB012091</td> <td>CB012091 LB08D01 m</td>	59	18.5	374	14	CB012091	CB012091 LB08D01 m
11 <td>57</td> <td>17.9</td> <td>359</td> <td>14</td> <td>CB011883</td> <td>CB011883 LB03N02 m</td>	57	17.9	359	14	CB011883	CB011883 LB03N02 m
12 <td>52</td> <td>16.3</td> <td>789</td> <td>28</td> <td>BZ782051</td> <td>BZ782051 A1SP1C26</td>	52	16.3	789	28	BZ782051	BZ782051 A1SP1C26
13 <td>52</td> <td>16.3</td> <td>791</td> <td>28</td> <td>BZ782064</td> <td>BZ782064 A1SP2C19</td>	52	16.3	791	28	BZ782064	BZ782064 A1SP2C19
14 <td>52</td> <td>16.3</td> <td>795</td> <td>28</td> <td>BZ782081</td> <td>BZ782081 A1SP2C4 M</td>	52	16.3	795	28	BZ782081	BZ782081 A1SP2C4 M
15 <td>42</td> <td>13.2</td> <td>840</td> <td>28</td> <td>BZ782314</td> <td>BZ782314 A2AP1C47</td>	42	13.2	840	28	BZ782314	BZ782314 A2AP1C47
16 <td>42</td> <td>13.2</td> <td>120</td> <td>9</td> <td>A1327878</td> <td>A1327878 j0g06a1.f</td>	42	13.2	120	9	A1327878	A1327878 j0g06a1.f
17 <td>42</td> <td>13.2</td> <td>141</td> <td>9</td> <td>A1327879</td> <td>A1327879 j0g06a1.f</td>	42	13.2	141	9	A1327879	A1327879 j0g06a1.f
18 <td>42</td> <td>13.2</td> <td>213</td> <td>9</td> <td>A1209736</td> <td>A1209736 ctg08a1.f</td>	42	13.2	213	9	A1209736	A1209736 ctg08a1.f
19 <td>42</td> <td>13.2</td> <td>318</td> <td>9</td> <td>A1213025</td> <td>A1213025 y6f01a1.f</td>	42	13.2	318	9	A1213025	A1213025 y6f01a1.f
20 <td>41</td> <td>12.9</td> <td>704</td> <td>13</td> <td>BQ751285</td> <td>BQ751285 EST631848</td>	41	12.9	704	13	BQ751285	BQ751285 EST631848
21 <td>41</td> <td>12.9</td> <td>725</td> <td>13</td> <td>BQ752001</td> <td>BQ752001 EST632564</td>	41	12.9	725	13	BQ752001	BQ752001 EST632564
22 <td>41</td> <td>12.9</td> <td>806</td> <td>13</td> <td>BQ751015</td> <td>BQ751015 EST631578</td>	41	12.9	806	13	BQ751015	BQ751015 EST631578
23 <td>41</td> <td>12.9</td> <td>806</td> <td>13</td> <td>BQ751484</td> <td>BQ751484 EST632047</td>	41	12.9	806	13	BQ751484	BQ751484 EST632047
24 <td>36</td> <td>11.3</td> <td>150</td> <td>12</td> <td>BM361006</td> <td>BM361006 A00318-F</td>	36	11.3	150	12	BM361006	BM361006 A00318-F
25 <td>36</td> <td>11.3</td> <td>150</td> <td>12</td> <td>BM361064</td> <td>BM361064 A00414-R</td>	36	11.3	150	12	BM361064	BM361064 A00414-R
26 <td>36</td> <td>11.3</td> <td>157</td> <td>12</td> <td>BM361387</td> <td>BM361387 A00705-R</td>	36	11.3	157	12	BM361387	BM361387 A00705-R
27 <td>36</td> <td>11.3</td> <td>157</td> <td>12</td> <td>BM361430</td> <td>BM361430 A00748-R</td>	36	11.3	157	12	BM361430	BM361430 A00748-R
28 <td>35</td> <td>11.0</td> <td>140</td> <td>12</td> <td>BP517053</td> <td>BP517053 BP517053</td>	35	11.0	140	12	BP517053	BP517053 BP517053
29 <td>35</td> <td>11.0</td> <td>146</td> <td>12</td> <td>BP508427</td> <td>BP508427 BP508427</td>	35	11.0	146	12	BP508427	BP508427 BP508427
30 <td>35</td> <td>11.0</td> <td>214</td> <td>10</td> <td>BP251183</td> <td>BP251183 EST418443</td>	35	11.0	214	10	BP251183	BP251183 EST418443
31 <td>35</td> <td>11.0</td> <td>268</td> <td>14</td> <td>CF780131</td> <td>CF780131 tad04c11.</td>	35	11.0	268	14	CF780131	CF780131 tad04c11.
32 <td>35</td> <td>11.0</td> <td>298</td> <td>14</td> <td>CA303199</td> <td>CA303199 ta004e02.</td>	35	11.0	298	14	CA303199	CA303199 ta004e02.
33 <td>35</td> <td>11.0</td> <td>320</td> <td>28</td> <td>AZ925653</td> <td>AZ925653 4910.e234</td>	35	11.0	320	28	AZ925653	AZ925653 4910.e234
34 <td>35</td> <td>11.0</td> <td>332</td> <td>14</td> <td>CA301641</td> <td>CA301641 ta006a11.</td>	35	11.0	332	14	CA301641	CA301641 ta006a11.
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36 <td>35</td> <td>11.0</td> <td>360</td> <td>28</td> <td>AZ923094</td> <td>AZ923094 4908.ge87</td>	35	11.0	360	28	AZ923094	AZ923094 4908.ge87
37 <td>35</td> <td>11.0</td> <td>370</td> <td>14</td> <td>CD566941</td> <td>CD566941 tgc12f11.</td>	35	11.0	370	14	CD566941	CD566941 tgc12f11.
38 <td>35</td> <td>11.0</td> <td>376</td> <td>14</td> <td>CD567121</td> <td>CD567121 tdb47a02.</td>	35	11.0	376	14	CD567121	CD567121 tdb47a02.
39 <td>35</td> <td>11.0</td> <td>384</td> <td>28</td> <td>BZ304161</td> <td>BZ304161 KD2793.q1</td>	35	11.0	384	28	BZ304161	BZ304161 KD2793.q1
40 <td>40</td> <td>11.0</td> <td>392</td> <td>28</td> <td>AZ923588</td> <td>AZ923588 4908.gf22</td>	40	11.0	392	28	AZ923588	AZ923588 4908.gf22
41 <td>35</td> <td>11.0</td> <td>407</td> <td>28</td> <td>AZ923857</td> <td>AZ923857 4908.gf22</td>	35	11.0	407	28	AZ923857	AZ923857 4908.gf22
42 <td>35</td> <td>11.0</td> <td>414</td> <td>14</td> <td>CA301545</td> <td>CA301545 ta008b08.</td>	35	11.0	414	14	CA301545	CA301545 ta008b08.
43 <td>35</td> <td>11.0</td> <td>419</td> <td>14</td> <td>CA301933</td> <td>CA301933 ta011a07.</td>	35	11.0	419	14	CA301933	CA301933 ta011a07.
44 <td>35</td> <td>11.0</td> <td>420</td> <td>14</td> <td>CA303244</td> <td>CA303244 ta005c12.</td>	35	11.0	420	14	CA303244	CA303244 ta005c12.
45 <td>35</td> <td>11.0</td> <td>422</td> <td>14</td> <td>CA302907</td> <td>CA302907 ta004b10.</td>	35	11.0	422	14	CA302907	CA302907 ta004b10.

## ALIGNMENTS

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF880267 735 bp mRNA linear EST 31-OCT-2003  
tric081xc18.b2.T.reesei mycelial culture, Version 6 October 2003  
Hypocrea jecorina CDNA clone tric081xc18, mRNA sequence.  
CF880267  
CF880267.1 GI:38134949  
EST.  
Hypocrea jecorina (anamorph: Trichoderma reesei)  
Hypocrea jecorina  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 735)  
Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D.,  
Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and  
Dean,R.A.  
Analysis of the protein processing and secretion pathways in a  
Trichoderma reesei EST dataset  
Unpublished (2003)  
Contact: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: Tr-F1 primer.

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1. 735  
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Hypocrea jecorina cDNA clone tric024xb14, mRNA sequence.  
ACCESSION  
CF870552 GI:38125234  
VERSION  
CF870552.1 GI:38125234  
SOURCE  
EST.  
Hypocrea jecorina (anamorph: Trichoderma reesei)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
REFERENCE  
1 (bases 1 to 739)  
Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D., Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and Dean,R.A.  
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset  
JOURNAL  
Unpublished (2003)  
CONTACT: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph\_dean@ncsu.edu  
Seq primer: LT-F1 primer.  
LOCATION/Qualifiers  
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VERSION  
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
REFERENCE  
1 (bases 1 to 755)  
Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D., Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and Dean,R.A.  
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset  
JOURNAL  
Unpublished (2003)  
CONTACT: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph\_dean@ncsu.edu  
Seq primer: LT-F1 primer.  
LOCATION/Qualifiers  
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RESULT 4  
CB900742 796 bp mRNA linear EST 02-JUL-2003  
LOCUS  
DEFINITION  
tric024xb14.T.reesei mycelial culture, Version 3 april Hypocrea jecorina cDNA clone tric024xb14, mRNA sequence.  
ACCESSION  
CB900742 GI:30115400  
VERSION  
CB900742.1 GI:30115400  
KEYWORDS  
EST.

SOURCE  
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)  
Hypocrea jecorina  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE  
AUTHORS 1 (bases 1 to 796)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE  
JOURNAL MEDLINE 22803314  
PUBMED 12788920  
COMMENT Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
Seq primer: LT-F1 primer.

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and Nitrogen sources and concentrations."

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Qy 63 TTGGCCCGCCAGTATTCGGCGGCATGCTGT 96  
Db 160 TTGGCCCGCCAGTATTCGGCGGCATGCTGT 193

RESULT 5  
CB900860 808 bp mRNA linear EST 02-JUL-2003  
LOCUS tric024x104 T. reesei mycelial culture, Version 3 april Hypocrea  
DEFINITION jecorina cDNA clone tric024x104, mRNA sequence.  
ACCESSION CB900860  
VERSION CB900860.1 GI:30115518  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 808)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE  
JOURNAL MEDLINE 22803314  
PUBMED 12788920  
COMMENT Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA

REFERENCE  
AUTHORS 1 (bases 1 to 808)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE  
JOURNAL MEDLINE 22803314  
PUBMED 12788920  
COMMENT Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA

FEATURES  
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culture grown from 24 hrs to 6 days with varying Carbon  
and Nitrogen sources and concentrations."

ORIGIN

Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
Seq primer: LT-F1 primer.

FEATURES  
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ORIGIN  
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Qy 3 AAATGCGATAGTATGATGATTCGAGATTCAGTATCGATCTTTGAACGCACA 62  
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Qy 63 TTGGCCCGCCAGTATTCGGCGGCATGCTGT 96  
Db 156 TTGGCCCGCCAGTATTCGGCGGCATGCTGT 189

RESULT 6  
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LOCUS tric081xc18 T. reesei mycelial culture, Version 3 april Hypocrea  
DEFINITION jecorina cDNA clone tric081xc18, mRNA sequence.  
ACCESSION CB907036  
VERSION CB907036.1 GI:30121694  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 840)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

TITLE  
JOURNAL MEDLINE 22803314  
PUBMED 12788920  
COMMENT Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
Seq primer: LT-F1 primer.

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and Nitrogen sources and concentrations."

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Best Local Similarity 100.0%; Pred. No. 1.2e-38;  
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DB 63 TTGGCGCCGCCAGTATTCGCGCGCATGCTGT 96  
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RESULT 7  
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LOCUS mgn009xj23f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgn009xj23 5', mRNA sequence.  
ACCESSION BM870292 GI:30404719  
VERSION BM870292.2 GI:30404719  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
REFERENCE 1 (bases 1 to 169)  
AUTHORS Eboile,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatnagar,K. and Dean,R.A.  
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
JOURNAL Unpublished (2002)  
COMMENT On Mar 7, 2002 this sequence version replaced gi:19237974.  
CONTACT: Eboile DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-eboile@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person; Best nr hit (April, 22, 2003) gb|AA179278.1| unknown  
|Saccharomyces cerevisiae| 79.1e-14  
PCR Primers  
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BACKWARD: T7 primer  
Plate: mgn009 row: J column: 23  
Seq primer: T3.

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predominantly 5' reads. T7 primer on XhoI side of insert.  
Nitrogen starvation library. Cells were inoculated into  
minimal medium and grown for two days with shaking (150  
rpm) at room temperature. Culture was harvested, blended,  
inoculated into minimal medium as above for 24 h. Cells  
were harvested, washed with water and inoculated into  
minimal medium base lacking nitrogen source for 6 h.  
Sequences were processed by one of two methods. Where a  
full-length alignment to the M. grisea genome sequence was  
available, the EST sequence was trimmed according to the  
alignment, otherwise sequence quality was assessed using  
phredPhrap version 991019 and trimmed according to phd  
files (0.05) and for vector seqs."

ORIGIN  
Query Match 22.3%; Score 71; DB 12; Length 169;  
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QY 3 AATGCGATGAATGTAATTCGAGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 62  
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DB 63 TTGGCGCCGCC 73  
99 TTGGCGCCGCC 109

RESULT 8  
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DEFINITION commune cDNA 5', mRNA sequence.  
ACCESSION CF800463 GI:37818860  
VERSION CF800463.1 GI:37818860  
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SOURCE Schizophyllum commune  
ORGANISM Schizophyllum commune  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
Agaricales; Schizophyllum commune  
REFERENCE 1 (bases 1 to 147)  
AUTHORS Foster,K.D., Belsler,A.E., Buchanan,S., Huck,M., Devoll,T.,  
Hittinger,C.T., Green,A., Lilly,W.W. and Gachman,A.C.  
TITLE Expressed sequence tags from Schizophyllum commune nitrogen-replete  
and nitrogen-limited libraries, 2003  
JOURNAL Unpublished (2003)  
COMMENT Contact: Gachman AC  
Biology Department  
Southeast MO State University  
1 University Plaza, Cape Girardeau, MO 63701, USA  
Tel: 5736512361  
Fax: 5739866433  
Email: agachman@semo.edu  
Seq primer: T3  
POLYA=Yes.

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/db\_xref="taxon:5334"  
/clone\_lib="6HR Nitrogen-limited Schizophyllum library"  
/issue\_type="mycelium"  
/note="Vector: lambda Zap; Site 1: EcoRI; Site 2: XhoI;  
4-day-old mycelia of Schizophyllum commune were  
transferred from minimal (nitrogen-replete) medium to  
low-nitrogen medium. RNA was extracted six hours after  
transfer and cDNAs prepared."

ORIGIN  
Query Match 18.5%; Score 59; DB 14; Length 147;  
Best Local Similarity 100.0%; Pred. No. 3.4e-20;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATGAATGTAATTCGAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC 61  
32 AATGCGATGAATGTAATTCGAGAAATTCAGTGAATCATCGAATCTTTGAACGCAC 90

RESULT 9  
BM347000 190 bp mRNA linear EST 07-JUN-2002  
LOCUS A1.3D11 Heterobasidion annosum infection stage cDNA library  
DEFINITION Heterobasidion annosum cDNA clone A1.3D11 similar to putative  
ribosomal RNA protein [Arabidopsis thaliana], mRNA sequence.  
ACCESSION BM347000

VERSION BM347000.1 GI:18083915  
KEYWORDS EST.  
SOURCE Heterobasidion annosum  
ORGANISM Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Schizophyllaceae; Heterobasidion  
REFERENCE 1 (bases 1 to 190)  
AUTHORS Karlsson,M., Olson,A. and Stenlid,J.  
TITLE Expressed sequences from the basidiomycetous tree pathogen Heterobasidion annosum during early infection of Scots pine  
JOURNAL Fungal Genet. Biol. 39 (1), 51-59 (2003)  
MEDLINE 22627971  
PUBMED 12742063  
COMMENT Contact: Magnus Karlsson  
Forest Mycology & Pathology  
Swedish University of Agricultural Sciences  
Box 7026, SE-750 07, Uppsala, Sweden  
Tel: +46 18 671806  
Fax: +46 18 673599  
Email: Magnus.Karlsson@mykopat.slu.se  
Seq primer: 54#8217.TripLx2 MK Seq.  
Location/Qualifiers  
1. 190  
/organism="Heterobasidion annosum"  
/mol\_type="mRNA"  
/strain="TC 32-1 (P)"  
/db\_xref="taxon:13563"  
/clone="A1\_3D11"  
/tissue\_type="Mycelia"  
/dev\_stage="Mycelia after 6 h & 72 h of challenge with pine seedling roots"  
/clone\_lib="Heterobasidion annosum infection stage cDNA library"  
/note="Vector: Lambda; Heterobasidion annosum mycelia were challenged by pinus sylvestris seedling roots for 6 h & 72 h and the cDNA library was made from a mix of the two stages"

ORIGIN  
Query Match 18.5%; Score 59; DB 12; Length 190;  
Best Local Similarity 100.0%; Pred. No. 3.6e-20;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAATCGAATAGTATGTAATTCGAGATTCAGTCAATCATGAACTTTGAACGCAC 61  
Db 52 AAATCGAATAGTATGTAATTCGAGATTCAGTCAATCATGAACTTTGAACGCAC 110

RESULT 10  
LOCUS CB012091 374 bp mRNA linear EST 30-JUN-2003  
DEFINITION Lb08D01 mycelium of Laccaria bicolor grown for three weeks Laccaria bicolor cDNA 5', mRNA sequence.  
ACCESSION CB012091  
VERSION CB012091.1 GI:32334717  
KEYWORDS EST.  
SOURCE Laccaria bicolor  
ORGANISM Laccaria bicolor  
REFERENCE Agarricales; Tricholomataceae; Laccaria.  
AUTHORS 1 (bases 1 to 374)  
Peter,M., Courty,P.-E., Kohler,A., Delaruelle,C., Martin,D., Tagu,D., Frey-Klett,P., Duplessis,S., Chalot,M., Podila,G. and Martin,P.  
TITLE Analysis of expressed sequence tags from the ectomycorrhizal basidiomycetes Laccaria bicolor and Pisolithus microcarpus  
JOURNAL New Phytol. 159 (1), 117-129 (2003)  
COMMENT Contact: Martin PM  
Equipe de Microbiologie Forestiere  
Institut National de la Recherche Agronomique  
Centre INRA de Nancy, 54280 Champenoux, France  
Tel: +33 383 39 40 80

Fax: +33 383 39 40 69  
Email: fmartin@nancy.inra.fr  
Insert length: 374 Std Error: 0.00  
Seq primer: Fornat 5' AAGCGCCCATGTTGTTGTAACC.  
Location/Qualifiers  
1. 374  
/organism="Laccaria bicolor"  
/mol\_type="mRNA"  
/cultiivar="S238N"  
/db\_xref="taxon:29883"  
/dev\_stage="three-weeks-old"  
/clone\_lib="mycelium of Laccaria bicolor grown for three weeks"  
/note="Organ: free-living vegetative mycelium; Vector: pTriplEx2; Laccaria bicolor Maire Orton; cDNA library from mycelium of Laccaria bicolor grown for three weeks on agar-plates containing high sugar (20 g/l glucose, 5 g/l maltose) Pachlewski medium. The cDNA library was constructed from 1 ug of total RNA using the SMART cDNA synthesis kit (Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. The resulting cDNA was packed into lambda phages using the Gigapack III Gold packaging kit (Stratagene, La Jolla, CA). The pTriplEx2 phagemid clones in Escherichia coli were obtained by using the mass in vivo excision protocol according to the manufacturer's instructions (Clontech)."

ORIGIN  
Query Match 18.5%; Score 59; DB 14; Length 374;  
Best Local Similarity 100.0%; Pred. No. 4e-20;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAATCGAATAGTATGTAATTCGAGATTCAGTCAATCATGAACTTTGAACGCAC 61  
Db 229 AAATCGAATAGTATGTAATTCGAGATTCAGTCAATCATGAACTTTGAACGCAC 287

RESULT 11  
LOCUS CB011883 359 bp mRNA linear EST 30-JUN-2003  
DEFINITION Lb03N02 mycelium of Laccaria bicolor grown for three weeks Laccaria bicolor cDNA 5', mRNA sequence.  
ACCESSION CB011883  
VERSION CB011883.1 GI:32334509  
KEYWORDS EST.  
SOURCE Laccaria bicolor  
ORGANISM Laccaria bicolor  
REFERENCE Agarricales; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Eukaryota; Fungi; Tricholomataceae; Laccaria.  
AUTHORS 1 (bases 1 to 359)  
Peter,M., Courty,P.-E., Kohler,A., Delaruelle,C., Martin,D., Tagu,D., Frey-Klett,P., Duplessis,S., Chalot,M., Podila,G. and Martin,P.  
TITLE Analysis of expressed sequence tags from the ectomycorrhizal basidiomycetes Laccaria bicolor and Pisolithus microcarpus  
JOURNAL New Phytol. 159 (1), 117-129 (2003)  
COMMENT Contact: Martin PM  
Equipe de Microbiologie Forestiere  
Institut National de la Recherche Agronomique  
Centre INRA de Nancy, 54280 Champenoux, France  
Tel: +33 383 39 40 80  
Fax: +33 383 39 40 69  
Email: fmartin@nancy.inra.fr  
Insert length: 359 Std Error: 0.00  
Seq primer: Fornat 5' AAGCGCCCATGTTGTTGTAACC.  
Location/Qualifiers  
1. 359  
/organism="Laccaria bicolor"  
/mol\_type="mRNA"  
/cultiivar="S238N"  
/db\_xref="taxon:29883"  
/dev\_stage="three-weeks-old"  
/clone\_lib="mycelium of Laccaria bicolor grown for three weeks"

weeks"  
/note="Organ: free-living vegetative mycelium; Vector: pTriplEx2; Laccaria bicolor Maire Otonari; cDNA library from mycelium of Laccaria bicolor grown for three weeks on agar-plates containing high sugar (20 g/l glucose, 5 g/l maltose) Pachlewski medium. The cDNA library was constructed from 1 ug of total RNA using the SMART cDNA synthesis kit (Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. The resulting cDNA was packed into lambda phages using the Gigapack III Gold packaging kit (Stratagene, La Jolla, CA). The pTriplEx2 phagemid clones in Escherichia coli were obtained by using the mass in vivo excision protocol according to the manufacturer's instructions (Clontech)."

## ORIGIN

Query Match 17.9%; Score 57; DB 14; Length 359;  
Best Local Similarity 100.0%; Pred. No. 4.6e-19;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATGCGATATGATATGATGCAATTCAGTCAATCATGCAATCTTTGAACG 59  
|||||  
Db 303 AATGCGATATGATATGATGCAATTCAGTCAATCATGCAATCTTTGAACG 359

RESULT 12 789 bp DNA linear GSS 14-MAR-2003  
LOCUS BZ782051  
DEFINITION AISP2C6 Microbotryum mating type chromosome and autosome random fragments Microbotryum violaceum genomic clone AISP2C6, genomic survey sequence.

ACCESSION BZ782051 GI:28960826  
VERSION BZ782051.1 GI:28960826  
KEYWORDS GSS.  
SOURCE Microbotryum violaceum  
ORGANISM Microbotryum violaceum

REFERENCE 1 (bases 1 to 789)  
AUTHORS Hood, M.E., Antonovics, J. and Koskella, B.  
TITLE Shared forces of sex chromosome evolution in haploids and diploids  
JOURNAL Unpublished (2003)  
COMMENT Contact: Hood ME  
Department of Biology  
University of Virginia  
Gilmer Hall, Charlottesville, VA 22903, USA  
Tel: 434 243 5077  
Fax: 434 982 5626  
Email: michael.hood@virginia.edu  
random fragment isolated from A1 mating type chromosome; BLASTx  
similarity to Transcript Antisense to Ribosomal RNA and BLASTn  
similarity to nuclear ribosomal RNA  
Class: shotgun  
High quality sequence stop: 789.

FEATURES  
source  
1. 789  
Location/Qualifiers  
/organism="Microbotryum violaceum"  
/mol\_type="genomic DNA"  
/strain="100-15lamole.1"  
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/clone="AISP2C6"  
/cell\_type="sporidia"  
/dev\_stage="post-meiotic"  
/clone\_lib="Microbotryum mating type chromosome and autosome random fragments"  
/note="Field Collected; specific host-Silene latifolia; country=Italy; common name= another smut; synonym=Ustilago violacea; Chromosome-specific bands were gel-isolated from electrophoretic karyotypes, triple digested (RsaI, MscI, and DraI), size-fractionated by electrophoresis for fragments between 200 to 1000 bp, cloned, and sequenced."

## FEATURES

source  
1. 789  
Location/Qualifiers  
/organism="Microbotryum violaceum"  
/mol\_type="genomic DNA"  
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/clone\_lib="Microbotryum mating type chromosome and autosome random fragments"  
/note="Field Collected; specific host-Silene latifolia; country=Italy; common name= another smut; synonym=Ustilago violacea; Chromosome-specific bands were gel-isolated from electrophoretic karyotypes, triple digested (RsaI, MscI, and DraI), size-fractionated by electrophoresis for fragments between 200 to 1000 bp, cloned, and sequenced."

## ORIGIN

Query Match 16.3%; Score 52; DB 28; Length 791;  
Best Local Similarity 100.0%; Pred. No. 2.4e-16;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GATTAATATGGAATTCGAAATTCAGTCAATCATGCAATCTTTGAACGCA 60  
|||||  
Db 93 GATTAATATGGAATTCGAAATTCAGTCAATCATGCAATCTTTGAACGCA 144

RESULT 13 791 bp DNA linear GSS 14-MAR-2003  
LOCUS BZ782064  
DEFINITION AISP2C19 Microbotryum mating type chromosome and autosome random fragments Microbotryum violaceum genomic clone AISP2C19, genomic survey sequence.

ACCESSION BZ782064 GI:28960852  
VERSION BZ782064.1 GI:28960852  
KEYWORDS GSS.  
SOURCE Microbotryum violaceum  
ORGANISM Microbotryum violaceum

REFERENCE 1 (bases 1 to 791)  
AUTHORS Hood, M.E., Antonovics, J. and Koskella, B.  
TITLE Shared forces of sex chromosome evolution in haploids and diploids  
JOURNAL Unpublished (2003)  
COMMENT Contact: Hood ME  
Department of Biology  
University of Virginia  
Gilmer Hall, Charlottesville, VA 22903, USA  
Tel: 434 243 5077  
Fax: 434 982 5626  
Email: michael.hood@virginia.edu  
random fragment isolated from A1 mating type chromosome; BLASTx  
similarity to Transcript Antisense to Ribosomal RNA and BLASTn  
similarity to nuclear ribosomal RNA  
Class: shotgun  
High quality sequence stop: 791.

FEATURES  
source  
1. 791  
Location/Qualifiers  
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/clone="AISP2C19"  
/cell\_type="sporidia"  
/dev\_stage="post-meiotic"  
/clone\_lib="Microbotryum mating type chromosome and autosome random fragments"  
/note="Field Collected; specific host-Silene latifolia; country=Italy; common name= another smut; synonym=Ustilago violacea; Chromosome-specific bands were gel-isolated from electrophoretic karyotypes, triple digested (RsaI, MscI, and DraI), size-fractionated by electrophoresis for fragments between 200 to 1000 bp, cloned, and sequenced."

## FEATURES

source  
1. 791  
Location/Qualifiers  
/organism="Microbotryum violaceum"  
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/clone\_lib="Microbotryum mating type chromosome and autosome random fragments"  
/note="Field Collected; specific host-Silene latifolia; country=Italy; common name= another smut; synonym=Ustilago violacea; Chromosome-specific bands were gel-isolated from electrophoretic karyotypes, triple digested (RsaI, MscI, and DraI), size-fractionated by electrophoresis for fragments between 200 to 1000 bp, cloned, and sequenced."

## ORIGIN

source  
1. 791  
Location/Qualifiers  
/organism="Microbotryum violaceum"  
/mol\_type="genomic DNA"  
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/note="Field Collected; specific host-Silene latifolia; country=Italy; common name= another smut; synonym=Ustilago violacea; Chromosome-specific bands were gel-isolated from electrophoretic karyotypes, triple digested (RsaI, MscI, and DraI), size-fractionated by electrophoresis for fragments between 200 to 1000 bp, cloned, and sequenced."

Query Match 16.3%; Score 52; DB 28; Length 791;  
Best Local Similarity 100.0%; Pred. No. 2.4e-16;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GATTAATATGGAATTCGAAATTCAGTCAATCATGCAATCTTTGAACGCA 60  
|||||  
Db 695 GATTAATATGGAATTCGAAATTCAGTCAATCATGCAATCTTTGAACGCA 644

RESULT 14 795 bp DNA linear GSS 14-MAR-2003  
LOCUS BZ782081  
DEFINITION AISP2C4 Microbotryum mating type chromosome and autosome random fragments Microbotryum violaceum genomic clone AISP2C4, genomic

survey sequence.

ACCESSION BZ782081 GI:28960886  
 VERSION BZ782081.1  
 KEYWORDS GSS  
 SOURCE Microbotryum violaceum  
 ORGANISM Microbotryum violaceum  
 Eukaryota; Fungi; Basidiomycota; Urediniomycetes;  
 Microbotryomycetidae; Microbotryales; Microbotryaceae;  
 Microbotryum

REFERENCE 1 (bases 1 to 795)  
 AUTHORS Hood,M.E., Antonovics,J. and Koskella,B.  
 TITLE Shared forces of sex chromosome evolution in haploids and diploids  
 JOURNAL Unpublished (2003)  
 COMMENT Department of Biology  
 University of Virginia  
 Gilmer Hall, Charlottesville, VA 22903, USA  
 Tel: 434 243 5077  
 Fax: 434 982 5626  
 Email: michael.hood@virginia.edu  
 random fragment isolated from Al mating type chromosome; BLASTx  
 similarity to Transcript Antisense to Ribosomal RNA and BLASTn  
 similarity to nuclear ribosomal RNA  
 Class: shotgun  
 High quality sequence stop: 795.

FEATURES  
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 /cell\_type="sporidia"  
 /dev\_stage="post-meiotic"  
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 violacea; Chromosome-specific bands were gel-isolated from  
 electrophoretic karyotypes, triple digested (Real, MscI,  
 and DraI), size-fractionated by electrophoresis for  
 fragments between 200 to 1000 bp, cloned, and sequenced."

ORIGIN

Query Match 16.3%; Score 52; DB 28; Length 795;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;  
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GATAAGTATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 99 GATAAGTATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCA 150

RESULT 15  
 BZ782314/c 840 bp DNA linear GSS 14-MAR-2003  
 LOCUS A2AP1C47 Microbotryum mating type chromosome and autosome random  
 DEFINITION fragments Microbotryum violaceum genomic clone A2AP1C47, genomic  
 survey sequence.  
 BZ782314  
 BZ782314.1 GI:28961356  
 GSS  
 SOURCE Microbotryum violaceum  
 ORGANISM Microbotryum violaceum  
 Eukaryota; Fungi; Basidiomycota; Urediniomycetes;  
 Microbotryomycetidae; Microbotryales; Microbotryaceae;  
 Microbotryum

REFERENCE 1 (bases 1 to 840)  
 AUTHORS Hood,M.E., Antonovics,J. and Koskella,B.  
 TITLE Shared forces of sex chromosome evolution in haploids and diploids  
 JOURNAL Unpublished (2003)  
 COMMENT Department of Biology  
 University of Virginia  
 Gilmer Hall, Charlottesville, VA 22903, USA  
 Tel: 434 243 5077  
 Fax: 434 982 5626  
 Email: michael.hood@virginia.edu  
 random fragment isolated from autosomes; BLASTx similarity to  
 Transcript Antisense to Ribosomal RNA and BLASTn similarity to  
 nuclear ribosomal RNA  
 Class: shotgun  
 High quality sequence stop: 840.

FEATURES  
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 /dev\_stage="post-meiotic"  
 /clone\_lib="Microbotryum mating type chromosome and  
 autosome random fragments"  
 /note="Field Collected; specific host=Silene latifolia;  
 country=Italy; common name= another smut; synonym=Ustilago  
 violacea; Chromosome-specific bands were gel-isolated from  
 electrophoretic karyotypes, triple digested (Real, MscI,  
 and DraI), size-fractionated by electrophoresis for  
 fragments between 200 to 1000 bp, cloned, and sequenced."

ORIGIN

Query Match 16.3%; Score 52; DB 28; Length 840;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GATAAGTATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 742 GATAAGTATGTGAATTCAGAAATTCAGTGAATCATCGAATCTTTGAACGCA 691

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 Job time : 2167.01 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 23:11:57 ; Search time 549.986 Seconds  
(without alignments)  
2394.501 Million cell updates/sec

Title: US-10-046-955-7  
Perfect score: 310  
Sequence: 1 aaatgcgataatgatactgtga.....ggataccgcgtgaactaa 310

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373663 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

1: Geneseq19908:.\*  
2: Geneseq19908:.\*  
3: Geneseq20005:.\*  
4: Geneseq2001as:.\*  
5: Geneseq2001bs:.\*  
6: Geneseq2002s:.\*  
7: Geneseq2003as:.\*  
8: Geneseq2003bs:.\*  
9: Geneseq2003cs:.\*  
10: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310	100.0	310	2	AAV70851 Internal
2	306.8	99.0	2293	4	AA516211 Fungus ge
3	302.8	97.7	534	7	ACC50001 Internal
4	265.8	85.7	502	3	AAA61893 Fungarium
5	249.8	80.6	561	2	AAV59009 F. avenac
6	248.6	80.2	659	6	ABV78724 C. sinens
7	240.2	77.5	319	2	AAV70850 Internal
8	194.4	62.7	522	7	ACC49999 Internal
9	194.4	62.7	522	7	ACC50002 Internal
10	193.8	62.5	661	6	ABV78721 C. sinens
11	193.4	62.4	582	2	AAV65100 T. harzia
12	187.6	60.5	546	2	AAV62596 Fungarium
13	187.6	60.5	546	2	AAV59007 F. poae 1
14	186.6	60.2	504	2	AAV62591 Fungarium
15	186.6	60.2	504	2	AAV62591 Fungarium
16	186.6	60.2	504	2	AAV59028 F. culmor
17	186.6	60.2	504	2	AAV59011 Phomopsis
18	185	59.7	545	2	AAV62593 Fungarium
19	183.2	59.1	545	2	AAV59030 F. monili
20	180.4	58.2	503	2	AAV05401 Fungarium
21	180.4	58.2	503	2	AAV62592 Fungarium
22	180.4	58.2	503	2	AAV59029 F. gramin
23	180.4	58.2	503	2	AAV59029 F. gramin

24	179.2	57.8	521	7	ACC50000 Internal
25	175	56.5	569	2	AAV65101 T. harzia
26	174.2	56.2	504	2	AAV62596 Fungarium
27	168.2	54.3	569	2	AAV65099 T. harzia
28	166.2	53.6	545	2	AAV05403 Microdoch
29	163.8	52.8	608	2	AAV90110 Phomopsis
30	157.8	50.9	537	3	AAZ91725 Rosellini
31	151	48.7	632	6	ABV78709 C. sinens
32	151	48.7	632	6	ABV78706 C. sinens
33	151	48.7	664	6	ABV78703 C. sinens
34	151	48.7	667	6	ABV78712 C. sinens
35	149.4	48.2	615	5	AAV76260 Cordyceps
36	149.4	48.2	625	6	ABV78718 C. sinens
37	149.4	48.2	659	6	ABV78715 C. sinens
38	147.8	47.7	549	3	AAZ91723 Rosellini
39	147.8	47.7	549	3	AAZ91724 Rosellini
40	141.8	45.7	382	3	AAA72783 S. 88 rRNA
41	139	44.8	605	2	AAV90108 Eutypella
42	137.6	44.4	537	6	ABA01153 Deuteromy
43	136.6	43.9	652	7	ABZ20765 Muscodor
44	136	43.9	365	2	AAV70847 Sequence
45	136	43.9	587	2	AAV43269 Sequence

## ALIGNMENTS

RESULT 1  
AAV70851  
ID AAV70851 standard; DNA; 310 BP.  
AC AAV70851;  
AC 17-OCT-2003 (revised)  
DT 26-FEB-1999 (first entry)  
DT Internal transcribed spacer 2 (ITS2) and adjacent regions.  
XX  
XX  
XX Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger;  
KW A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;  
KW M. racemosus; M. plumbeus; M. indicus; A. fumigatus;  
KW M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus;  
KW R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;  
KW Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;  
KW Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.  
XX  
XX  
XX Gibberella fujikuroi.  
OS  
OS  
OS W09850584-A2.  
XX  
XX  
XX 12-NOV-1998.  
PD  
XX 01-MAY-1998; 98WO-US008926.  
PF  
XX 02-MAY-1997; 97US-0045400P.  
PR  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX Morrison CJ, Reiss B, Aldorevich L, Choi JS;  
PI WPI; 1999-034737/03.  
XX  
XX New nucleic acid probes for filamentous fungi - for detecting e.g.  
PT Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,  
PT Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix  
PT species.  
XX  
XX Claim 1; Page 12; 45pp; English.  
PS  
XX The present sequence represents an internal transcribed spacer 2 (ITS2)  
XX and adjacent regions. Probes can be derived from the present sequence  
XX which are species-specific. The specification also describes ITS2  
XX sequence-derived probes for identifying a species selected from

CC Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,  
 CC Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,  
 CC M. indicus, M. circinalis, F. circinalis, Rhizopus oryzae, R.  
 CC Microsporus, R. circinalis, R. stolonifer, Rhizomucor pusillus, Ascidia  
 CC corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph  
 CC of Scodoporiopsis aplosporum), Penicillium notatum, or Sporothrix  
 CC schenckii. The probes can be used for differentiating filamentous fungal  
 CC species from each other and from other medically important fungi.  
 CC (Updated on 17-Oct-2003 to standardise OS field)

XX Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 310; DB 2; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-98;  
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATGCATAGTAATGTAATGCAAAATTCAGTGAATCATGTAATCTTTGAACGACA 60  
 DB 1 AAATGCATAGTAATGTAATGCAAAATTCAGTGAATCATGTAATCTTTGAACGACA 60

QY 61 TTGGCGCCCGCAGATATTCGCGCGCATGCGCTGTTGAGCGTCAATTCACCTCAAGCC 120  
 DB 61 TTGGCGCCCGCAGATATTCGCGCGCATGCGCTGTTGAGCGTCAATTCACCTCAAGCC 120

QY 121 CCGGGGTTTGGTGTGGGATTCGCGCAGCCCTTGCGGCAAGCGCGCGCAAAATCTAGTG 180  
 DB 121 CCGGGGTTTGGTGTGGGATTCGCGCAGCCCTTGCGGCAAGCGCGCGCAAAATCTAGTG 180

QY 181 GCGGTCCTGCTGAGCTTTCATTCGCTAGTATGTAATAAACCCTCGCACTGTGACGCGCGC 240  
 DB 181 GCGGTCCTGCTGAGCTTTCATTCGCTAGTATGTAATAAACCCTCGCACTGTGACGCGCGC 240

QY 241 GCGCAACCGCTTAAACCCCACTTCTGATTTGACTTGGATCGATGAGTAATACCG 300  
 DB 241 GCGCAACCGCTTAAACCCCACTTCTGATTTGACTTGGATCGATGAGTAATACCG 300

QY 301 CTGAACCTTAA 310  
 DB 301 CTGAACCTTAA 310

RESULT 2  
 AAS16211 standard; DNA; 2293 BP.

XX AAS16211;  
 AC AAS16211;  
 XX 29-JAN-2002 (first entry)  
 DT  
 XX Fungus genomic DNA spanning 18S, 5.8S and 28S rRNA and ITS sequences.  
 DE  
 XX Gibberellin, 18S rRNA, internal transcribed spacer region, ITS1; ITS2;  
 KM 5.8S rRNA; LTB-1027; species differentiation; GA\_4; GA\_3; GA\_7;  
 KM flowering; fruit cell elongation; apple; pear; grape; fruit;  
 XX russet control; fungus; ds.

OS Gibberella fujikuroi.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..1774  
 FT /\*tag= a  
 FT /note= "18S rRNA gene"  
 FT 1775..1921  
 FT /\*tag= b  
 FT /note= "ITS1 region"  
 FT 1922..2078  
 FT /\*tag= c  
 FT /note= "5.8S rRNA gene"  
 FT 2079..2243  
 FT /\*tag= d  
 FT /note= "ITS2 region"  
 FT 2244..2293  
 FT misc\_feature /\*tag= e

FT /note= "28S rRNA gene"  
 XX US6287800-B1.  
 PN 11-SBP-2001.  
 XX 23-AUG-2000; 2000US-00645073.  
 PF 31-AUG-1999; 99US-0151770P.  
 XX (GALL/) GALLIAZZO J L.  
 PA (LEEM/) LEE M D.  
 XX Galliazzo JL, Lee MD;  
 PI WPI; 2001-662197/76.  
 DR  
 XX A new method for producing a mixture of gibberellins from Gibberella  
 PT fujikuroi results in high titers of GA4 and GA7 useful to promote  
 PT flowering and fruit growth in the fruit growing industry.  
 XX Example 4; Col 9-12; 7pp; English.

XX This sequence represents a genomic DNA sequence containing the 18S rRNA  
 CC gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S  
 CC rRNA sequences from a mutant strain of Gibberella fujikuroi (LTB-1027) of  
 CC the invention. This region of DNA is highly variable and can be used for  
 CC species and strain differentiation. The LTB-1027 mutant produces a  
 CC mixture of gibberellins which is at least 70 % GA<sub>4</sub> and GA<sub>7</sub>.  
 CC Gibberellin GA<sub>4</sub> and GA<sub>7</sub> promote flowering and fruit cell elongation,  
 CC and are used by growers of apples, pears and grapes to produce larger  
 CC fruits and earlier harvests. The mixture of GA<sub>3</sub>, GA<sub>4</sub> and GA<sub>7</sub> achieved  
 CC using the method of this invention should be particularly useful in the  
 CC apple industry where GA<sub>4</sub> has been found more effective in russet control  
 CC and in promoting fruit set. This method produces GA<sub>4</sub> and GA<sub>7</sub> in much  
 CC higher titers than prior art methods

XX Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 U; 0 Other;

Query Match 99.0%; Score 306.8; DB 4; Length 2293;  
 Best Local Similarity 99.4%; Pred. No. 1.7e-96;  
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAATGCATAGTAATGTAATGCAAAATTCAGTGAATCATGTAATCTTTGAACGACA 60  
 DB 1972 AAATGCATAGTAATGTAATGCAAAATTCAGTGAATCATGTAATCTTTGAACGACA 2031

QY 61 TTGGCGCCCGCAGATATTCGCGCGCATGCGCTGTTGAGCGTCAATTCACCTCAAGCC 120  
 DB 2032 TTGGCGCCCGCAGATATTCGCGCGCATGCGCTGTTGAGCGTCAATTCACCTCAAGCC 2091

QY 121 CCGGGGTTTGGTGTGGGATTCGCGCAGCCCTTGCGGCAAGCGCGCCCGCAAAATCTAGTG 180  
 DB 2092 CCGGGGTTTGGTGTGGGATTCGCGCAGCCCTTGCGGCAAGCGCGCCCGCAAAATCTAGTG 2151

QY 181 GCGGTCCTGCTGAGCTTTCATTCGCTAGTATGTAATAAACCCTCGCACTGTGACGCGCGC 240  
 DB 2152 GCGGTCCTGCTGAGCTTTCATTCGCTAGTATGTAATAAACCCTCGCACTGTGACGCGCGC 2211

QY 241 GCGCAACCGCTTAAACCCCACTTCTGATTTGACTTGGATCGATGAGTAATACCG 300  
 DB 2212 GCGCAACCGCTTAAACCCCACTTCTGATTTGACTTGGATCGATGAGTAATACCG 2271

QY 301 CTGAACCTTAA 310  
 DB 2272 CTGAACCTTAA 2281

RESULT 3  
 ACC50001  
 ID ACC50001 standard; DNA; 534 BP.  
 XX ACC50001;

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XX 14-JUL-2003 (first entry)
DT Internal transcribed spacer RNA encoding sequence #3.
DE
XX Mitochondria; fungal pathogen; ds.
XX
XX Fusicurium proliferatum.
OS
XX WO2003027635-A2.
XX
XX 03-APR-2003.
PD
XX 19-SEP-2002; 2002WO-US030311.
PF
XX 24-SEP-2001; 2001US-00961755.
PR
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX Beck UJ, Barnett CJ,
PI
XX WPI; 2003-363229/34.
XX
XX Detecting a fungal pathogen, useful for monitoring disease development,
PT comprises subjecting the DNA to PCR amplification using at least one
PT primer having sequence identity with at least 10 contiguous nucleotides
PT of Fusicurium spp.
XX
XX Claim 5, Page 38-39; 44pp; English.
XX
XX This invention relates to the detection of a fungal pathogen comprising
XX isolating DNA from a plant leaf infected with a pathogen. The methods and
XX primers are useful for identifying fungal isolates of fungal pathogens
XX and monitoring of disease development in plant populations. The present
XX sequence represents an internal transcribed spacer RNA encoding sequence
XX
XX Sequence 534 BP; 135 A; 149 C; 130 G; 120 T; 0 U; 0 Other;
SQ
Query Match 97.7%; Score 302.8; DB 7; Length 534;
Best Local Similarity 99.3%; Pred. No. 2.2e-95;
Matches 304; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAATGCGATTAAGTAATGTAATGCAAAATTCAGTGAATTCGAACTTTGAACGACCA 60
DB 229 AAATGCGATTAAGTAATGTAATGCAAAATTCAGTGAATTCGAACTTTGAACGACCA 288
QY 61 TTGGCGCCGCGCAGTAATTCGCGCGGCATGCTGTTCGAGCGTCATTTCAACCTTCAGCC 120
DB 289 TTGGCGCCGCGCAGTAATTCGCGCGGCATGCTGTTCGAGCGTCATTTCAACCTTCAGCC 348
QY 121 CCCGGGTTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCGCGCAAAATTTAGTG 180
DB 349 CCCGGGTTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCGCGCAAAATTTAGTG 408
QY 181 GCGGCTGCTGCGAGCTTCATTTGCGTAGTAATAACCTTCGCAACGTTACGGGCGC 240
DB 409 GCGGCTGCTGCGAGCTTCATTTGCGTAGTAATAACCTTCGCAACGTTACGGGCGC 468
QY 241 GCGCAAGCGTTAAACCCCAACTTCTGAATGTTGACCTCGAGTACGTAAGTAATACCG 300
DB 469 GCGCAAGCGTTAAACCCCAACTTCTGAATGTTGACCTCGAGTACGTAAGTAATACCG 528
QY 301 CTGAAC 306
DB 529 CTGAAC 534

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DT 15-SEP-2003 (revised)
DT 14-NOV-2000 (first entry)
DE
XX Fusicurium sp. MF6381 rDNA internal transcribed spacer (ITS) region.
XX
XX Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469;
XX HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
XX acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;
XX symptomatic infection; asymptomatic infection; potential HIV exposure;
XX combination therapy; ds.
XX
XX Fusicurium sp; MF6381.
OS
XX WO200006132-A1.
XX
XX 22-JUN-2000.
PD
XX 09-DEC-1999; 99WO-US029356.
PF
XX 14-DEC-1998; 98US-0112168P.
PR
XX (MERI ) MERCK & CO INC.
PA
XX Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;
PI Dombrowski AW;
PI WPI; 2000-431606/37.
XX
XX New steroid compounds are HIV integrase inhibitors used for treating HIV
XX infection and AIDS.
PT
XX
XX Disclosure; Page 14; 113pp; English.
XX
XX The invention relates to novel steroid compounds derived from the African
XX soil fungus Fusicurium sp. MF6381 (ATCC 74469) which act as inhibitors of
XX HIV integrase. The invention encompasses cultures of Fusicurium sp. MF6381.
XX The invention also relates to a composition comprising a compound of the
XX invention in combination with an AIDS antiviral agent, an immunomodulator
XX and an antileukemic agent. The compounds of the invention may be used in
XX the inhibition of HIV integrase and in the prevention and treatment of
XX HIV infection. A wide range of state of HIV infection may be treated;
XX AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex);
XX both symptomatic and asymptomatic HIV infection; and actual or potential
XX exposure to HIV. The compounds may be used to isolate HIV integrase
XX mutants which are potentially useful as screening tools for antiviral
XX compounds. The compounds may also be used to establish or determine the
XX site at which other antivirals bind to HIV integrase (e.g., by
XX competitive inhibition). The present sequence represents the ribosomal
XX DNA (rDNA) internal transcribed spacer (ITS) region of Fusicurium sp.
XX MF6381, which may be used to characterize MF6381. (Updated on 15-SEP-2003
XX to standardise OS field)
SQ
Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 U; 0 Other;
Query Match 85.7%; Score 265.8; DB 3; Length 502;
Best Local Similarity 93.8%; Pred. No. 2e-82;
Matches 288; Conservative 0; Mismatches 17; Indels 2; Gaps 1;
QY 1 AAATGCGATTAAGTAATGTAATGCAAAATTCAGTGAATTCGAACTTTGAACGACCA 60
DB 196 AAATGCGATTAAGTAATGTAATGCAAAATTCAGTGAATTCGAACTTTGAACGACCA 255
QY 61 TTGGCGCCGCGCAGTAATTCGCGCGGCATGCTGTTCGAGCGTCATTTCAACCTTCAGCC 120
DB 256 TTGGCGCCGCGCAGTAATTCGCGCGGCATGCTGTTCGAGCGTCATTTCAACCTTCAGCC 315
QY 121 CCCGGGTTTGGTGTGGGATCGGCAAGCCCT--TTGGGCAAGCGCGCGCGCGCAAAATTAG 178
DB 316 CCCGGGTTTGGTGTGGGATCGGCGCTGCTGTCTACCGGCTCCCGCGCGCAAAATTAG 375
QY 179 TTGGCGTCTGCTGCACTTCATTTGCGTAGTAATAACCTTCGCAACTGTGACGCGC 238
DB 376 TTGGCGTCTGCTGCACTTCATTTGCGTAGTAATAACCTTCGCAACTGTGACGCGC 435

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QY 239 GCGGCAAGCCGTTAAACCCCACTTCTGAATGTGACCTCGATCAGTAGAATACC 238  
 Db 436 GCGGCAAGCCGTTAAACCCCACTTCTGAATGTGACCTCGATCAGTAGAATACC 495  
 QY 299 CGCTGAA 305  
 Db 496 CGCTGAA 502

## RESULT 5

AAVS9009 standard; DNA; 561 BP.

XX AAVS9009;  
 XX  
 XX 17-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 06-JAN-1999 (first entry)

XX F. avenaceum internal transcribed spacer.

XX Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;  
 KW fungal pathogen identification; infection identification; ss.

XX Gibberella avenacea.

XX Key Location/Qualifiers  
 FT misc\_feature 31..181  
 FT /tag= a  
 FT /note= "ITS1"  
 FT 339..504  
 FT /tag= b  
 FT /note= "ITS2"

XX US5827695-A.

XX 27-OCT-1998.

XX 04-AUG-1997; 97US-00905314.

XX 04-AUG-1997; 97US-00905314.

XX (NOVS ) NOVARTIS FINANCE CORP.

XX Beck JJ;

XX WPI; 1998-593995/50.

XX Wheat pathogen internal transcribed spacer sequences - used as a basis  
 PT for primers for the species-specific polymerase chain reaction detection  
 PT of the pathogens.

XX Claim 1; Col 29-30; 20pp; English.

XX This sequence represents an internal transcribed spacer (ITS) sequence of  
 CC the invention. The primer pairs, based on the ITS sequences, are used for  
 CC the PCR amplification detection of wheat Microdochium and Fusarium fungal  
 CC pathogens, especially M. nivale, F. graminearum, F. culmorum, F.  
 CC avenaceum, F. poae, F. moniliforme or F. roseum. The two different  
 CC strains of fungi show different symptoms during infection, which may or  
 CC may not be due to infection. Early identification of the strain causing  
 CC the infection allows early, and more specific fungicidal treatment.  
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to  
 CC correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 561 BP; 145 A; 152 C; 135 G; 126 T; 0 U; 3 Other;

Query Match 80.6%; Score 249.8; DB 2; Length 561;

Best Local Similarity 91.6%; Pred. No. 8.2e-77;  
 Matches 285; Conservative 1; Mismatches 23; Indels 2; Gaps 2;

QY 1 AAATGCGATTAAGTATGTGAAATTCAGTAGATCATCGAATCTTTGAACGACCA 60

Db 232 AAATGCGATTAAGTATGTGAAATTCAGTAGATCATCGAATCTTTGAACGACCA 291  
 QY 61 TTGCGCCCGCAGATATTCTGCGGCGCATCCTGTTGAGCGTCAATTTCAACCTCAAGCC 120  
 Db 292 TTGCGCCCGCAGTGTATTCGCGGCGCATCCTGTTGAGCGTCAATTTCAACCTCAAGCC 351  
 QY 121 CCGGGTTTGGTGTGGGATGCGCAAGCCCTTGCGGC- AAGCCGGCCCGGAATCTAGT 179  
 Db 352 CCGGGTTTGGTGTGGGATGCGCTCTGCTTGGCGGTCGCGCCGCCGGAATACATT 411  
 QY 180 GCGGCTCGCTGACACTTCCATTGCGTAGTAAACCTCGCAACTGTACGGGCG 239  
 Db 412 GCGGCTCGCTGACACTTCCATTGCGTAGTAAACCTCGCAACTGTACGGGCG 471  
 QY 240 CCGGCAAGCCGTTAAACCCCACTTCTGAATGTGACCTCGGATCAGTAGAATACC 299  
 Db 472 CCGGCAATGCCG-TAAACCCCAACTTCTGAATGTGACCTCGGATCAGTAGAATACC 530  
 QY 300 GCTGAACCTTAA 310  
 Db 531 GCTGAACCTTAA 541

## RESULT 6

ABV78724 standard; rRNA; 659 BP.

XX ABV78724;  
 AC  
 XX 14-JAN-2003 (first entry)

XX C. sinensis rRNA sequence #23.

XX Ribosome rRNA sequence #23.

XX Ribosome ribonucleic acid; rRNA; Cordyceps crassisporea; classification;  
 KW Cordyceps sinensis; ss.

XX Cordyceps sinensis.

XX JP2002204696-A.

XX 23-JUL-2002.

XX 12-JAN-2001; 2001JP-00004805.

XX 12-JAN-2001; 2001JP-00004805.

XX (HEAL-) HEALTHWAY KK.

XX (KANE/) KANESHIRO N.

XX WPI; 2002-639075/69.

XX Ribosome RNA gene base sequence of Cordyceps sinensis for classification  
 PT of seeds of Cordyceps sinensis.

XX 26; Page 25; 33pp; Japanese.

XX The invention relates to a novel base sequence which is part of a fully  
 CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassisporea.  
 CC The base sequences can be used for the classification of Cordyceps  
 CC sinensis. The sequence represents a C. sinensis rRNA sequence of the  
 CC invention

XX Sequence 659 BP; 183 A; 173 C; 160 G; 143 T; 0 U; 0 Other;

Query Match 80.2%; Score 248.6; DB 6; Length 659;

Best Local Similarity 91.6%; Pred. No. 2.3e-76;  
 Matches 285; Conservative 0; Mismatches 24; Indels 2; Gaps 2;

QY 1 AAATGCGATTAAGTATGTGAAATTCAGTAGATCATCGAATCTTTGAACGACCA 60  
 Db 260 AAATGCGATTAAGTATGTGAAATTCAGTAGATCATCGAATCTTTGAACGACCA 319

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Oy 61 TTGCGCCGCGCAGTATCTGCGGCGGCGATGCTGTTCAGAGCGTATTTCACACCTCAAGCC 120
    |||||
Db 320 TTGCGCCGCGGCTGATATTCGGGCGGCGATGCTGTTCAGAGCGTATTTCACACCTCAAGCC 379
Oy 121 CCCGGGTTTGTTGGTGAGATCGGCAAGCCCTTGGCGG-AGCCGCGCCCGGAAATCTAGT 179
    |||||
Db 380 CCCGGGTTTGTTGGTGAGATCGGCTGTGCTTCAGCGGCGGTGCGCCCGCGAAATATACAT 439
Oy 180 GCGCGTCTCGCTGCGCTTCATTCGCTAGTATGATGATGATGATGATGATGATGATGATGATGAT 239
    |||||
Db 440 GCGCGTCTCGCTGCGCTTCATTCGCTAGTATGATGATGATGATGATGATGATGATGATGATGAT 499
Oy 240 GCGCGAAGCCGCTTAACCCCGCACTTCTGAATGTTGACCTCGGATCAGATGAGATGATGATGAT 299
    |||||
Db 500 GCGCGATGCTCG- TAAACCCCGCACTTCTGAATGTTGACCTCGGATCAGATGAGATGATGATGAT 558
Oy 300 GCTGAACCTTAA 310
    |||||
Db 559 GCTGAACCTTAA 569

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## RESULT 7

ABV78700  
ID ABV78700 standard; RNA; 647 BP.

ABV78700;

14-JAN-2003 (first entry)

C. crassispora rRNA sequence #2.

Ribosome ribonucleic acid; rRNA; *Cordyceps crassispora*; classification;

*Cordyceps sinensis*; ss.

*Cordyceps crassispora*.

JP2002204696-A.

23-JUL-2002.

12-JAN-2001; 2001JP-00004805.

12-JAN-2001; 2001JP-00004805.

(HEAL-) HEALTHWAY KK.

(KANE/) KANESHIRO N.

WPI; 2002-639075/69.

Ribosome rRNA gene base sequence of *Cordyceps sinensis* for classification of seeds of *Cordyceps sinensis*.

2; Page 12; 33pp; Japanese.

The invention relates to a novel base sequence which is part of a fully defined ribosome ribonucleic acid (rRNA) gene of *Cordyceps crassispora*. The base sequences can be used for the classification of *Cordyceps sinensis*. The sequence represents a *C. crassispora* rRNA sequence of the invention

Sequence 647 BP; 166 A; 178 C; 160 G; 143 T; 0 U; 0 Other;

Query Match 79.9%; Score 247.8; DB 6; Length 647;

Best Local Similarity 91.6%; Pred. No. 4.4e-76;

Matches 285; Conservative 0; Mismatches 22; Indels 4; Gaps 2;

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Oy 1 AAATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
    |||||
Db 245 AAATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304
Oy 61 TTGCGCCGCGCAGTATCTGCGGCGGCGATGCTGTTCAGAGCGTATTTCACACCTCAAGCC 120
    |||||
Db 305 TTGCGCCGCGCAGTATCTGCGGCGGCGATGCTGTTCAGAGCGTATTTCACACCTCAAGCC 364

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Oy 121 CCCGGGTTTGTTGGTGAGATCGGCAAGCCCTTGGCGGCGGCGCCCGGAAATCTAGTG 180
    |||||
Db 365 CCCGGGTTTGTTGGTGAGATCGGCTGTGCTTCAGCGGCGGTGCGCCCGCGAAATCTAGTG 424
Oy 181 GCGGCTCTGCTGACGCTTCCATTCGCTAGTATGATGATGATGATGATGATGATGATGATGATGAT 240
    |||||
Db 425 GCGGCTCTGCTGATGCTTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
Oy 241 GCGCAAGCCGTTAAACCCCGCACTTCTGAATG-TTGACTTCGATCAGTATGATGATGATGATGAT 299
    |||||
Db 482 GCGCAAGCCGTTAAACCCCGCACTTCTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 541
Oy 300 GCTGAACCTTAA 310
    |||||
Db 542 GCTGAACCTTAA 552

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## RESULT 8

AAV70850  
ID AAV70850 standard; DNA; 319 BP.

AAV70850;

26-FEB-1999 (first entry)

Internal transcribed spacer 2 (ITS2) and adjacent regions.

Internal transcribed spacer 2; ITS2; probe; *Aspergillus flavus*; *A. niger*;

*A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*; *Mucor rouxii*;

*M. racemosus*; *M. plumbeus*; *M. indicus*; *A. fumigatus*;

*M. circinellus*; *F. circinelloides*; *Rhizopus oryzae*; *R. microsporus*;

*R. circinans*; *R. stolonifer*; *Rhizomucor pusillus*; *Abidia corymbifera*;

*Cunninghamella elegans*; *Pseudallescheria boydii*; *Scedosporium apiospermum*;

*Penicillium notatum*; *Sporothrix schenckii*; filamentous fungus; ss.

*Fusarium solani*.

WO9850584-A2.

12-NOV-1998.

01-MAY-1998; 98WO-US008926.

02-MAY-1997; 97US-0045400P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Morrison CJ, Reiss E, Aldorevich L, Choi JS;

WPI; 1999-034737/03.

New nucleic acid probes for filamentous fungi - for detecting e.g.

*Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Abidia*,

*Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix*

species.

Claim 1; Page 12; 45pp; English.

The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species-specific. The specification also describes ITS2

sequence-derived probes for identifying a species selected from

*Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,

*Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,

*M. indicus*, *M. circinellus*; *F. circinelloides*; *Rhizopus oryzae*; *R.*

*microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia*

*corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph

of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix*

schenckii. The probes can be used for differentiating filamentous fungal

species from each other and from other medically important fungi

Sequence 319 BP; 77 A; 96 C; 84 G; 62 T; 0 U; 0 Other;

Query Match	62.7%	Score	194.4	DB	7	Length	522
Best Local Similarity	84.3%	Pred. No.	2e-57				
Matches	258	Conservative	0	Mismatches	36	Indels	12
				Gaps			3

  

QY	1	AAATGCGATAAGTATGATGCAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA	60
DB	229	AAATGCGATAAGTATGATGCAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA	288
QY	61	TTGGCGCCCGGCAGTAATTCGGCGGGCATGCTGTTCGAGCGGTCAATTCACCCCTCAAGCC	120
DB	289	TTGGCGCCCGGCAGTAATTCGGCGGGCATGCTGTTCGAGCGGTCAATTCACCCCTCAAGCC	348
QY	121	CCCGGGTTTGATGTTGGGGAATCGGCAAGCCCTTGGCGGCAACCGGCCCCGGAATCTAAGT	180
DB	349	C-----AGCTTGATGTTGGGACATCGGCAATGCGCTTCCCGCAAAATTGAATG	398
QY	181	GCGGTTCGCTGCAGCTTCCATTTCCGTAAGTATGTAATACCTTCGCAATCGTAACCGGGGC	240
DB	399	GCGGTTCACG-TCGAGCTTCCATACGGAAGTATGTAATACCTTCGTAATCGTAATCTGTGC	457
QY	241	GGCGAAGCGGTTAAACCCCAACTTCGAATGTTGACCTCGGATCAGGTAGGAATPACCG	300
DB	458	GGCGAAGCGGTTAAA-CCCAACTTCGAATGTTGACCTCGGATCAGGTAGGAATPACCG	516
QY	301	CTGAAC	306
DB	517	CTGAAC	522

XX	ACC50002
XX	ACC50002 standard; DNA; 522 BP.
XX	ACC50002;
XX	27-OCT-2003 (revised)
XX	14-JUL-2003 (first entry)
XX	Internal transcribed spacer RNA encoding sequence #4.
XX	Mitochondria; fungal pathogen; ds.
XX	Gibberella moniliformis.
XX	WO2003027635-A2.
XX	03-APR-2003.
XX	19-SEP-2002; 2002WO-US030311.
XX	24-SEP-2001; 2001US-00961755.
XX	(SYGN ) SYNGENTA PARTICIPATIONS AG.
XX	Beck UJ, Barnett CJ;
XX	WPI; 2003-363229/34.
XX	Detecting a fungal pathogen, useful for monitoring disease development,
XX	comprises subjecting the DNA to PCR amplification using at least one
XX	primer having sequence identity with at least 10 contiguous nucleotides
XX	of Fusarium spp.
XX	Claim 5; Page 39; 44pp; English.
XX	This invention relates to the detection of a fungal pathogen comprising
XX	isolating DNA from a plant leaf infected with a pathogen. The methods and
XX	primers are useful for identifying fungal isolates of fungal pathogens
XX	and monitoring of disease development in plant populations. The present
XX	sequence represents an internal transcribed spacer RNA encoding sequence-
XX	(updated on 27-OCT-2003 to standardise OS field)
XX	Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 62.7%; Score 194.4; DB 7; Length 522;  
Best Local Similarity 84.3%; Pred. No. 28-57; Mismatches 36; Indels 12; Gaps 3;  
Matches 258; Conservative 0; Mismatches 36; Indels 12; Gaps 3;

QY 1 AATGCGATTAAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGCACA 60  
DB 229 AATGCGATTAAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGCACA 288  
QY 61 TTGGCCCGCCGAGTATTCGCGCGGCGATGCTGTTGAGCGTCAATTCACCCCAAGCC 120  
DB 289 TTGGCCCGCCGAGTATTCGCGCGGCGATGCTGTTGAGCGTCAATTCACCCCAAGCC 348  
QY 121 CCCGGGTTGGTGTGGGATGGCAAGCCCTGCGGCAAGCCGCCCGGAATTTAGTG 180  
DB 349 C-----AGTTGGTGTGGGATGGCAAGCCCTGCGGCAAGCCGCCCGGAATTTAGTG 398  
QY 181 GCGGCTCGCTGCACTTCATTCGAGTGAATAAACCCTGCACTGTACGGCGGC 240  
DB 399 GCGGCTCGCTGCACTTCATTCGAGTGAATAAACCCTGCACTGTACGGCGGC 457  
QY 241 GCGCAAGCGGTTAAACCCCAACTTCTGAGTGTGACCTCGAGTACGATAGGATACCCG 300  
DB 458 GCGCAAGCGGTTAAACCCCAACTTCTGAGTGTGACCTCGAGTACGATAGGATACCCG 516  
QY 301 CTGAC 306  
DB 517 CTGAC 522

RESULT 11  
ABV78721  
ID ABV78721 standard; rRNA; 661 BP.  
XX AC ABV78721;  
XX DT 14-JAN-2003 (first entry)  
XX DE C. sinensis rRNA sequence #20.  
XX KW Ribosome ribonucleic acid; rRNA; Cordyceps crassisporea; classification;  
XX KW Cordyceps sinensis; ss.  
XX OS Cordyceps sinensis.  
XX PN JP2002204696-A.  
XX PD 23-JUL-2002.  
XX PE 12-JAN-2001; 2001JP-00004805.  
XX PR 12-JAN-2001; 2001JP-00004805.  
XX PA (HEAL-) HEALTHWAY KK.  
XX PA (KANE/) KANESHIRO N.  
XX DR WPI; 2002-639075/69.  
XX PT Ribosome RNA gene base sequence of Cordyceps sinensis for classification  
XX PT of seeds of Cordyceps sinensis.  
XX PS 23; Page 24; 33pp; Japanese.  
XX CC The invention relates to a novel base sequence which is part of a fully  
CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassisporea.  
CC The base sequence can be used for the classification of Cordyceps  
CC sinensis. The sequence represents a C. sinensis rRNA sequence of the  
CC invention  
XX SQ Sequence 661 BP; 176 A; 192 C; 168 G; 123 T; 0 U; 2 Other;

Query Match 62.5%; Score 193.8; DB 6; Length 661;  
Best Local Similarity 83.6%; Pred. No. 3.6e-57;

Matches 260; Conservative 0; Mismatches 37; Indels 14; Gaps 3;

QY 1 AATGCGATTAAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGCACA 60  
DB 269 AATGCGATTAAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGCACA 328  
QY 61 TTGGCCCGCCGAGTATTCGCGCGGCGATGCTGTTGAGCGTCAATTCACCCCAAGCC 120  
DB 329 TTGGCCCGCCGAGTATTCGCGCGGCGATGCTGTTGAGCGTCAATTCACCCCAAGCC 388  
QY 121 CCCG-GGTTGGTGTGGGATGGCAAGCCCTTGGCGCAAGCCGCCCGGAATTTAGT 179  
DB 389 CCAGGCGGCTGTGTGGGAGCCGGC-----CCGGCGGCCCGCCCAATTCAGT 437  
QY 180 GCGGCTCGCTGCACTTCATTCGAGTGAATAAACCCTGCACTGTACGGCGGC 239  
DB 438 GCGCAAGCGGTTAAACCCCAACTTCTGAGTGTGACCTCGAGTACGATAGGATACCC 495  
QY 240 GCGCAAGCGGTTAAACCCCAACTTCTGAGTGTGACCTCGAGTACGATAGGATACCC 299  
DB 496 GCGTACGCGCGTAAAGCCCAACTTCTGAGTGTGACCTCGAGTACGATAGGATACCC 555  
QY 300 GCTGAACCTTAA 310  
DB 556 GCTGAACCTTAA 566

RESULT 12  
AAT65100  
ID AAT65100 standard; DNA; 582 BP.  
XX AC AAT65100;  
XX DT 17-OCT-2003 (revised)  
XX DT 17-FEB-1998 (first entry)  
XX DE T. harzianum IMI 352940 5.8 S rRNA gene regions ITS1-ITS4.  
XX KW ITS1-ITS4 region; 5.8S rRNA; filamentous fungi; Trichoderma harzianum;  
XX KW liquid formulation; T. viride; gene recipient; increase activity;  
XX KW biological control agent; plant disease; biodegradation;  
XX KW biofixation; leaching; ss.  
XX OS Hypocrea lixii; strain IMI 352940.  
XX PN WO9716974-A1.  
XX PD 15-MAY-1997.  
XX PE 06-NOV-1996; 96WO-ES000206.  
XX PR 07-NOV-1995; 95ES-00002266.  
XX PA (URSA-) UNIV SALAMANCA.  
XX PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.  
XX PI Monte Vazquez E, Grondona Espana I, Garcia Ancha I;  
XX DR WPI; 1997-280728/25.  
XX PT Liquid formulation of Trichoderma harzianum and Trichoderma viride  
XX PT strains - are used as biological control agents against diseases of  
XX PT plants and plant material and as biofixation agents.  
XX PS Disclosure; Page 26; 37pp; Spanish.  
XX CC The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA  
CC gene from the filamentous fungi Trichoderma harzianum strain IMI 352940.  
CC A novel liquid formulation based on strains of T. harzianum and T.  
CC viride, has the following composition (w/v%): 0.1-6 sorbitol; 0.02-2  
CC K3PO3; 0.05-2 KNO3; 0.002-1 MgSO4.7H2O; 0.02-2 (NH4)H2PO4; 0.02-2 copper;  
CC 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron; 0.02-2  
CC manganese; and a biological component comprising at least one of: T.

CC hazianum IMI 352939 (3 x 105 to 10 x 107 conidia/ml), T. hazianum IMI 352940 (3 x 105 to 10 x 107 conidia/ml), T. hazianum CECT 20179 and/or T. viride CECT 20178. The Trichoderma fungi, alone or in combination, are used as gene recipients to increase activity of the formulation as a biological control agent against diseases of plants and plant material and biological entites causing biodegradation, and as a biofixation (leaching) agent. It is particularly used e.g. in agriculture, forestry and gardening; for controlling microorganisms which damage food and its packaging; construction materials, raw materials and manufactured products. The antagonistic capacity of the four types of T. hazianum and one type of T. viride over other soil fungi makes them useful for control of plant diseases. Use of this formulation allows reduced application of polluting chemical pesticides and is thus more eco-friendly. (updated on 17-OCT-2003 to standardise OS field)

CC XX Sequence 582 BP, 129 A; 178 C; 142 G; 133 T; 0 U; 0 Other;

Query Match 62.4%; Score 193.4; DB 2; Length 582;  
Best Local Similarity 85.9%; Pred. No. 4,7e-57;  
Matches 274; Conservative 0; Mismatches 36; Indels 9; Gaps 5;

QY 1 AATGCGATTAAGTATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60  
Db 264 AATGCGATTAAGTATGTAATTCAGTGAATCATCGAATCTTTGAACGCACA 323

QY 61 TTGGCGCCGCGCAGTATCTGGCGGGGCAATGCTGTTCAGAGGTCATTCAACCCCTCAAGCC 120  
Db 324 TTGGCGCCGCGCAGTATCTGGCGGGGCAATGCTGTTCAGAGGTCATTCAACCCCTCAAGCC 383

QY 121 C-----CCGGTTTGTTGGTTGGGATCGCAAGCCCTT-GCGGCAGACCGCGCCCGAAT 174  
Db 384 CCTCGCCGCCCTCGGGGTTGGGATCGGCCCTCCTTAGGGGTGGCCCTCTCCGAAT 443

QY 175 CTATGGCGGCTCTGCTGCGACCTTCCATTGGTATGTG-TAAACCTCCGAAGTGTAC 223  
Db 444 ACAATGGGCTCTGCGCGACCCCTCTCTGGCAGTGTTCACACTCCCATCGGAGC 503

QY 234 GCGCGCGGCGCA-AGCGTTAAACCCCAACTCTG-AATGTTGACTCGGATCAGGTAG 291  
Db 504 GCGCGCGGCTCCACGCGCTTTAAACCCCAACTCTGAAATGTTGACTCGGATCAGGTAG 563

QY 292 GAATACCCGCTGAACCTTAA 310  
Db 564 GAATACCCGCTGAACCTTAA 582

RESULT 13  
AAV62596 standard; DNA, 546 BP.  
AC AAV62596;  
XX 17-DEC-1998 (first entry)  
DE Fusarium poae PCR amplified ITS region consensus DNA sequence.  
XX Internal transcribed spacer; ITS; ribosomal RNA; RNA; fungal pathogen;  
KM Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;  
KM Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;  
KM PCR; nucleic acid detection; ss.  
XX Fusarium poae.  
OS  
FH Key location/Qualifiers  
FT misc\_feature 1..30  
FT /tag= a  
FT /note= "3' end of small subunit rRNA gene"  
FT misc\_feature 31..180  
FT /tag= b  
FT /note= "ITS 1"  
FT misc\_feature 181..337  
FT /tag= c

FT /note= "5.8S rRNA gene"  
FT misc\_feature 338..489  
FT /tag= d  
FT /note= "ITS 2"  
FT misc\_feature 490..546  
FT /tag= e  
FT /note= "5' end of large subunit rRNA gene"  
FN US5814453-A.  
FN 29-SEP-1998.  
PD 02-JUL-1997; 97US-00887480.  
PF 19-APR-1995; 95MO-US004712.  
PR 15-OCT-1996; 96US-00722187.  
XX (NOVS ) NOVARTIS FINANCE CORP.  
PA Beck JI;  
PI WPI; 1998-541745/46.  
DR DNA isolated from fungal RNA, and its internal transcribed spacer  
XX sequence - used for detecting fungal pathogens in plant tissue.  
PT Example; Col 87-88; 56bp; English.  
PS  
XS This represents the consensus DNA sequence of the internal transcribed  
CC spacer (ITS) region that was PCR amplified from Fusarium poae isolates, T  
CC -427, T-534 and T-756. The invention provides a DNA molecule isolated  
CC from the ribosomal RNA (rRNA) gene region of a fungal pathogen, where the  
CC DNA molecule consists of an ITS sequence selected from ITS1 and ITS2 of  
CC Fusarium culmorum, Fusarium graminearum, Fusarium moniliforme, Septoria  
CC avenae or Microdochium nivale. A method for detecting F. graminearum, F.  
CC culmorum, F. moniliforme, F. poae, F. avenaceum and M. nivale isolates is  
CC also provided. The method comprises isolating DNA from a plant leaf  
CC infected with at least one of the above pathogens and amplifying parts of  
CC the ITS sequence of the pathogen(s) by PCR using specific primers from  
CC within these sequences. The pathogen(s) are detected by visualising the  
CC amplified part of the ITS sequence  
XX  
SQ Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;

Query Match 60.5%; Score 187.6; DB 2; Length 546;  
Best Local Similarity 84.5%; Pred. No. 4,9e-55;  
Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;

QY 1 AATGCGATTAAGTATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60  
Db 231 AATGCGATTAAGTATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGCACA 290

QY 61 TTGGCGCCGCGCAGTATCTGGCGGGGCAATGCTGTTCAGAGGTCATTCAACCCCTCAAGCC 120  
Db 291 TTGGCGCCGCGCAGTATCTGGCGGGGCAATGCTGTTCAGAGGTCATTCAACCCCTCAAGCC 350

QY 121 CCCGGTTTGTTGGTTGGGATCGCAAGCCCTTGGGGAAGCGCGCCCGGAATTAATAGT 180  
Db 351 C---AGCTTGGTGGG-----ATCTGTGCAACAGCTCCCAATTAATGATG 398

QY 181 GCGGTTCTGCTGCACTTCATTTGCGTGTAGTAAACCTCGCAACGTGTACGCGGCGC 240  
Db 399 GCGGTCAGG-TGACCTTCATAGGTAGTAAATTTACATCTGTTACTGTTATCTGTCG 457

QY 241 GCGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACTCGGATCAGTAGGAATACCG 300  
Db 458 GCGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACTCGGATCAGTAGGAATACCG 516

QY 301 CTGAACCTTAA 310  
Db 517 CTGAACCTTAA 526



ID	AAV59007	standard; DNA; 546 BP.
AC	AAV59007;	
XX		
XX		
DT	25-MAR-2003	(revised)
DT	06-JAN-1999	(first entry)
XX		
DE	F. poae internal transcribed spacer.	
XX		
KW	Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;	
KW	fungal pathogen identification; infection identification; ss.	
XX		
OS	Fusarium poae.	
XX		
PH	Key	Location/Qualifiers
FT	misc_feature	31..180
FT		/tag= a
FT		/note= "ITS1"
FT	misc_feature	338..489
FT		/tag= b
FT		/note= "ITS2"
XX		
PN	US5827695-A.	
PD	27-OCT-1998.	
XX		
PF	04-AUG-1997; 97US-00905314.	
PR	04-AUG-1997; 97US-00905314.	
PA	(NOVS ) NOVARTIS FINANCE CORP.	
XX		
PL	Beck UJ;	
XX		
DR	WPI; 1998-593995/50.	
XX		
PT	Wheat pathogen internal transcribed spacer sequences - used as a basis	
PT	for primers for the species-specific polymerase chain reaction detection	
PT	of the pathogens.	
XX		
PS	Claim 1; Col 25-26; 20pp; English.	
XX		
CC	This sequence represents an internal transcribed spacer (ITS) sequence of	
CC	the invention. The primer pairs, based on the ITS sequences, are used for	
CC	the PCR amplification detection of wheat Microdochium and Fusarium fungal	
CC	pathogens, especially M. nivale, F. graminearum, F. culmorum, F.	
CC	avenaceum, F. poae, F. moniliforme or F. roseum. The two different	
CC	strains of fungi show different symptoms during infection, which may or	
CC	may not be due to infection. Early identification of the strain causing	
CC	the infection allows early, and more specific fungicidal treatment.	
CC	(Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to	
XX	correct PR field.)	
XX		
SQ	Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 U; 0 Other;	
Query Match	60.5%; Score 187.6; DB 2; Length 546;	
Best Local Similarity	84.5%; Pred. No. 4.9e-55;	
Matches 262; Conservative	0; Mismatches 34; Indels 14; Gaps 4	
Db	1 AATCGAATAAGTAATGTGAATTGCAGAAATTCAGTAGATCATGATCTTTGAAGCACA 60	
Db	231 AATTCGATAGTAATGTGAATTGCAGATTCAGTAATCATGATCTTTGAAGCACA 290	
Db	61 TTGCGCCCGCCAGTATTCTGCGGGGAGCCCTGTTGAGCGCTGATTCAACCTCAAGCC 120	
Db	291 TTGCGCCCGCCAGTATTCTGCGGGGAGCATCTGTTGAGCGCTGATTCAACCTCAAGCC 350	
Db	121 CCCGGGTTTGCTGTTGGGGAGATGCGCAAGCCCTTGCGGCAAGCCGCGCCGGAATCTAGTC 180	
Db	351 C---AGCTTGAGTGGG-----ATCTGTGTGCAACAACAGTCCCAATTGATTG 398	

Oy		181	GGGCGTCTGCACACTTCATTTGGTAGTATAAAACCCTTGCAACGTGACGGGGC	248
Db		399	GGGGTCAGC-TCGACCTTCAGAGCGTGAATTACATCATGTTACTGTATCCGTGC	457
Oy		241	GGCCAAGCCGTTAAACCCCAACTCTGAAATTGACCTCGATCAGTAGAATACCCG	300
Db		468	GGCCACGCCGCTTAA-CCCCAACCTCTGAATTTTAACCTCGAATCAGTAGAATACCCG	516
Oy		301	CTGAACCTTAA 310 	
Db		517	CTGAACCTTAA 526 	
<hr/>				
RESULT 15				
ID	AAT05400	standard; DNA; 504 BP.		
XX	AAT05400;			
AC	AAT05400;			
DT	04-JUN-1996	(first entry)		
DE	Fusarium culmorum internal transcribed spacer sequence.			
XX				
KM	Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;			
KM	Pseudocercospora heparichnoides; Mycosphaerella fljensis; PCR;			
KW	Mycosphaerella musicola; amplification; primer; ribosomal RNA gene;			
KW	internal transcribed region; strain; capture; colourimetric assay;			
KW	isolate; development; population; random amplified polymorphic DNA; ss.			
XX				
OS	Fusarium culmorum.			
PN	WO9529260-A2.			
PD	02-NOV-1995.			
XX				
PF	19-APR-1995; 95MO-US004712.			
PR	25-APR-1994; 94US-00233608.			
PA	(CIBA ) CIBA GEIGY AG.			
PI	Ligon JM, Beck JI;			
DR	WPJ; 1995-383005/49.			
PT	DNA encoding intervening transcribed sequence - used for detection of			
PT	plant fungal pathogens.			
PS	Claim 1; Page 54-55; 65pp; English.			
XX				
CC	A novel method for the detection of plant pathogenic strains of fungi			
CC	e.g. Septoria nodorum, S.tritici, Pseudocercospora heparichnoides,			
CC	Mycosphaerella fljensis, M.muscola or Fusarium spp, involves the PCR			
CC	amplification of sequences found in the internal transcribed region (ITS)			
CC	of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93			
CC	and AAT05357-72. These primers are derived from the ITS sequences of			
CC	these fungi (AAT05394-T05404 and AQ94398) and are strain specific. The			
CC	amplification products of the reactions using these primers can be used			
CC	with the capture primers AAT05378-93 in colourimetric assays. The primers			
CC	and ITS DNAs can be used for the detection of specific fungal pathogen			
CC	isolates and in monitoring disease development in plant populations			
XX				
SQ	Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;			
<hr/>				
Query Match	60.2%; Score 186.6; DB 2; Length 504;			
Beet Local Similarity	82.6%; Pred. NO. 1.1e-54;			
Matches 252; Conservative	1; Mismatches 40; Indels 12; Gaps 3			
Oy	1	AAATGCATAGTATGATGCAATTCGAAAATTCAGAGATCATCGATCTTTGAAGCAC	60	
Db	212	AAATGCATAGTATGATGCAATTCGAAAATTCAGAGATCATCGATCTTTGAAGCAC	271	
Oy	61	TTGGCGCCGCGAGTATCTTGGCGGGCATCCTGTTGAGCGGTCAITTCACCTCAAGC	120	

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Db      272  TTGGCCCGCCAGATATTCTGGCGGGCATGCTGTTGAGGCTCATTTCAACCTCAAGCC 331
QY      121  CCCGGTTTGGTGTGGGATCGCAAGCCCTTGGGAAAGCGGCCCGGAATCTAGTG 180
Db      332  C--AGCTTGGTGTGGG-----AGTCAGACTCTGCTGCACCTCCCAAAATACATG 380
QY      181  GCGGTCGCGTGCAGCTTCCATTGCGTAGTAAACCTCGCACTGGTAAGCGGCGC 240
Db      381  GCGGTACGTCGRAGCTTCCATAGCGTAGTAATTTACATATCGTTACTGGTAATCGTGC 440
QY      241  GGCCTAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGTAGAATACCCG 300
Db      441  GGCYAGCCCGTTAA--CCCCAATTCTGAATGTTGACCTCGATCAGTAGAATACCCG 499
QY      301  CTGAA 305
Db      500  CTGAA 504

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 Job time : 551.986 secs

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## OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 2524.91 Seconds  
(without alignments)  
5321.503 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310

Sequence: 1 aaatgcataagtaatgta.....ggaatacccgctgaactta 310

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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

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1: gb ba:*
2: gb htg:*
3: gb in:*
4: gb om:*
5: gb ov:*
6: gb pat:*
7: gb ph:*
8: gb pl:*
9: gb pr:*
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11: gb sts:*
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15: em ba:*
16: em fun:*
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23: em pat:*
24: em ph:*
25: em pl:*
26: em ro:*
27: em sts:*
28: em sy:*
29: em un:*
30: em htg hum:*
31: em htg inv:*
32: em htg other:*
33: em htg mus:*
34: em htg pln:*
35: em htg rod:*
36: em htg mam:*
37: em htg vrt:*
38: em sy:*
39: em htgo hum:*
40: em htgo mus:*
41: em htgo other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	6 AR206401	AR206401 Sequence
2	310	100.0	310	6 BD083592	BD083592 Nucleic a
3	310	100.0	310	6 AF117922	AF117922 Gdbere11
4	306.8	99.0	351	8 AF162903	AF162903 Fusarium
5	306.8	99.0	556	8 AF455422	AF455422 Gdbere11
6	306.8	99.0	556	8 AF455460	AF455460 Gdbere11
7	306.8	99.0	558	8 FPUORRNA	X94176 Fusarium fu
8	306.8	99.0	558	8 FPUORRNA	X94171 Fusarium pr
9	306.8	99.0	562	8 AY237110	AY237110 Fusarium
10	306.8	99.0	569	8 AF452163	AF452163 Pythium u
11	306.8	99.0	596	8 AF291061	AF291061 Fusarium
12	306.8	99.0	2293	6 AR168094	AR168094 Sequence
13	305.2	98.5	531	8 AF158303	AF158303 Fusarium
14	305.2	98.5	540	8 AF158304	AF158304 Fusarium
15	303.6	97.9	540	8 AF158302	AF158302 Fusarium
16	302.8	97.7	534	8 FPU34557	U34557 Fusarium fu
17	302.8	97.7	534	8 FPU34558	U34558 Fusarium pr
18	301.2	97.2	534	8 FPU61670	U61670 Fusarium an
19	301.2	97.2	534	8 FPU61693	U61693 Fusarium sp
20	300.8	97.0	502	8 AF165873	AF165873 Gdbere11
21	299.6	96.6	534	8 FPU34574	U34574 Fusarium ph
22	297.2	95.9	559	8 FREDRRA	X94169 Fusarium re
23	296.4	95.6	534	8 FPU34567	U34567 Fusarium sp
24	296.4	95.6	534	8 FPU61692	U61692 Fusarium sp
25	294.8	95.1	534	8 FPU34564	U34564 Fusarium sp
26	294.2	94.9	541	8 AF158307	AF158307 Fusarium
27	294.2	94.9	541	8 AF158309	AF158309 Fusarium
28	294.2	94.9	559	8 FDLARRNA	X94177 Fusarium dl
29	291	93.9	527	8 FPU61687	U61687 Fusarium gl
30	290.8	93.8	521	8 FPU61691	U61691 Fusarium sp
31	290.2	93.6	535	8 FPU34573	U34573 Fusarium ac
32	290	93.5	535	8 FPU34565	U34565 Fusarium re
33	289.2	93.2	522	8 FCU61678	U61678 Fusarium co
34	289	93.2	542	8 AF008920	AF008920 Fusarium
35	288.6	93.1	535	8 FPU34572	U34572 Fusarium dl
36	288.4	93.0	349	8 AF162897	AF162897 Fusarium
37	288.4	93.0	529	8 AF158312	AF158312 Fusarium
38	288.4	93.0	557	8 FNYGRRNA	X94174 Fusarium ny
39	284.4	91.7	533	8 FNU34568	U34568 Fusarium ny
40	284.4	91.7	533	8 FPU34575	U34575 Fusarium ud
41	278.2	89.7	543	8 FPU34581	U34581 Fusarium bu
42	272.4	87.9	532	8 FPU34560	U34560 Fusarium th
43	272.2	87.8	434	8 AY243055	AY243055 Ascomycet
44	270.8	87.4	520	8 FPU61690	U61690 Fusarium sp
45	270.8	87.4	1458	8 AF310981	AF310981 Fusarium

## ALIGNMENTS

RESULT 1  
LOCUS AR206401 310 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 7 from patent US 6372430.  
ACCESSION AR206401  
VERSION AR206401.1 GI:21504992  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 310)  
AUTHORS Morrison,C.D., Reles,E., Aidorevich,L. and Choi,J.Soo.  
TITLE Nucleic acids for detecting Aspergillus species and other filamentous fungi  
JOURNAL Patent: US 6372430-A 7 16-APR-2002;



Best Local Similarity 100.0%; Pred. No. 1.2e-85;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGCGATAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCGACA 60  
DB 1 AATGCGATAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCGACA 60  
QY 61 TTGGCCCGCGCGAGTATCTGGCGGAGATGCCCTGTTCAGCGCATTTCAACCCCTCAAGCC 120  
DB 61 TTGGCCCGCGCGAGTATCTGGCGGAGATGCCCTGTTCAGCGCATTTCAACCCCTCAAGCC 120  
QY 121 CCCGGGTTTGTGTGTGGGAGATCGGCAAGCCCTTGGCGCAAGCCGCGCCCGGAATCTAGTG 180  
DB 121 CCCGGGTTTGTGTGTGGGAGATCGGCAAGCCCTTGGCGCAAGCCGCGCCCGGAATCTAGTG 180  
QY 181 GCGGTCTGCTGCTGACGCTTCATTCGTAGTAGTAAACCTTCGCAACTGTGTACGCGCGCC 240  
DB 181 GCGGTCTGCTGCTGACGCTTCATTCGTAGTAGTAAACCTTCGCAACTGTGTACGCGCGCC 240  
QY 241 GCGCAAGCGCGTTAAACCCCACTTCGTAGTAGTAAACCTTCGCAACTGTGTACGCGCGCC 300  
DB 241 GCGCAAGCGCGTTAAACCCCACTTCGTAGTAGTAAACCTTCGCAACTGTGTACGCGCGCC 300  
QY 301 CTGAACCTTAA 310  
DB 301 CTGAACCTTAA 310

RESULT 4  
AF162903  
LOCUS  
DEFINITION

AF162903 351 bp DNA linear PLN 04-AUG-1999  
Fusarium proliferatum 5.8S ribosomal RNA gene, partial sequence;  
internal transcribed spacer 2, complete sequence; and 28S ribosomal  
RNA gene, partial sequence.

ACCESSION  
AF162903  
VERSION  
AF162903.1 GI:5690392

KEYWORDS  
Fusarium proliferatum

ORGANISM

Fusarium proliferatum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella  
fujikuroi complex.  
1 (bases 1 to 351)  
Min.B.R.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji  
Dong, Chong Ro-Gu, Seoul 110-743, Korea

FEATURES  
source  
1..351  
Location/Qualifiers

/organism="Fusarium proliferatum"  
/mol\_type="genomic DNA"  
/strain="6787"  
/db\_xref="taxon:42674"

rRNA  
129..293  
/product="5.8S ribosomal RNA"

misc\_RNA  
294..351  
/product="internal transcribed spacer 2"

rRNA  
/product="28S ribosomal RNA"

ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 351;  
Best Local Similarity 99.4%; Pred. No. 1.2e-84;

Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGCGATAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCGACA 60  
DB 22 AATGCGATAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCGACA 81  
QY 61 TTGGCCCGCGCGAGTATCTGGCGGAGATGCCCTGTTCAGCGCATTTCAACCCCTCAAGCC 120  
DB 82 TTGGCCCGCGCGAGTATCTGGCGGAGATGCCCTGTTCAGCGCATTTCAACCCCTCAAGCC 141

QY 121 CCCGGGTTTGTGTGTGGGAGATCGGCAAGCCCTTGGCGGAGCCGCGCCCGGAATCTAGTG 180  
DB 142 CCCGGGTTTGTGTGTGGGAGATCGGCAAGCCCTTGGCGGAGCCGCGCCCGGAATCTAGTG 201

QY 181 GCGGTCTGCTGCTGACGCTTCATTCGTAGTAGTAAACCTTCGCAACTGTGTACGCGCGCC 240  
DB 202 GCGGTCTGCTGCTGACGCTTCATTCGTAGTAGTAAACCTTCGCAACTGTGTACGCGCGCC 261

QY 241 GCGCAAGCGCGTTAAACCCCACTTCGTAGTAGTAAACCTTCGCAACTGTGTACGCGCGCC 300  
DB 262 GCGCAAGCGCGTTAAACCCCACTTCGTAGTAGTAAACCTTCGCAACTGTGTACGCGCGCC 321

QY 301 CTGAACCTTAA 310  
DB 322 CTGAACCTTAA 331

RESULT 5  
AF455422  
LOCUS  
DEFINITION

AF455422 556 bp DNA linear PLN 16-JUN-2003  
Gibberella fujikuroi isolate w518 small subunit ribosomal RNA  
gene, partial sequence; internal transcribed spacer 1, 5.8S  
ribosomal RNA gene and internal transcribed spacer 2, complete  
sequence; and large subunit ribosomal RNA gene, partial sequence.

ACCESSION  
AF455422  
AF455422.1 GI:21666850

VERSION  
AF455422  
KEYWORDS  
Gibberella fujikuroi (anamorph: Fusarium fujikuroi)

ORGANISM

Gibberella fujikuroi  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella  
fujikuroi complex.  
1 (bases 1 to 556)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (04-DEC-2001) Laboratory for Mycology and Molecular  
Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Graz A  
8036, Austria

FEATURES  
source  
1..556  
Location/Qualifiers

/organism="Gibberella fujikuroi"  
/mol\_type="genomic DNA"  
/isolate="wb518"  
/db\_xref="taxon:5127"

rRNA  
49..247  
/product="small subunit ribosomal RNA"

misc\_RNA  
248..353  
/product="internal transcribed spacer 1"

rRNA  
354..518  
/product="5.8S ribosomal RNA"

misc\_RNA  
519..556  
/product="internal transcribed spacer 2"

rRNA  
/product="large subunit ribosomal RNA"

ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 556;  
Best Local Similarity 99.4%; Pred. No. 1.3e-84;

Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGCGATAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCGACA 60  
DB 247 AATGCGATAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCGACA 306  
QY 61 TTGGCCCGCGCGAGTATCTGGCGGAGATGCCCTGTTCAGCGCATTTCAACCCCTCAAGCC 120  
DB 307 TTGGCCCGCGCGAGTATCTGGCGGAGATGCCCTGTTCAGCGCATTTCAACCCCTCAAGCC 366

Qy	12	CCGGGGTTTGGTGTGAGGATCGGCAAGCCCTTGGGGGAACCGGGCCCCAAATCTAGTG	180
Db	367	CCGGGGTTTGGTGTGTGGGAATCGGCGAGCCCTTGGCGGAAGCCGCCCCGAATCTAGTG	426
Qy	181	GCGGCTCTCGTCGACGCTTCATTTGCGTGTAGTAAACCTTCGCAACTGTATCGGGCGC	240
Db	427	GCGGCTCTCGTGTGAGCTTCATTTGGGTGTAGTAAACCTTCGCACTGTATCGGGCGC	486
Qy	241	GGCCAAAGCGTTAAACCCCAACTTCTGAATTTGACTCGGATCAGGTAGAAATCCG	300
Db	487	GGCCAAAGCGTTAAACCCCAACTTCTGAATTTGACTCGGATCAGGTAGAAATCCG	546
Qy	301	CTGAACCTTAA	310
Db	547	CTGAACCTTAA	556

RESULT 6	AF455460	556 bp	DNA	linear	PLN 16-rUN-2003
LOCUS	AF455460				
DEFINITION	Gibberella fujikuroi isolate wh355 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence.				
ACCESSION	AF455460				
VERSION	AF455460.1	GI:21666892			

SOURCE ORGANISM	(anamorph: Fusarium fujikuroi)
Gibberella fujikuroi	
Gibberella fujikuroi	

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella  
futiluroi complex

REFERENCE  
AUTHORS  
1 (bases 1 to 556)  
Buzina, W., Braun, H., Freudenschuss, K., Lackner, A. and  
Stamberger, H.

TITLE	JOURNAL	REFERENCE
Fungal biodiversity as found in natural habitats	Med. Mycol. 41 (2), 149-161 (2003)	1
Fungal biodiversity as found in natural habitats	Med. Mycol. 41 (2), 149-161 (2003)	2

**AUTHORS**  
Buzina, W., Braun, H., Freudenschuss, K., Lackner, A. and  
Stamberger, H.

**JOURNAL** Submitted (04-DEC-2001) Laboratory for Mycology and Molecular Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Graz A 8036, Austria

FEATURES	Location/Qualifiers
source	1. .556

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/organism="Gibberella fujikuroi"
/mol_type="genomic DNA"
/isolate="b3cc"
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rRNA <1.48

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misc_RNA      49.247
/product="internal transcribed spacer 1"
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/product="5.8S ribosomal RNA"
354 518
miesc pna

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/product="Internal transcribed spacer 2"
519. .>556
rRNA

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# ORIGIN

Query Match	99.0%;	Score 306.8;	DB 8;	Length 556;
Best Local Similarity	99.4%;	Pred. No. 1.3e-84;		
Matches 308; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 AAATCGATACTATGTGATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACA 60

61 TTGCGCCCCGCCAGTATTTCTGGCGGCGATGCGCTGTTTCGAGCGTCATTTCAACCCCTAAGCC 120

Db	30	TTGCGGCCCCAGAGTATCTGGCGGGCATGCTGTTCCAGAGCGTCAATTCAACCCCTCAAGCC	36
Qy	121	CCGGGGTTTGATGTGGGGATTCGGAGAACCCCTTCCGGCAACCGGCCCCGAATCTTAGTG	180
Db	367	CCGGGGTTTGATGTGGGGATTCGGAGAACCCCTTCCGGCAACCGGCCCCGAATCTTAGTG	426
Qy	181	GGGATCTGCTCAGCTTCCATTGGGTAGTAGTAAAACTTCGCAACTGTACGCGGCGC	240
Db	427	GGGATCTGCTCAGCTTCCATTGGGTAGTAGTAAAACTTCGCAACTGTACGCGGCGC	486
Qy	241	GGCCAAAGCGTTAAACCCCAACTTCGATGTTGACCTCGGATCAGTAGAGTAATCCCG	300
Db	487	GGCCAAAGCGTTAAACCCCAACTTCGATGTTGACCTCGGATCAGTAGAGTAATCCCG	546
Qy	301	CTGAACCTTAA	310
Db	547	CTGAACCTTAA	556

RESULT 7  
FFUJRNA  
LOCUS

LOCUS	558 bp	DNA	linear	PLN 14-JUN-2001
EFU0KRNA				
DEFINITION	Fusarium fujikuroi 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial)			

Accession X94176 X93900  
 Internal transcribed spacer 1 (ITS1) and  
 internal transcribed spacer 2 (ITS2).

## KEYWORDS

SOURCE Gibberella fujikuroi (anamorph: Fusarium fujikuroi)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordaria  
Hymenochaetales; Nectriaceae; Gibberella

REFERENCE

1. LUGANOV COMPLEX.

TITLE	DESCRIPTION	DATE	BY
Discordant groupings of <i>Fusarium</i> spp. from sections E			

JOURNAL  
REFERENCE  
Mycologia 88, 361-368 (1996)  
2 (pages 1 to 558)

Submitted (08-DEC-1995) C. Waalwijk, Research inst. for Plant

COMMENT On Jun 15, 2001 this sequence version replaced gi:1103564.. Overlaps with X78260.

FEATURES	Location/Qualifiers
source	1. .558

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/mol_type="genomic DNA"
/strain="CBS 221-76"
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/db\_xref="taxon:5127"

RNA	<1. .30
18S	1.00
28S	1.00
5S	1.00
5.8S	1.00
5.9S	1.00
6S	1.00
7S	1.00
8S	1.00
9S	1.00
10S	1.00
11S	1.00
12S	1.00
13S	1.00
14S	1.00
15S	1.00
16S	1.00
17S	1.00
18S	1.00
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21S	1.00
22S	1.00
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94S	1.00
95S	1.00
96S	1.00
97S	1.00
98S	1.00
99S	1.00
100S	1.00

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misc feature
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31..177
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qen

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rRNA
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  178.335
  /gene="5.8 rRNA"
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misc\_feature

2RN7

## ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 558;  
 Beef Local Similarity 99.4%; Pred. No. 1.3e-84;  
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATCGATTAAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCACA 60  
 DB 229 AATCGATTAAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCACA 288  
 QY 61 TTGGCCCGCCGCAAGTATTCGCGGGGATGCTGTTGAGCGTCAATTCACCTCAAGCC 120  
 DB 289 TTGGCCCGCCGCAAGTATTCGCGGGGATGCTGTTGAGCGTCAATTCACCTCAAGCC 348  
 QY 121 CCCGGGTTGGTGTGGGATGGCAAGCCCTTGGGGCAAGCCGCCGAATCTAGTG 180  
 DB 349 CCCGGGTTGGTGTGGGATGGCAAGCCCTTGGGGCAAGCCGCCGAATCTAGTG 408  
 QY 181 GCGGTCTGCTGACGCTTCATTCGAGTAGTAAACCTCGCAACTGTGAGCGGCGC 240  
 DB 409 GCGGTCTGCTGACGCTTCATTCGAGTAGTAAACCTCGCAACTGTGAGCGGCGC 468  
 QY 241 GCGCAAGCGGTTAAACCCCAACTTCTGATGTGAACCTCGATCAGTAGAATACCG 300  
 DB 469 GCGCAAGCGGTTAAACCCCAACTTCTGATGTGAACCTCGATCAGTAGAATACCG 528  
 QY 301 CTGAACCTTAA 310  
 DB 529 CTGAACCTTAA 538

RESULT 8  
 PPRORNA  
 LOCUS 558 bp DNA linear PLN 14-JUN-2001

DEFINITION Fusarium proliferatum 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2).

VERSION X94171.X93904

ACCESSION X94171.1 GI:1122873

KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.

## SOURCE

ORGANISM Fusarium proliferatum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.

REFERENCE 1 Maalwijk, C., de Koning, J.R.A., Baayen, R.P. and Gams, W.  
 Discordant groupings of *Fusarium* spp. from sections *Elegans*, *Liaseola* and *Diamnia* a based on ribosomal ITS1 and ITS2 sequences

JOURNAL Mycologia 88, 361-368 (1996)  
 REFERENCE 2 (bases 1 to 558)  
 AUTHORS Maalwijk, C.  
 TITLE Direct Submission

COMMENT Submitted (08-DEC-1995) C. Maalwijk, Research Inst. for Plant Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS  
 JOURNAL On Jun 15, 2001 this sequence version replaced gi:1103572.  
 OVERLAPS Overlaps with X78260.

## FEATURES

source 1..558  
 location/Qualifiers  
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 /organism="Fusarium proliferatum"  
 /mol\_type="genomic DNA"  
 /strain="CBS 217.76"  
 /specific\_host="Cattleya"  
 /db\_xref="taxon:42674"  
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 /gene="18S rRNA"  
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 /gene="18S rRNA"  
 /product="18S ribosomal RNA"  
 31..177  
 /note="internal transcribed spacer 1, ITS1"

gene

178..335  
 /gene="5.8 rRNA"

rRNA

178..335  
 /gene="5.8 rRNA"

misc\_feature

336..500  
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gene

501..558  
 /gene="28S rRNA"

rRNA

501..558  
 /gene="28S rRNA"

## ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 558;  
 Beef Local Similarity 99.4%; Pred. No. 1.3e-84;  
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATCGATTAAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCACA 60  
 DB 229 AATCGATTAAGTATGTAATGCAAAATTCAGTGAATCATGATCTTTGAAGCACA 288  
 QY 61 TTGGCCCGCCGCAAGTATTCGCGGGGATGCTGTTGAGCGTCAATTCACCTCAAGCC 120  
 DB 289 TTGGCCCGCCGCAAGTATTCGCGGGGATGCTGTTGAGCGTCAATTCACCTCAAGCC 348  
 QY 121 CCCGGGTTGGTGTGGGATGGCAAGCCCTTGGGGCAAGCCGCCGAATCTAGTG 180  
 DB 349 CCCGGGTTGGTGTGGGATGGCAAGCCCTTGGGGCAAGCCGCCGAATCTAGTG 408  
 QY 181 GCGGTCTGCTGACGCTTCATTCGAGTAGTAAACCTCGCAACTGTGAGCGGCGC 240  
 DB 409 GCGGTCTGCTGACGCTTCATTCGAGTAGTAAACCTCGCAACTGTGAGCGGCGC 468  
 QY 241 GCGCAAGCGGTTAAACCCCAACTTCTGATGTGAACCTCGATCAGTAGAATACCG 300  
 DB 469 GCGCAAGCGGTTAAACCCCAACTTCTGATGTGAACCTCGATCAGTAGAATACCG 528  
 QY 301 CTGAACCTTAA 310  
 DB 529 CTGAACCTTAA 538

## RESULT 9

AY237110

LOCUS AY237110 562 bp DNA linear PLN 09-APR-2003

DEFINITION Fusarium sp. 03001 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8 ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AY237110  
 VERSION AY237110.1 GI:29691499

KEYWORDS Fusarium sp. 03001  
 SOURCE Fusarium sp. 03001

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 562)  
 AUTHORS Afunian, M.R. and Heiang, T.

TITLE Direct Submission  
 JOURNAL Submitted (14-FEB-2003) Environmental Biology, University of Guelph, Guelph, ON N1G 2W1, Canada  
 location/Qualifiers  
 1..562

FEATURES  
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 /isolate="03001"  
 /db\_xref="taxon:227081"  
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 /product="18S ribosomal RNA"  
 41..186  
 /product="internal transcribed spacer 1"  
 187..345

misc\_RNA  
346..510  
/product="5.8 ribosomal RNA"

rRNA  
511..>562  
/product="28S ribosomal RNA"

## ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 562;  
Best Local Similarity 99.4%; Pred. No. 1.3e-84;  
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAATGCGATTAAGTAATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 60  
DB 239 AAATGCGATTAAGTAATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 298  
QY 61 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTTCCAGCGCTCATTTCAACCTTCAAGCC 120  
DB 239 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTTCCAGCGCTCATTTCAACCTTCAAGCC 358  
QY 121 CCCGGGTTTGGTGGGGATCGGCAAGCCCTTGGCGGAGCCGGCCCGGAAATCTAGT 180  
DB 359 CCCGGGTTTGGTGGGGATCGGCAAGCCCTTGGCGGAGCCGGCCCGGAAATCTAGT 418  
QY 181 GCGGCTCTGCTGACGCTTCATTCGTAAGTAATAACCTTCGCACTGTGACGCGCGC 240  
DB 419 GCGGCTCTGCTGACGCTTCATTCGTAAGTAATAACCTTCGCACTGTGACGCGCGC 478  
QY 241 GGGCAAGCGGTTAAACCCCAACTTCGTAATGTTGACTCGGATCAGATGAGTAATACCG 300  
DB 479 GGGCAAGCGGTTAAACCCCAACTTCGTAATGTTGACTCGGATCAGATGAGTAATACCG 538  
QY 301 CTGAACCTTAA 310  
DB 539 CTGAACCTTAA 548

RESULT 10  
AF452163 569 bp DNA linear PLN 27-DEC-2001  
LOCUS Pythium ultimum var. sporangiiiferum isolate 308276R 18S ribosomal  
DEFINITION RNA gene, partial sequence.  
ACCESSION AF452163  
VERSION AF452163.1 GI:17980882  
KEYWORDS Pythium ultimum var. sporangiiiferum  
SOURCE Pythium ultimum var. sporangiiiferum  
ORGANISM Pythium  
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;

REFERENCE 1 (bases 1 to 569)  
AUTHORS Moorman,G.W., Geisler,D.M., Kang,S. and Kim,S.  
TITLE Pythium species and a population identification using DNA markers  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 569)  
AUTHORS Moorman,G.W., Geisler,D.M., Kang,S. and Kim,S.  
TITLE Pythium species and a population identification using DNA markers  
JOURNAL Submitted (26-NOV-2001) Plant Pathology, Pennsylvania State  
Direct Submission University, 210 Buckhout Laboratory, University Park, PA 16802, USA  
LOCATION/Qualifiers

FEATURES  
source  
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/organism="Pythium ultimum var. sporangiiiferum"  
/mol\_type="genomic DNA"  
/variety="sporangiiiferum"  
/isolate="308276R"  
/db\_xref="taxon:115421"  
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/product="18S ribosomal RNA"

## ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 569;  
Best Local Similarity 99.4%; Pred. No. 1.3e-84;  
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAATGCGATTAAGTAATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 60

DB 246 AAATGCGATTAAGTAATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 305  
QY 61 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTTCCAGCGCTCATTTCAACCTTCAAGCC 120  
DB 306 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTTCCAGCGCTCATTTCAACCTTCAAGCC 365  
QY 121 CCCGGGTTTGGTGGGGATCGGCAAGCCCTTGGCGGAGCCGGCCCGGAAATCTAGT 180  
DB 366 CCCGGGTTTGGTGGGGATCGGCAAGCCCTTGGCGGAGCCGGCCCGGAAATCTAGT 425  
QY 181 GCGGCTCTGCTGACGCTTCATTCGTAAGTAATAACCTTCGCACTGTGACGCGCGC 240  
DB 426 GCGGCTCTGCTGACGCTTCATTCGTAAGTAATAACCTTCGCACTGTGACGCGCGC 485  
QY 241 GGGCAAGCGGTTAAACCCCAACTTCGTAATGTTGACTCGGATCAGATGAGTAATACCG 300  
DB 486 GGGCAAGCGGTTAAACCCCAACTTCGTAATGTTGACTCGGATCAGATGAGTAATACCG 545  
QY 301 CTGAACCTTAA 310  
DB 546 CTGAACCTTAA 555

RESULT 11  
AF291061 596 bp DNA linear PLN 18-SEP-2001  
LOCUS Fusarium proliferatum NRRL 31071 18S ribosomal RNA, partial  
DEFINITION sequence; internal transcribed spacer 1, 5.8S ribosomal RNA, and  
internal transcribed spacer 2, complete sequence; 28S ribosomal  
RNA, partial sequence.  
ACCESSION AF291061  
VERSION AF291061.1 GI:15637128  
KEYWORDS Fusarium proliferatum  
SOURCE Fusarium proliferatum  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella  
fujikuroi complex.  
REFERENCE 1 (bases 1 to 596)  
AUTHORS Kwon,S.-I., van Dohnon,C.D. and Anderson,A.J.  
TITLE Gene sequence analysis of an opportunistic wheat pathogen, an  
isolate of Fusarium proliferatum  
JOURNAL Can. J. Bot. 79 (9), 1115-1121 (2001)  
REFERENCE 2 (bases 1 to 596)  
AUTHORS Kwon,S.-I. and Anderson,A.J.  
TITLE Direct Submission  
JOURNAL Submitted (31-JUL-2000) Biology, Utah State University, Logan, UT  
84322-5305, USA  
LOCATION/Qualifiers

FEATURES  
source  
1..596  
/organism="Fusarium proliferatum"  
/mol\_type="genomic DNA"  
/strain="NRRL 31071"  
/specific\_host="Triticum aestivum cv. Super Dwarf"  
/db\_xref="taxon:42674"  
<1..596  
/note="contains 18S ribosomal RNA, internal transcribed  
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer  
2, 28S ribosomal RNA"

## ORIGIN

Query Match 99.0%; Score 306.8; DB 8; Length 596;  
Best Local Similarity 99.4%; Pred. No. 1.3e-84;  
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAATGCGATTAAGTAATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 60  
DB 267 AAATGCGATTAAGTAATGTAATTCGAAATTCAGTGAATCATGCAATCTTTGAACGACA 326  
QY 61 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTTCCAGCGCTCATTTCAACCTTCAAGCC 120  
DB 327 TTGGCCCCCGCCAGTATTTCTGGGGGCGCATGCTGTTTCCAGCGCTCATTTCAACCTTCAAGCC 386



QY 121 CCCGGGTTTGGTGGGGATCGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGT 180  
 DB 387 CCCGGGTTTGGTGGGGATCGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGT 446  
 QY 181 GCGGTCTGCTGCTGACCTTCCATTGGTGTAGTAAACCTTCGCACTGTACGGGGCC 240  
 DB 447 GCGGTCTGCTGCTGACCTTCCATTGGTGTAGTAAACCTTCGCACTGTACGGGGCC 506  
 QY 241 GGGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGGTAGTAATCCG 300  
 DB 507 GGGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGGTAGTAATCCG 566  
 QY 301 CTGAACCTTAA 310  
 DB 567 CTGAACCTTAA 576

## RESULT 12

LOCUS AR168094 2293 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 1 from patent US 6287800.  
 ACCESSION AR168094  
 VERSION AR168094.1 GI:17903914  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS Unpublished.  
 TITLE (bases 1 to 2293)  
 Giallazo, J.L. and Lee, M.D.  
 Production of high titers of gibberellins, GA4 and GA7, by  
 Gibberella fujikuroi strain IIRB-1027  
 Parent: US 6287800-A 1 11-SEP-2001;  
 Location/Qualifiers  
 1..2293  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 99.0%; Score 306.8; DB 6; Length 2293;  
 Best Local Similarity 99.4%; Pred. No. 1.5e-84;  
 Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AAATGCGATAGTATGATGCAAAATTCAGATGATCATTCGAATCTTTGAAGCACA 60  
 DB 1972 AAATGCGATAGTATGATGCAAAATTCAGATGATCATTCGAATCTTTGAAGCACA 2031  
 QY 61 TTGGGCGCGCAGATATTCGGCGGGCATGCTGTTCGAGCGTCATTTCAACCCCTCAAGCC 120  
 DB 2032 TTGGGCGCGCAGATATTCGGCGGGCATGCTGTTCGAGCGTCATTTCAACCCCTCAAGCC 2091  
 QY 121 CCCGGGTTTGGTGGGGATCGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGTG 180  
 DB 2092 CCCGGGTTTGGTGGGGATCGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGTG 2151  
 QY 181 GCGGTCTGCTGCTGACCTTCCATTGGTGTAGTAAACCTTCGCACTGTACGGGGCC 240  
 DB 2152 GCGGTCTGCTGCTGACCTTCCATTGGTGTAGTAAACCTTCGCACTGTACGGGGCC 2211  
 QY 241 GGGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGGTAGTAATCCG 300  
 DB 2212 GGGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGGTAGTAATCCG 2271  
 QY 301 CTGAACCTTAA 310  
 DB 2272 CTGAACCTTAA 2281

## RESULT 13

LOCUS AF158303 531 bp DNA linear PLN 21-MAR-2000  
 DEFINITION Fusarium sp. NRRL26794 18S ribosomal RNA gene, partial sequence;  
 Internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal

transcribed spacer 2, complete sequence; and 28S ribosomal RNA  
 gene, partial sequence.  
 AF158303  
 AF158303.1 GI:7106206  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Fusarium sp. NRRL 26794  
 Fusarium sp. NRRL 26794  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
 1 (bases 1 to 531)  
 O'Donnell, K., Nirenberg, H. I., Aoki, T. and Cigelnik, E.  
 A multigene phylogeny of the Gibberella fujikuroi species complex:  
 detection of additional phylogenetically distinct species  
 Mycoscience 41, 61-78 (2000)  
 2 (bases 1 to 531)  
 O'Donnell, K.  
 Direct Submission  
 Submitted (10-JUN-1999) Microbial Properties, NCAMR-USDA-ARS, 1815  
 N. University St., Peoria, IL 61604, USA  
 Location/Qualifiers  
 1..531  
 /organism="Fusarium sp. NRRL 26794"  
 /mol\_type="genomic DNA"  
 /strain="NRRL26794"  
 /db\_xref="taxon:100621"  
 <1..23  
 /product="18S ribosomal RNA"  
 24..169  
 /product="internal transcribed spacer 1"  
 170..328  
 /product="5.8S ribosomal RNA"  
 329..493  
 /product="internal transcribed spacer 2"  
 494..>531  
 /product="28S ribosomal RNA"

## ORIGIN

Query Match 98.5%; Score 305.2; DB 8; Length 531;  
 Best Local Similarity 99.0%; Pred. No. 4e-84;  
 Matches 307; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 AAATGCGATAGTATGATGCAAAATTCAGTGAATCATTCGAATCTTTGAAGCACA 60  
 DB 222 AAATGCGATAGTATGATGCAAAATTCAGTGAATCATTCGAATCTTTGAAGCACA 281  
 QY 61 TTGGGCGCGCAGATATTCGGCGGGCATGCTGTTCGAGCGTCATTTCAACCCCTCAAGCC 120  
 DB 282 TTGGGCGCGCAGATATTCGGCGGGCATGCTGTTCGAGCGTCATTTCAACCCCTCAAGCC 341  
 QY 121 CCCGGGTTTGGTGGGGATCGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGTG 180  
 DB 342 CTCGGGTTTGGTGGGGATCGCAAGCCCTTGGGGCAAGCCGGCCCGGAATCTAGTG 401  
 QY 181 GCGGTCTGCTGCTGACCTTCCATTGGTGTAGTAAACCTTCGCACTGTACGGGGCC 240  
 DB 402 GCGGTCTGCTGCTGACCTTCCATTGGTGTAGTAAACCTTCGCACTGTACGGGGCC 461  
 QY 241 GGGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGGTAGTAATCCG 300  
 DB 462 GGGCAAGCCGTTAAACCCCAACTTCTGAATGTTGACCTCGATCAGGTAGTAATCCG 521  
 QY 301 CTGAACCTTAA 310  
 DB 522 CTGAACCTTAA 531

## RESULT 14

LOCUS AF158304 540 bp DNA linear PLN 21-MAR-2000  
 DEFINITION Fusarium sp. NRRL28852 18S ribosomal RNA gene, partial sequence;  
 Internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal  
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA  
 gene, partial sequence.



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using BW model

Run on: October 1, 2004, 03:09:43 ; Search time 102.159 Seconds  
(without alignments)  
1683.989 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310

Sequence: 1 aaatgcgataagtaagtgtga.....sgaataccgcgtgaacttaa 310

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/6C\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/6D\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	US-09-423-233-7	Sequence 7, Appli
2	306.8	99.0	2293	US-09-645-073-1	Sequence 1, Appli
3	249.8	80.6	561	US-08-905-314A-24	Sequence 24, Appli
4	240.2	77.5	319	US-09-423-233-6	Sequence 6, Appli
5	231	74.5	583	US-08-652-127C-8	Sequence 8, Appli
6	225.2	72.6	531	US-08-652-127C-7	Sequence 7, Appli
7	224.2	72.3	581	US-08-652-127C-6	Sequence 6, Appli
8	197.8	63.8	594	US-08-652-127C-5	Sequence 5, Appli
9	187.6	60.5	546	US-08-887-480-96	Sequence 96, Appli
10	187.6	60.5	546	US-08-905-314A-22	Sequence 22, Appli
11	186.6	60.2	504	US-08-887-480-82	Sequence 82, Appli
12	186.6	60.2	504	US-08-905-314A-19	Sequence 19, Appli
13	186.6	60.2	504	US-08-722-187-82	Sequence 82, Appli
14	186.6	60.2	504	PCT-US95-04712-82	Sequence 82, Appli
15	185	59.7	611	US-08-986-727-4	Sequence 84, Appli
16	183.2	59.1	545	US-08-887-480-84	Sequence 84, Appli
17	183.2	59.1	545	US-08-905-314A-21	Sequence 21, Appli
18	180.4	58.2	503	US-08-887-480-83	Sequence 83, Appli
19	180.4	58.2	503	US-08-905-314A-20	Sequence 20, Appli
20	180.4	58.2	503	US-08-722-187-83	Sequence 83, Appli
21	180.4	58.2	503	PCT-US95-04712-83	Sequence 83, Appli
22	174.2	56.2	504	US-09-481-293-32	Sequence 32, Appli
23	166.2	53.6	545	US-08-722-187-85	Sequence 85, Appli
24	166.2	53.6	545	PCT-US95-04712-85	Sequence 85, Appli
25	163.8	52.8	608	US-08-986-727-3	Sequence 3, Appli
26	139	44.8	605	US-08-986-727-1	Sequence 1, Appli
27	136	43.9	365	US-09-423-233-3	Sequence 3, Appli

28	136	43.9	587	1	US-08-742-023-7	Sequence 7, Appli
29	136	43.9	587	3	US-08-968-505-7	Sequence 2, Appli
30	136	43.9	617	3	US-08-986-727-2	Sequence 2, Appli
31	131.4	42.4	364	4	US-09-423-233-2	Sequence 4, Appli
32	126.6	40.8	556	3	US-09-037-9908-7	Sequence 7, Appli
33	125.2	40.4	627	1	US-08-233-608-47	Sequence 47, Appli
34	125.2	40.4	627	2	US-08-887-480-47	Sequence 47, Appli
35	125.2	40.4	627	1	US-08-722-187-47	Sequence 47, Appli
36	125.2	40.4	627	5	PCT-US95-04712-47	Sequence 47, Appli
37	125	40.3	309	4	US-09-423-233-28	Sequence 28, Appli
38	124.4	40.1	536	4	US-09-517-790-5	Sequence 5, Appli
39	124.4	40.1	556	1	US-08-887-480-85	Sequence 85, Appli
40	124.4	40.1	556	1	US-08-905-314A-23	Sequence 23, Appli
41	124.4	40.1	580	3	US-08-742-023-6	Sequence 6, Appli
42	124.4	40.1	580	3	US-08-968-505-6	Sequence 6, Appli
43	123.6	39.9	626	1	US-08-233-608-3	Sequence 3, Appli
44	123.6	39.9	626	1	US-08-887-480-3	Sequence 3, Appli
45	123.6	39.9	626	2	US-08-722-187-3	Sequence 3, Appli

## ALIGNMENTS

```

RESULT 1
US-09-423-233-7
; Sequence 7, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09/423,233
; NUMBER OF SEQUENCE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-7

Query Match      100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 8.5e-93;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAATGCATTAAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
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DB      1 AAATGCCATAAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
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QY      61 TTGGCCCGCCAGTATTCGCGGGGATGCTGTTGAGCGTCAATTCACCTCAAGCC 120
|       |||
DB      61 TTGGCCCGCCAGTATTCGCGGGGATGCTGTTGAGCGTCAATTCACCTCAAGCC 120
|       |||

QY      121 CCGCGGTTTGTTGGGATTCGCAAGCCCTTCCGCAAGCCGCCCAAAATCTAGTG 180
|       |||
DB      121 CCGCGGTTTGTTGGGATTCGCAAGCCCTTCCGCAAGCCGCCCAAAATCTAGTG 180
|       |||

QY      181 GCGGTCGCGTCAATTCGAGTAGTAAGTAAGCCCTCGCAATGAGTAGGATACCCG 240
|       |||
DB      181 GCGGTCGCGTCAATTCGAGTAGTAAGTAAGCCCTCGCAATGAGTAGGATACCCG 240
|       |||

QY      241 GGCAGACCGTTAAACCCCACTTCGAAATGTTGACCTCGATCAGTAGGAATACCCG 300
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DB      241 GGCAGACCGTTAAACCCCACTTCGAAATGTTGACCTCGATCAGTAGGAATACCCG 300
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QY      301 CTGAACCTTAA 310
|       |||
DB      301 CTGAACCTTAA 310
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RESULT 2
US-09-645-073-1

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; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; APPLICANT: Galazzo, Jorge
; TITLE OF INVENTION: Production of High Titters of Gibberellins GA4 and GA7
; FILE REFERENCE: 102-01ND
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Gibberella fujikuroi
US-09-645-073-1

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Query Match      99.0%; Score 306.8; DB 3; Length 2293;
Best Local Similarity 99.4%; Pred. No. 2.2e-91;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 AAATGCGATTAAGTATGATGATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 60
DB 1972 AAATGCGATTAAGTATGATGATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 2031
QY 61 TTGGCCCCCGCAATGATTTGGCGGCGATGCGCTGTTCAGAGCGTCAATCCCTGAAGCC 120
DB 2032 TTGGCCCCCGCAATGATTTGGCGGCGATGCGCTGTTCAGAGCGTCAATCCCTGAAGCC 2091
QY 121 CCCGGGTTTGGTGTGGGGATTCGGCAAGCCCTTGGCGCAAGCGGCGCCGCAAAATCTAGTG 180
DB 2092 CCCGGGTTTGGTGTGGGGATTCGGCAAGCCCTTGGCGCAAGCGGCGCCGCAAAATCTAGTG 2151
QY 181 GCGGCTCGCTGCGAGCTTCATTCAGTAGTAAACCCCTCGCACTGCTAGCGCGCGC 240
DB 2152 GCGGCTCGCTGCGAGCTTCATTCAGTAGTAAACCCCTCGCACTGCTAGCGCGCGC 2211
QY 241 GCGCAACCGCTTAAACCCCACTTCGTGATGTTGACCTCGGATCAGGTGGAATACCCG 300
DB 2212 GCGCAACCGCTTAAACCCCACTTCGTGATGTTGACCTCGGATCAGGTGGAATACCCG 2271
QY 301 CTGAACCTTAA 310
DB 2272 CTGAACCTTAA 2281

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RESULT 3
US-08-905-314A-24
; Sequence 24, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium avenaceum
; INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note="3' end of small subunit"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..181
; OTHER INFORMATION: /note="ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 182..338
; OTHER INFORMATION: /note="5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 339..504
; OTHER INFORMATION: /note="ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 505..561
; OTHER INFORMATION: /note="5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
US-08-905-314A-24

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Query Match      80.6%; Score 249.8; DB 1; Length 561;
Best Local Similarity 91.6%; Pred. No. 7.8e-73;
Matches 285; Conservative 1; Mismatches 23; Indels 2; Gaps 2;

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QY 1 AAATGCGATTAAGTATGATGATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 60
DB 232 AAATGCGATTAAGTATGATGATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 291
QY 61 TTGGCCCCCGCAATGATTTGGCGGCGATGCGCTGTTCAGAGCGTCAATCCCTGAAGCC 120
DB 292 TTGGCCCCCGCAATGATTTGGCGGCGATGCGCTGTTCAGAGCGTCAATCCCTGAAGCC 351
QY 121 CCCGGGTTTGGTGTGGGGATTCGGCAAGCCCTTGGCGCAAGCGGCGCCGCAAAATCTAGT 179
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QY 180 GCGGCTCGCTGCGAGCTTCATTCAGTAGTAAACCCCTCGCACTGCTAGCGCGCGC 239
DB 412 GCGGCTCGCTGCGAGCTTCATTCAGTAGTAAACCCCTCGCACTGCTAGCGCGCGC 471
QY 240 GCGCAACCGCTTAAACCCCACTTCGTGATGTTGACCTCGGATCAGGTGGAATACCCG 299
DB 472 GCGCAACCGCTTAAACCCCACTTCGTGATGTTGACCTCGGATCAGGTGGAATACCCG 530
QY 300 GCTGAACCTTAA 310
DB 531 GCTGAACCTTAA 541

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RESULT 4
US-09-423-233-6
; Sequence 6, Application US/09423233

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Patent No. 6372430  
 GENERAL INFORMATION:  
 APPLICANT: The Government of the United States of America as  
 TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
 TITLE OF INVENTION: Other Filamentous Fungi  
 FILE REFERENCE: 03063-0341WP  
 CURRENT APPLICATION NUMBER: US/09/423,233  
 CURRENT FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 61  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 6  
 LENGTH: 319  
 TYPE: DNA  
 ORGANISM: Fusarium solani  
 US-09-423-233-6

Query Match 77.5%; Score 240.2; DB 4; Length 319;  
 Best Local Similarity 87.4%; Pred. No. 9,1e-70;  
 Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

QY 1 AAATGCCGTAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60  
 DB 3 AAATGCCGTAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 62  
 QY 61 TTGCGCCCGCCAGTATTCGCGGCGCATGCTGTTGAGCGCATTTCAACCCCTCAAGCC 120  
 DB 63 TTGCGCCCGCCAGTATTCGCGGCGCATGCTGTTGAGCGCATTTCAACCCCTCAAGCC 122  
 QY 121 CCCGGTTTGGTGTGGGGAATCGCGAAGCCCTTGGCGC-----AAGCCGCGCCCGAAA 173  
 DB 123 CCCGGCTTGGGATCGGGGATCGGGGAAGCCCTTGGCGGCAACAAGCCCGCCCAAA 182  
 QY 174 TCTAGTGGCGGTCTGCGTGCAGCTTCCATTTGGTGTAGTAAACCTTCGCACTGGTAC 233  
 DB 183 TACAGTGGCGGTCTGCGTGCAGCTTCCATTTGGTGTAGTAAACCTTCGCACTGGTAC 242  
 QY 234 GCGGCGCGCCAGCGCTTAAACCCCACTTCTGAATGTGACCTCGGATCAGGTAGA 293  
 DB 243 GCGGCGCGCCAGCGCTTAAACCCCACTTCTGAATGTGACCTCGGATCAGGTAGA 302  
 QY 294 ATACCCGCTGAACCTTAA 310  
 DB 303 ATACCCGCTGAACCTTAA 319

RESULT 5  
 US-08-652-127C-8  
 Sequence 8, Application US/08652127C  
 Patent No. 5792611  
 GENERAL INFORMATION:  
 APPLICANT: Richard C. Hamelin  
 TITLE OF INVENTION: DETECTION OF PLANT  
 NUMBER OF INVENTION: PATHOGEN FUNGI  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: George A. Seady  
 STREET: 880 Wellington Street, Suite 708  
 CITY: Ottawa  
 COUNTRY: Canada  
 ZIP: K1R 6K7  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/652,127C  
 FILING DATE: May 23, 1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: George A. Seady  
 REGISTRATION NUMBER: 24,034

REFERENCE/DOCKET NUMBER: 1898  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (613) 232-5815  
 TELEFAX: (613) 232-5831  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 583  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 US-08-652-127C-8

Query Match 74.5%; Score 231; DB 1; Length 583;  
 Best Local Similarity 90.4%; Pred. No. 1.3e-66;  
 Matches 281; Conservative 0; Mismatches 25; Indels 5; Gaps 3;

QY 1 AAATGCCGTAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60  
 DB 257 AAATGCCGTAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 316  
 QY 61 TTGCGCCCGCCAGTATTCGCGGCGCATGCTGTTGAGCGCATTTCAACCCCTCAAGCC 120  
 DB 317 TTGCGCCCGCCAGTATTCGCGGCGCATGCTGTTGAGCGCATTTCAACCCCTCAAGCC 376  
 QY 121 CCCGGTTTGGTGTGGGGAATCGCGAAGCCCTTGGCGCAAGCCCGCCGAAATCTAGTG 180  
 DB 377 CCCGGCTTGGTGTGGGGAATCGCGAAGCCCTTGGCGCAAGCCCGCCGAAATCTAGTG 435  
 QY 181 GCGGTCTGCTGCACTTCCATTCGTAAGTAAACCTTCGCACTGGATCAGCGCGC 240  
 DB 436 GCGGTCTGCTGTAAGTCTTCCATTCGTAAGTAAACCTTCGCACTGGATCAGCGCGC 492  
 QY 241 GCGCAAGCGCTTAAACCCCACTTCTGAATG-TTACCTGCGATCGTGAATGCC 299  
 DB 493 GCGCAAGCGCTTAAACCCCACTTCTGAATG-TTACCTGCGATCGTGAATGCC 552  
 QY 300 GCTGAACCTTAA 310  
 DB 553 GCTGAACCTTAA 563

RESULT 6  
 US-08-652-127C-7  
 Sequence 7, Application US/08652127C  
 Patent No. 5792611  
 GENERAL INFORMATION:  
 APPLICANT: Richard C. Hamelin  
 TITLE OF INVENTION: DETECTION OF PLANT  
 NUMBER OF INVENTION: PATHOGEN FUNGI  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: George A. Seady  
 STREET: 880 Wellington Street, Suite 708  
 CITY: Ottawa  
 COUNTRY: Canada  
 ZIP: K1R 6K7  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/652,127C  
 FILING DATE: May 23, 1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: George A. Seady  
 REGISTRATION NUMBER: 24,034  
 REFERENCE/DOCKET NUMBER: 1898  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (613) 232-5815  
 TELEFAX: (613) 232-5831

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 531  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-652-127C-7

Query Match 72.6%; Score 225.2; DB 1; Length 531;  
Best Local Similarity 88.8%; Pred. No. 9.9e-65;  
Matches 277; Conservative 0; Mismatches 30; Indels 5; Gaps 3;

QY 1 AATGCGATAGTAATGTAATGTAATGCAAAATTCAGTATCATCATCATCTTTGAACGACA 60  
DB 203 AATGCGATAGTAATGTAATGTAATGCAAAATTCAGTATCATCATCTTTGAACGACA 262  
QY 61 TTGCGCCCGCCAGTATTTCTGGGGGCGATGCTGTTGAGCGTCAATTCACCTCAAGCC 120  
DB 263 TTGCGCCCGCCAGTATTTCTGGGGGCGATGCTGTTGAGCGTCAATTCACCTCAAGCC 322  
QY 121 CCCGGGTTTGGTGTGGGAGTCGCGAAG-CCCTTGGCGGCAAGCGGCGCCGAATCTAGT 179  
DB 323 CCCGGGTTTGGTGTGGGAGTCGCGAAG-CCCTTGGCGGCGGCGGCGGCGCTCTTAATATATAGT 382  
QY 180 GCGGCTCTGCTGCGAGCTTCGATTCGATAGTAAACCTCGCAACTGGTACGCGGCG 239  
DB 383 GCGGCTCTGCTGATAGTCTTCTGCGATAGTACACCTGCG--ACTGAAAACAGCG 439  
QY 240 CGGCGAAGCGCTTAAACCCCACTTCTG-AATGTTGACCTGGATCAGGTAGGAATACC 298  
DB 440 CGGCGAAGCGCTTAAACCCCACTTCTGAAAGGTTGACCTGGATCAGGTAGGAATACC 499  
QY 299 CGCTGAACCTTAA 310  
DB 500 CGCTGAACCTTAA 511

## RESULT 7

US-08-652-127C-6  
Sequence 6, Application US/08652127C  
Patent No. 5792611  
GENERAL INFORMATION:  
APPLICANT: Richard C. Hamelin  
TITLE OF INVENTION: DETECTION OF PLANT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: George A. Seaby  
STREET: 880 Wellington Street, Suite 708  
CITY: Ottawa  
COUNTRY: Canada  
ZIP: K1R 6K7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,127C  
FILING DATE: May 23, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George A. Seaby  
REGISTRATION NUMBER: 24,034  
REFERENCE/DOCKET NUMBER: 1898  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (613) 232-5815  
TELEFAX: (613) 232-5831  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 581  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-652-127C-6

Query Match 72.3%; Score 224.2; DB 1; Length 581;  
Best Local Similarity 88.5%; Pred. No. 2.2e-64;  
Matches 276; Conservative 1; Mismatches 30; Indels 5; Gaps 3;

QY 1 AATGCGATAGTAATGTAATGTAATGCAAAATTCAGTATCATCATCATCTTTGAACGACA 60  
DB 253 AATGCGATAGTAATGTAATGTAATGCAAAATTCAGTATCATCATCTTTGAACGACA 312  
QY 61 TTGCGCCCGCCAGTATTTCTGGGGGCGATGCTGTTGAGCGTCAATTCACCTCAAGCC 120  
DB 313 TTGCGCCCGCCAGTATTTCTGGGGGCGATGCTGTTGAGCGTCAATTCACCTCAAGCC 372  
QY 121 CCCGGGTTTGGTGTGGGAGTCGCGAAG-CCCTTGGCGGCAAGCGGCGCCGAATCTAGT 179  
DB 373 CCCGGGTTTGGTGTGGGAGTCGCGAAG-CCCTTGGCGGCGGCGGCGGCGCTCTTAATATATAGT 432  
QY 180 GCGGCTCTGCTGCGAGCTTCGATTCGATAGTAAACCTCGCAACTGGTACGCGGCG 239  
DB 433 GCGGCTCTGCTGATAGTCTTCTGCGATAGTACACCTGCG--ACTGAAAACAGCG 489  
QY 240 CGGCGAAGCGCTTAAACCCCACTTCTG-AATGTTGACCTGGATCAGGTAGGAATACC 298  
DB 490 CGGCGAAGCGCTTAAACCCCACTTCTGAAAGGTTGACCTGGATCAGGTAGGAATACC 549  
QY 299 CGCTGAACCTTAA 310  
DB 550 CGCTGAACCTTAA 561

## RESULT 8

US-08-652-127C-5  
Sequence 5, Application US/08652127C  
Patent No. 5792611  
GENERAL INFORMATION:  
APPLICANT: Richard C. Hamelin  
TITLE OF INVENTION: DETECTION OF PLANT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: George A. Seaby  
STREET: 880 Wellington Street, Suite 708  
CITY: Ottawa  
COUNTRY: Canada  
ZIP: K1R 6K7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,127C  
FILING DATE: May 23, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George A. Seaby  
REGISTRATION NUMBER: 24,034  
REFERENCE/DOCKET NUMBER: 1898  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (613) 232-5815  
TELEFAX: (613) 232-5831  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 594  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-652-127C-5

Query Match 63.8%; Score 197.8; DB 1; Length 594;  
 Best Local Similarity 85.0%; Pred. No. 1.1e-55;  
 Matches 211; Conservative 0; Mismatches 37; Indels 11; Gaps 4;

QY 1 AAATCGATAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTTGAACGACA 60  
 DB 258 AAATCGATAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTTGAACGACA 317  
 QY 61 TTGCCCCCGCCAGTATTCGCGGGGCGATCCCTGTTGAGCGTATTTCAACCTTCAAGCC 120  
 DB 318 TTGCGCCCGCCAGTATTCGCGGGGCGATCCCTGTTGAGCGTATTTCAACCTTCAAGCA 377  
 QY 121 CC-----CGGGTTGGTGTGGGATCGGCAAG-----CCCTTGCGGCAAGCCGCCCGCA 172  
 DB 378 CCTTGCGGAGCTTGGTGTGGGATCGGCGCGCTTCCGCGGTGCGCGCTCCCGCA 437  
 QY 173 ATCTAGTGGCGGCTCTGCTGAGCTTCCATTGCGTAGTAAACCTTGGCACTGCTGA 232  
 DB 438 ATCTAGTGGCGGCTCTGCTGAGCTTCCATTGCGTAGTAAACCTTGGCACTGCTGA 495  
 QY 233 CCGGCGCGGCGCCAGCCGTTAAACCCCACTTCTGAAT-GTTGACCTTGGATCGGTAG 291  
 DB 496 CTCGGGTGGCGGCGCCAGTAAACCCCACTTCTTCTGTTGACCTTGGATCGGTAG 555  
 QY 292 GAATACCGCGCTGAACCTTAA 310  
 DB 556 GACTACCGCGCTGAACCTTAA 574

RESULT 9  
 US-08-887-480-96  
 Sequence 96, Application US/08887480  
 Patent No. 5814453

GENERAL INFORMATION:  
 APPLICANT: Beck, James J  
 TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
 TITLE OF INVENTION: Polymerase Chain Reaction  
 NUMBER OF SEQUENCES: 96  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 58145Jartis Corporation  
 STREET: 520 White Plains Road  
 CITY: Tarrytown  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10591

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/887,480  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/722,187  
 FILING DATE: 15-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-541-8587  
 TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 96:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 546 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 STRAIN: *Fusarium poae*

INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)  
 INDIVIDUAL ISOLATE: sequence  
 IMMEDIATE SOURCE:  
 CLONE: pCRPpoae1427(1-2), pCRPpoae1534(2-2), and  
 CLONE: pCRPpoae1756(3-1)  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1..30  
 OTHER INFORMATION: /note= "3' end of small subunit  
 OTHER INFORMATION: rRNA gene"  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 31..180  
 OTHER INFORMATION: /note= "ITS 1"  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 338..489  
 OTHER INFORMATION: /note= "ITS 2"  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 490..546  
 OTHER INFORMATION: /note= "5' end of large subunit  
 OTHER INFORMATION: rRNA gene"  
 US-08-887-480-96

Query Match 60.5%; Score 187.6; DB 1; Length 546;  
 Best Local Similarity 84.5%; Pred. No. 2.5e-52;  
 Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;

QY 1 AAATCGATAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTTGAACGACA 60  
 DB 231 AAATCGATAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTTGAACGACA 290  
 QY 61 TTGCGCCCGCCAGTATTCGCGGGGCGATCCCTGTTGAGCGTATTTCAACCTTCAAGCC 120  
 DB 291 TTGCGCCCGCCAGTATTCGCGGGGCGATCCCTGTTGAGCGTATTTCAACCTTCAAGCC 350  
 QY 121 CCGGCGGTTGGTGTGGGATCGGCAAGCCCTTGCGGCAAGCCGCCCGCAATCTAGTG 180  
 DB 351 C---AGCTTGGTGTGG-----ATCTGTGCAACACAGTCCCAATTTGATTG 398  
 QY 181 GCGGCTCGCTGAGCTTCCATTGCGTAGTAAACCTTGGCACTGTGACGCGGC 240  
 DB 399 GCGGTACAG-TGAGCTTCCATAGCGTAGTAAATTTACATCGTTACGTGAATCGTGC 457  
 QY 241 GCGCAAGCCGTTAAACCCCACTTCTGAATGTTGACCTTGGATCGATGAGTAAATACCG 300  
 DB 458 GCGCAAGCCGTTAAACCCCACTTCTGAATGTTGACCTTGGATCGATGAGTAAATACCG 516  
 QY 301 CTGAACCTTAA 310  
 DB 517 CTGAACCTTAA 526

RESULT 10  
 US-08-905-314A-22  
 Sequence 22, Application US/08905314A  
 Patent No. 5827695

GENERAL INFORMATION:  
 APPLICANT: Beck, James J.  
 TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
 TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 5827695artis Corporation Patent Department  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: NC  
 COUNTRY: USA

```

ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium poae
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
IMMEDIATE SOURCE:
CLONE: PCRpoaeT427(1-2), PCRpoaeT534(2-2), and
PCRpoaeT756(3-1)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..180
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 181..337
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 338..489
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-22
Query Match 60.5%; Score 187.6; DB 1; Length 546;
Best Local Similarity 84.5%; Pred. No. 2.5e-52;
Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;
QY 1 AAATGCATAGTAATGTGAATTCGAAATTCAGTGAATGATCTTTGAACGACG 60
DB 231 AAATGCATAGTAATGTGAATTCGAAATTCAGTGAATGATCTTTGAACGACG 290
QY 61 TTGGCCCGCCAGATTCGCGGGGCGATGCTGTTCGAGGCGATTTCAACCTCAAGCC 120
DB 291 TTGGCCCGCCAGATTCGCGGGGCGATGCTGTTCGAGGCGATTTCAACCTCAAGCC 350
QY 121 CCGGGTTTGTGTGGGATCGGCAAGCCCTTGCAGCAAGCCGCCCGCAATCTAGTG 180
DB 351 C--AGCTGTGTGGG-----ATCTGTGTGCAACACAGTCCCAATTTGATTTG 398
QY 181 GCGGTCTCGTGCAGCTTCATTCGTAAGTAAGTAACCTCGCAACTGGTACGCGGCGC 240

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DB 399 GCGGTACG-TGAGTTCATAGCGTAGTAATTACACATCGTACTGTAACTCGC 457
QY 241 GGCCAGCCGTTAAACCCCACTTGAATGTGACCTCGATCAGTAGAATACCGC 300
DB 458 GGCCAGCCGTTAA-CCCACTTGAATGTGACCTCGATCAGTAGAATACCGC 516
QY 301 CTGAAGTTAA 310
DB 517 CTGAAGTTAA 526
RESULT 11
US-08-887-480-82
Sequence 82, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..12
OTHER INFORMATION: /note= "3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 13..161
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 162..318
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 319..472

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```

? OTHER INFORMATION: /note="ITS 2"
?
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 473_504
? OTHER INFORMATION: /note="5' end of large subunit"
? OTHER INFORMATION: rRNA gene"
? OS-08-887-480-82

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Query Match	60.2%	Score 186.6;	DB 1;	Length 504;
Best Local Similarity	82.6%;	Pred. No. 5.2e-52;		
Matches 252; Conservative	1;	Mismatches 40;	Indels 12;	Gaps 3

QY	AAAATGGGATAGAGTAAAGTGAATTTGCAAAATTAGTGAATCATCGAATCTTTTGAACGACA	60	
Db	212	AAATGGCATAGAAAGTGAATTGCGAATTCAGTGAATCATCGAATCTTTGAACGACA	2711
QY	61	TTAGGGCCCGCAGATATTTCGGGGGCGATGCCCTGTGAGCGCATTTCAACCCCTCAAGCC	120
Db	272	TTGCGCCCGCCAGTATTTCTGGGGGCGATGCCCTGTGAGCGCATTTCAACCCCTCAAGCC	3311
QY	121	CCCGGGTTTGGTTGGGGATCGGCAAGCCCTTGGGGGCAAGCCGGCCCCCGAATCTAGTG	180
Db	332	C---ACCTTGGTGTGGG-----AGTCGAGTCTGTGCACTCCCCAAATATCATTG	380
QY	181	GGGCTTCGCTGAGGCTTCATTTGCTAGTAAACCCCTCGCACTGTGATCGCGGCGC	240
Db	381	GGGCTACGTCGAGGCTTCATAGGTAGTAAATTTACATATCGTACGTAAATCGTCGC	440
QY	241	GGCCAAAGCGGTTAAACCCCACTTCTGATGTGACCTCGGATCAGGTAGAAATACCG	300
Db	441	GGCTACGCGGTTAAA-CCCCAATCTTGATATGTGACCTCGGATCAGGTAGAAATACCG	499
QY	301	CTGAA	305
Db	500	CTGAA	504

RESULT 12  
US-08-905-314A-19

Sequence 19, Application US/08905314A  
Patent No. 5827695  
GENERAL INFORMATION:  
APPLICANT: Beck, James J.  
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5827695attis Corporation Patent Department  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 20779-2257  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent-in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,314A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CQC 1944  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8689  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid

```

1  STRANDEDNESS: single
2  TOPOLOGY: linear
3  MOLECULE TYPE: DNA (genomic)
4  ORIGINAL SOURCE:
5  ORGANISM: Fusarium culmorum
6  INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
7  INDIVIDUAL ISOLATE: (consensus sequence)
8  FEATURE:
9  NAME/KEY: misc_feature
10 LOCATION: 1..12
11 OTHER INFORMATION: /note= "3' end of small subunit"
12 OTHER INFORMATION: rRNA gene"
13 FEATURE:
14 NAME/KEY: misc_feature
15 LOCATION: 13..161
16 OTHER INFORMATION: /note= "ITS 1"
17 FEATURE:
18 NAME/KEY: misc_feature
19 LOCATION: 162..318
20 OTHER INFORMATION: /note= "5.8S rRNA gene"
21 FEATURE:
22 NAME/KEY: misc_feature
23 LOCATION: 319..472
24 OTHER INFORMATION: /note= "ITS 2"
25 FEATURE:
26 NAME/KEY: misc_feature
27 LOCATION: 473..504
28 OTHER INFORMATION: /note= "5' end of large subunit"
29 OTHER INFORMATION: rRNA gene"
30 OS-08-905-314A-19

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Query Match	60.2%	Score 186.6;	DB 1;	Length 504;
Best Local Similarity	82.6%	Pred. No. 5.2e-52;		
Matches 252; Conservative	1;	Mismatches 40;	Indels 12;	Gaps 3

Qy	1	AAATGCGATTAATAATGTGAATTGCAAAATCAGTGAAATCATCGAAATCTTTGAACGCACA	60
Db	212	AAATGCGATTAATAATGTGAATTGCAAAATCAGTGAAATCATCGAAATCTTTGAACGCACA	271
Qy	61	TTGCGCGCCGCGATTTCTGGCGGGCATGCTGTTCCAGGTCATTTCAACCTTCGAAGCC	120
Db	272	TTGCGCGCCGCGATTTCTGGCGGGCATGCTGTTCCAGGTCATTTCAACCTTCGAAGCC	331
Qy	121	CCCGGGTTTGATGTGGGGATCGCGAAGCCCTTCGCGAAGCCGGCCCGGCAAAATCTTAGTG	180
Db	332	C---AGCTTGATGTGGG-----AGCTGCAATCTCGTGCACTCCCAATATCAATTG	380
Qy	181	GGGCTCTGCTGACGCTTCATTTGGTATGTAATAAACCTTCGCAATTGTAACGGCGCC	240
Db	381	GGGCTCACCTCGACCTTCATTTGGTATGTAATAATAATCGTTACTGGTAATCGTCGC	440
Qy	241	GGCGAAGCGTTAAACCCCAACTTCTGAATGTGACCTCGAGTCAGTATGAGATATACCG	300
Db	441	GGCTAAGCGCTTAA-CCCAACTTCTGAATGTGACCTCGAGTCAGTATGAGATATACCG	499
Qy	301	CTGAA 305	
Db	500	CTGAA 504	

### RESULT 13

US-08-722-187-82  
Sequence 82, Application US/08722187  
Patent No. 5,955,274  
GENERAL INFORMATION:  
APPLICANT: Ligon, James M  
APPLICANT: Beck, James J  
TITLE OF INVENTION: Detection of Fungal Pathogens using the  
TITLE OF INVENTION: Polymerase Chain Reaction  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ciba-Geigy Corporation  
STREET: 7 Skyline Drive

```

City: Hawthorne
State: NY
Country: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
US-08-722-187-82

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Query Match          60.2%; Score 186.6; DB 2; Length 504;
Best Local Similarity 82.6%; Pred. No. 5.2e-52;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;

QY 1 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB 212 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 271
QY 61 TTGGCCCGCCGAGTAATTCGCGGGGCAATGCTGTTTCAAGGCTCATTTCAACCTCAAGCC 120
DB 272 TTGGCCCGCCGAGTAATTCGCGGGGCAATGCTGTTTCAAGGCTCATTTCAACCTCAAGCC 331
QY 121 CCCGGGTTTGGTGTGGGGATCGCAAGCCCTTCGCGCAAGCCGCGCAAAATCTAGTG 180
DB 332 C---AGCTTGGTGTGGG-----AGCTGCAAGTCTGCTGCACCTCCCAATAACATTTG 380
QY 181 GCGGCTCTGCTGCGAGCTTCCATTTCGTAAGTAATAACCTTCGCACTGGTACGGCGCG 240
DB 381 GCGGCTCTGCTGCGAGCTTCCATTTCGTAAGTAATAACCTTCGCACTGGTACGGCGCG 440
QY 241 GGCAGACCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCGAGTGAATACCGG 300
DB 441 GGCAGACCGCGTTAA-CCCAACTTCTGAATGTTGACCTCGGATCGAGTGAATACCGG 499
QY 301 CTGAA 305
DB 500 CTGAA 504

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RESULT 14
PCT-US95-04712-82
Sequence 82, Application PC/TUS9504712
GENERAL INFORMATION:
APPLICANT: Ligon, James M

```

```

APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
PCT-US95-04712-82

```

```

Query Match          60.2%; Score 186.6; DB 5; Length 504;
Best Local Similarity 82.6%; Pred. No. 5.2e-52;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;

QY 1 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
DB 212 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA 271
QY 61 TTGGCCCGCCGAGTAATTCGCGGGGCAATGCTGTTTCAAGGCTCATTTCAACCTCAAGCC 120
DB 272 TTGGCCCGCCGAGTAATTCGCGGGGCAATGCTGTTTCAAGGCTCATTTCAACCTCAAGCC 331
QY 121 CCCGGGTTTGGTGTGGGGATCGCAAGCCCTTCGCGCAAGCCGCGCGCAAAATCTAGTG 180
DB 332 C---AGCTTGGTGTGGG-----AGCTGCAAGTCTGCTGCACCTCCCAATAACATTTG 380
QY 181 GCGGCTCTGCTGCGAGCTTCCATTTCGTAAGTAATAACCTTCGCACTGGTACGGCGCG 240
DB 381 GCGGCTCTGCTGCGAGCTTCCATTTCGTAAGTAATAACCTTCGCACTGGTACGGCGCG 440
QY 241 GGCAGACCGTTAAACCCCAACTTCTGAATGTTGACCTCGGATCGAGTGAATACCGG 300
DB 441 GGCAGACCGCGTTAA-CCCAACTTCTGAATGTTGACCTCGGATCGAGTGAATACCGG 499
QY 301 CTGAA 305
DB 500 CTGAA 504

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Search completed: October 1, 2004, 08:05:40  
Job time : 103.159 secs

RESULT 15  
US-08-986-727-4

/ Sequence 4, Application US/08986727  
/ Patent No. 6080543

## GENERAL INFORMATION:

/ APPLICANT: ENGEL, Stacia R.  
/ APPLICANT: DESCENZO, Richard A.

/ APPLICANT: IRELAN, Nancy A.

/ TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS

/ NUMBER OF SEQUENCES: 38

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

/ STREET: P. O. Box 1404

/ CITY: Alexandria

/ STATE: Virginia

/ COUNTRY: United States

/ ZIP: 22113-1404

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/986,727

/ FILING DATE: 08-DEC-1997

/ CLASSIFICATION: 435

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Ekstrom, Richard C.

/ REGISTRATION NUMBER: 37,027

/ REFERENCE/DOCKET NUMBER: 009773-012

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (703) 836-6620

/ TELEFAX: (703) 836-2021

/ INFORMATION FOR SEQ ID NO: 4:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 611 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: DNA (genomic)

/ US-08-986-727-4

Query Match 59.7%; Score 185; DB 3; Length 611;  
Best Local Similarity 83.1%; Pred. No. 1.9e-51;

Matches 260; Conservative 0; Mismatches 45; Indels 8; Gaps 4;

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Oy 1 AAATCGATTAAGTATGTAATTCGCAAAATTCAGTGAATCATCGAATCTTTGAACGACCA 60
Db 283 AAATCGATTAAGTATGTAATTCGCAAAATTCAGTGAATCATCGAATCTTTGAACGACCA 342
Oy 61 TTGCGCCGCCGAGTATTCGCGGCGCATGCTGTTGAGCGTCATTTCAACCCCTCAAGCC 120
Db 343 TTGCGCCCTCTGCGTATTCGAGGAGGCGATGCTGTTGAGCGTCATTTCAACCCCTCAAG-- 400
Oy 121 CCCGGGTTGGTGTGGGATGCGAAGCCCTTGCGGCAAGCCGCCGCAATTAATAGTG 180
Db 401 -CTTGGCTTGGTGTGGGATGCGAAGCCCTTGCGGCAAGCCGCCGCAATTAATCAAGTG 459
Oy 181 GCGGCTCGCTGCACTTCATTCGATGTAATAACCTTCGCAACTG--GTACGCGGC 238
Db 460 GCGAGCTCGC--CAGGACCCCGAGCGCAGTATTAACCTTCGCTCCGAGAGGCCCTTGGC 517
Oy 239 GCGGCAAGCCGTTAAACCCCACTTCTGAATG-TTGAACCTCGATCAGGTAGGAATAC 297
Db 518 GGTGCGCTGCGCTTAACCCCACTTCTGAATGTTGACCTCGATCAGGTAGGAATAC 577
Oy 298 CCGCTGAACCTTA 310
Db 578 CCGCTGAACCTTA 590
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SEQ ID NO 5  
 LENGTH: 522  
 TYPE: DNA  
 ORGANISM: Fusarium subglutinans  
 US-09-961-755A-5

Query Match 62.7%; Score 194.4; DB 10; Length 522;  
 Best Local Similarity 84.3%; Pred. No. 2.1e-60;  
 Matches 258; Conservative 0; Mismatches 36; Indels 12; Gaps 3;

QY 1 AAATCGATAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60  
 DB 229 AAATCGATAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 288  
 QY 61 TTGCGCCGCCAGATATTTCTGGCGGCATGCTGTTGAGCGCATTTCAACCCCTCAAGCC 120  
 DB 289 TTGCGCCGCCAGATATTTCTGGCGGCATGCTGTTGAGCGCATTTCAACCCCTCAAGCC 348  
 QY 121 CCCGGGTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 180  
 DB 349 C-----AGCTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 398  
 QY 181 GCGGTCTGCTGCAGCTTCCATTCGTAGTAGTAAACCCTCGCACTGTGACGGCGCC 240  
 DB 399 GCGGTCTGCTGCAGCTTCCATTCGTAGTAGTAAACCCTCGCTACTGTATATGTGCGC 457  
 QY 241 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGGTAGGAATACCG 300  
 DB 458 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGGTAGGAATACCG 516  
 QY 301 CTGAAC 306  
 DB 517 CTGAAC 522

RESULT 5  
 US-09-961-755A-8  
 ; Sequence 8, Application US/09961755A  
 ; Publication No. US20030113722A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beck, Jim  
 ; APPLICANT: Barnett, Jason  
 ; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the  
 ; FILE REFERENCE: 60055  
 ; CURRENT APPLICATION NUMBER: US/09/961,755A  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 8  
 ; LENGTH: 522  
 ; TYPE: DNA  
 ; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)  
 US-09-961-755A-8

Query Match 62.7%; Score 194.4; DB 10; Length 522;  
 Best Local Similarity 84.3%; Pred. No. 2.1e-60;  
 Matches 258; Conservative 0; Mismatches 36; Indels 12; Gaps 3;

QY 1 AAATCGATAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60  
 DB 229 AAATCGATAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 288  
 QY 61 TTGCGCCGCCAGATATTTCTGGCGGCATGCTGTTGAGCGCATTTCAACCCCTCAAGCC 120  
 DB 289 TTGCGCCGCCAGATATTTCTGGCGGCATGCTGTTGAGCGCATTTCAACCCCTCAAGCC 348  
 QY 121 CCCGGGTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 180  
 DB 349 C-----AGCTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 398  
 QY 181 GCGGTCTGCTGCAGCTTCCATTCGTAGTAGTAAACCCTCGCACTGTGACGGCGCC 240

DB 399 GCGGTCTGCTGCAGCTTCCATTCGTAGTAGTAAACCCTCGCACTGTGACGGCGCC 457  
 QY 241 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGGTAGGAATACCG 300  
 DB 458 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGGTAGGAATACCG 516  
 QY 301 CTGAAC 306  
 DB 517 CTGAAC 522

RESULT 6  
 US-09-961-755A-6  
 ; Sequence 6, Application US/09961755A  
 ; Publication No. US20030113722A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beck, Jim  
 ; APPLICANT: Barnett, Jason  
 ; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the  
 ; FILE REFERENCE: 60055  
 ; CURRENT APPLICATION NUMBER: US/09/961,755A  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 6  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Gibberella zeae  
 US-09-961-755A-6

Query Match 57.8%; Score 179.2; DB 10; Length 521;  
 Best Local Similarity 83.3%; Pred. No. 7.9e-55;  
 Matches 255; Conservative 0; Mismatches 38; Indels 13; Gaps 4;

QY 1 AAATCGATAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60  
 DB 229 AAATCGATAAGTATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAAGCACA 288  
 QY 61 TTGCGCCGCCAGATATTTCTGGCGGCATGCTGTTGAGCGCATTTCAACCCCTCAAGCC 120  
 DB 289 TTGCGCCGCCAGATATTTCTGGCGGCATGCTGTTGAGCGCATTTCAACCCCTCAAGCC 348  
 QY 121 CCCGGGTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 180  
 DB 349 C---AGCTTGGTGTGGGATCGGCAAGCCCTTGGCGCAAGCCGCCCGCAATCTAGTG 397  
 QY 181 GCGGTCTGCTGCAGCTTCCATTCGTAGTAGTAAACCCTCGCACTGTGACGGCGCC 240  
 DB 398 GCGGTCTGCTGCAGCTTCCATTCGTAGTAGTAAACCCTCGCACTGTGACGGCGCC 456  
 QY 241 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGGTAGGAATACCG 300  
 DB 457 GGGCAAGCGGTTAAACCCCAACTCTGAATGTGACCTCGGATGAGGTAGGAATACCG 515  
 QY 301 CTGAAC 306  
 DB 516 CTGAAC 521

RESULT 7  
 US-10-121-740-2  
 ; Sequence 2, Application US/10121740  
 ; Publication No. US200301186425A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Strobel, Gary  
 ; APPLICANT: Manaker, Denise  
 ; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF  
 ; FILE REFERENCE: AQ 2019.40  
 ; CURRENT APPLICATION NUMBER: US/10/121,740  
 ; CURRENT FILING DATE: 2002-04-11  
 ; PRIOR APPLICATION NUMBER: 60/283,902

;; PRIOR FILING DATE: 2002-03-11  
;; PRIOR APPLICATION NUMBER: 60/363,072  
;; PRIOR FILING DATE: 2001-04-16  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 652  
;; TYPE: DNA  
;; ORGANISM: Muscudor albus  
US-10-121-740-2

Query Match 43.9%; Score 136.2; DB 15; Length 652;  
Best Local Similarity 71.7%; Pred. No. 5.3e-39;  
Matches 223; Conservative 0; Mismatches 78; Indels 10; Gaps 3;

QY 1 AATGCGATAGTATGTGATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60  
DB AAATGCGATAGTATGTGATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 388  
QY 61 TTGGGCCCCGACGATTTCTGGCGGCGATGCTGTTGACAGGTGATTTCAACCTCAAGCC 120  
DB TTGGGCCCCGACGATTTCTGGCGGCGATGCTGTTGACAGGTGATTTCAACCTCAAGCC 448  
QY 121 CCCGGGTTTGATGTTGGGAGATCGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 180  
DB 449 CTGTTGCTTAGCGTTGGAGACC-----TACGGGCACTGCCGCTAGCTCCCTAAAGTATG 503  
QY 181 GCGGCTCGCTGACGCTTCATTCAGTAGTAAACCTCGCACT-GGTACGCGGCG 239  
DB 504 GCGGAGTTGGTTC---TCACTCTAGGCGGTAGTAAATCTATCTCGCTCTGTAGTGTTC 559  
QY 240 CCGGCAAGCGGTAAACCCCACTTGTGAATGTGACCTCGATCGGTAGGAATATCCC 259  
DB 560 CCGGCCCCCTGCGTAAACCCCTATATCAAAAGGTGACCTCGATCGGTAGGAATATCCC 619  
QY 300 GCTGAACCTTAA 310  
DB 620 GCTGAACCTTAA 630

RESULT 8  
US-10-623-432-2  
;; Sequence 2, Application US/10623432  
;; Publication No. US20040141955A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Strobel, Gary  
;; APPLICANT: Manke, Denise  
;; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF  
;; TITLE OF INVENTION: USE  
;; FILE REFERENCE: AQ 2019.40  
;; CURRENT APPLICATION NUMBER: US/10/623,432  
;; CURRENT FILING DATE: 2003-07-17  
;; PRIOR APPLICATION NUMBER: US/10/121,740  
;; PRIOR FILING DATE: 2002-04-11  
;; PRIOR APPLICATION NUMBER: 60/283,902  
;; PRIOR FILING DATE: 2002-03-11  
;; PRIOR APPLICATION NUMBER: 60/363,072  
;; PRIOR FILING DATE: 2001-04-16  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 652  
;; TYPE: DNA  
;; ORGANISM: Muscudor albus  
US-10-623-432-2

Query Match 43.9%; Score 136.2; DB 17; Length 652;  
Best Local Similarity 71.7%; Pred. No. 5.3e-39;  
Matches 223; Conservative 0; Mismatches 78; Indels 10; Gaps 3;

QY 1 AATGCGATAGTATGTGATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60  
DB 329 AATGCGATAGTATGTGATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 388

QY 61 TTGGGCCCCGACGATTTCTGGCGGCGATGCTGTTGACAGGTGATTTCAACCTCAAGCC 120  
DB 389 TTGGGCCCCGACGATTTCTGGCGGCGATGCTGTTGACAGGTGATTTCAACCTCAAGCC 448  
QY 121 CCCGGGTTTGATGTTGGGAGATCGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 180  
DB 449 CTGTTGCTTAGCGTTGGAGACC-----TACGGGCACTGCCCGTAGCTCCCTAAAGTATG 503  
QY 181 GCGGCTCGCTGACGCTTCATTCAGTAGTAAACCTCGCACT-GGTACGCGGCG 239  
DB 504 GCGGAGTTGATTC---TCACTCTAGGCGGTAGTAAATCTATCTCGCTCTGATGTTG 559  
QY 240 CCGGCAAGCGGTAAACCCCACTTGTGAATGTGACCTCGATCGGTAGGAATATCCC 259  
DB 560 CCGGCCCCCTGCGTAAACCCCTATATCAAAAGGTGACCTCGATCGGTAGGAATATCCC 619  
QY 300 GCTGAACCTTAA 310  
DB 620 GCTGAACCTTAA 630

RESULT 9  
US-10-046-955-3  
;; Sequence 3, Application US/10046955  
;; Publication No. US20030129600A1  
;; GENERAL INFORMATION:  
;; APPLICANT: The Government of the United States of America, as Represented by the  
;; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease  
;; APPLICANT: Control and Prevention  
;; APPLICANT: Morrison, Christine J.  
;; APPLICANT: Reiss, Etrol  
;; APPLICANT: Ahdorovich, Lilianna  
;; APPLICANT: Choi, Jong Soo  
;; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
;; TITLE OF INVENTION: Other Filamentous Fungi  
;; FILE REFERENCE: 6395-62064  
;; CURRENT APPLICATION NUMBER: US/10/046,955  
;; CURRENT FILING DATE: 2002-06-04  
;; PRIOR APPLICATION NUMBER: US 09/423,233  
;; PRIOR FILING DATE: 2000-06-27  
;; PRIOR APPLICATION NUMBER: PCT/US98/08926  
;; PRIOR FILING DATE: 1998-05-01  
;; PRIOR APPLICATION NUMBER: US 60/045,400  
;; PRIOR FILING DATE: 1997-05-02  
;; NUMBER OF SEQ ID NOS: 61  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 3  
;; LENGTH: 365  
;; TYPE: DNA  
;; ORGANISM: Aspergillus niger  
US-10-046-955-3

Query Match 43.9%; Score 136; DB 15; Length 365;  
Best Local Similarity 69.0%; Pred. No. 4.7e-39;  
Matches 218; Conservative 0; Mismatches 90; Indels 8; Gaps 2;

QY 1 AATGCGATAGTATGTGATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60  
DB 52 AATGCGATAGTATGTGATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 111  
QY 61 TTGGGCCCCGACGATTTCTGGCGGCGATGCTGTTGACAGGTGATTTCAACCTCAAGCC 120  
DB 112 TTGGGCCCCGACGATTTCTGGCGGCGATGCTGTTGACAGGTGATTTCAACCTCAAGCC 169  
QY 121 CCCGGGTTTGATGTTGGGAGATCGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 180  
DB 170 CAGCGTTTGATGTTGGGAGATCGCAAGCCCTTGCGGCAAGCCGCCGAAATCTAGTG 229  
QY 181 GCGGCTCGCTGACGCTTCATTCAGTAGTAAACCTCGCACT-GGTACGCGGCG 234  
DB 230 GCGGCAAGCGGTAAACCCCACTTGTGAATGTGACCTCGATCGGTAGGAATATCCC 289



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Qy 235 CGGCGCGCCGCAAGCCGTTAAACCCCACTTCTGATGTGACCTCGATCGATGAGGAA 294
Db 290 CGGCGCGCCGCGAGCTTATCCAAACATTTTTCAGAGTTACCTCGATCAGGAGGA 349
Qy 295 TACCGCTGAACCTTAA 310
Db 350 TACCGCTGAACCTTAA 365

RESULT 10
US-10-046-955-2
; Sequence 2, Application US/10046955
; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reis, Errol
; APPLICANT: Aidorevich, Liliiana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT FILING DATE: 2002-06-04
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-046-955-2

Query Match 42.4%; Score 131.4; DB 15; Length 364;
Best Local Similarity 68.1%; Pred. No. 2,3e-37;
Matches 213; Conservative 0; Mismatches 96; Indels 4; Gaps 2;

Qy 1 AAATCGATTAAGTAATGTAATGCAAAATTCAGTAATCGAATCTTTGAACGACA 60
Db 52 AAATCGATTAAGTAATGTAATGCAAAATTCAGTAATCGAATCTTTGAACGACA 111
Qy 61 TTGGCGCCGCGAGTATTCGCGCGGAGCTGTTGCGAGCGTCAATTGAACCTCAAGCC 120
Db 112 TTGGCGCCGCGAGTATTCGCGCGGAGCTGTTGCGAGCGTCAATTGAACCTCAAG 170
Qy 121 CCCGGGTTGGTGTGGGATTCGCGCAAGCCCTTGGCGGCAAGCCGCGCCGGAATCTAGT 180
Db 171 CACGGCTTGTGTGGGAGCTGCGAGCGTATGGGCGTGTCACTGCTGTAGGCGCCGCGC 230
Qy 181 GCGGCTCTGCTGACGCTTCAATTGCGTA--GTAATAAACCTTCGCAACTGTAACGCG 237
Db 238 GCGGCGCAAGCGCTTAAACCCCACTTCTGATGTGACCTCGATCGATGAGGAAATAC 297
Qy 291 GCGGCGCAAGCGCTTAAACCCCACTTCTGATGTGACCTCGATCGATGAGGAAATAC 350
Db 351 CCGCTGAACCTTAA 363

RESULT 11
US-10-046-955-28
; Sequence 28, Application US/10046955
; Publication No. US20030129600A1
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; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reis, Errol
; APPLICANT: Aidorevich, Liliiana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT FILING DATE: 2002-06-04
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 28
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Penicillium notatum
US-10-046-955-28

Query Match 40.3%; Score 125; DB 15; Length 309;
Best Local Similarity 69.0%; Pred. No. 4.7e-35;
Matches 216; Conservative 0; Mismatches 90; Indels 7; Gaps 3;

Qy 1 AAATCGATTAAGTAATGTAATGCAAAATTCAGTAATCGAATCTTTGAACGACA 60
Db 1 AAATCGATTAAGTAATGTAATGCAAAATTCAGTAATCGAATCTTTGAACGACA 59
Qy 61 TTGGCGCCGCGAGTATTCGCGCGGAGCTGTTGCGAGCGTCAATTGAACCTCAAGCC 120
Db 60 TTGGCGCCGCGAGTATTCGCGCGGAGCTGTTGCGAGCGTCAATTGAACCTCAAGCA 119
Qy 121 CCCGGGTTGGTGTGGGATTCGCGCAAGCCCTTGGCGGCAAGCCGCGCCGGAATCTAGT 180
Db 120 C--GGCTTGTGTGGGAGCTGCGGCTCTCGATCCGCGGAGAGCGGCCGAAAGGACGCG 176
Qy 181 GCGGCTCTGCTGACGCTTCAATTGCGTAAGTAATAACCTTCGCAACTGTAACGCG 237
Db 177 GCGGCAAGCGGCTCGGCTTCGAGCGTATGGGCGTGTGTCAACCGCTGTAGGCGCGC 236
Qy 238 GCGGCGCAAGCGGCTTAAACCCCACTTCTGATGTGACCTCGATCGATGAGGAAATAC 297
Db 237 GCGGCGCTTGGCGATCAACCAAAATTTTATTCAGGTTGACCTCGATCAGTACGATAC 296
Qy 298 CCGCTGAACCTTAA 310
Db 297 CCGCTGAACCTTAA 309

RESULT 12
US-09-766-173C-4
; Sequence 4, Application US/09766173C
; Patent No. US20020172945A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, George C.
; TITLE OF INVENTION: Materials and Methods for Detection of
; FILE REFERENCE: Oregon 99-09
; CURRENT FILING DATE: 2001-01-22
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: PCT/US01/01735
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
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SEQ ID NO 4  
 ; LENGTH: 641  
 ; TYPE: DNA  
 ; ORGANISM: Guignardia citricarpa  
 US-09-766-173C-4

Query Match 40.2%; Score 124.6; DB 9; Length 641;  
 Best Local Similarity 64.6%; Pred. No. 9.4e-35;  
 Matches 201; Conservative 0; Mismatches 109; Indels 1; Gaps 1;

QY 1 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60  
 DB 318 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 377  
 QY 61 TTGGGCCCCGCGAGTATTCGCGGGGCGATGCTGTTGAGGCGATTTCACCCCTCAAGCC 120  
 DB 378 TTGGGCCCCCTGGCATTCGCGGGGCGATGCTGTTGAGGCGATTTCACCCCTCAAGCT 437  
 QY 121 CCGCGGTTTGGTGTGGGAGATCGGCAGCCCTTGCGGCAAGCCGACC-CCGAATCTAGT 179  
 DB 438 CTGCTTGTATTTGGGCGACGTCGCTGCCGAGCGCGCTGGAAGACCTCGGCGACGCGCT 497  
 QY 180 GCGGCTCTGCTGCACTTCCATTGCGTAGTAAGTAAACCTTCGCACTGTGACGCGCG 239  
 DB 498 CTCAGCCTCGAGCGTAGTAAGTAAATATCTGCTTTGAGAGAGGGGCGCGCTGCGCGCG 557  
 QY 240 CCGCCAGCGGTAAACCCCACTCTGATGTGACCTCGATCGATGAGTAATACCC 239  
 DB 558 GACAATGACCTTGGTCTACTATTTTCCAAAGTTGACCTCGATCGATGAGTAATACCC 617  
 QY 300 GCTGAACCTTAA 310  
 DB 618 GCTGAACCTTAA 628

RESULT 13  
 US-10-121-740-4  
 ; Sequence 4, Application US/10121740  
 ; Publication No. US20030186425A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Strobel, Gary  
 ; APPLICANT: Manke, Denise  
 ; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF  
 ; FILE REFERENCE: AQ 2019.40  
 ; CURRENT APPLICATION NUMBER: US/10/121,740  
 ; CURRENT FILING DATE: 2002-04-11  
 ; PRIOR APPLICATION NUMBER: 60/283,902  
 ; PRIOR FILING DATE: 2002-03-11  
 ; PRIOR APPLICATION NUMBER: 60/363,072  
 ; PRIOR FILING DATE: 2001-04-16  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 650  
 ; TYPE: DNA  
 ; ORGANISM: Muscodor roseus  
 US-10-121-740-4

Query Match 40.1%; Score 124.2; DB 15; Length 650;  
 Best Local Similarity 71.4%; Pred. No. 1.3e-34;  
 Matches 222; Conservative 0; Mismatches 78; Indels 11; Gaps 4;

QY 1 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60  
 DB 329 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 388  
 QY 61 TTGGGCCCCGCGAGTATTCGCGGGGCGATGCTGTTGAGGCGATTTCACCCCTCAAGCC 120  
 DB 389 TTGGGCCCCATTACATTTCTAGTGGGCGATGCTGTTGAGGCGATTTC-ACCACTTAAGCC 447  
 QY 121 CCGCGGTTTGGTGTGGGAGTGGCAAGCCCTTGCGGCAAGCCGCCCGCAATCTAGTG 180

DB 448 CTGTGCTTAGAGCGTTGGAGCC-----TACGGCACTGCCCGTAGCTCCCTAAAGTATG 502  
 QY 181 GCGGCTCTGCTGAGCTTCATTTGCTAGTAAACCCCTCGCACT-GGTACGGGGG 239  
 DB 503 GCGAGTTGTTTC---TACTCTAGGCGTAGTAATCTATCTCGCTCTGAGTGGTTC 558  
 QY 240 CCGCCAGCGGTAAACCCCACTCTGATGTGACCTCGGATCAGGTAGGAATACCC 299  
 DB 559 CCGCCCTCGGTAAACCCCTTATATCAAGGTTGACCTCGGATCAGGTAGGAATACCC 618  
 QY 300 GCTGAACCTTAA 310  
 DB 619 GCTGAACCTTAA 629

RESULT 14  
 US-10-623-432-4  
 ; Sequence 4, Application US/10623432  
 ; Publication No. US20040141955A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Strobel, Gary  
 ; APPLICANT: Manke, Denise  
 ; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF  
 ; FILE REFERENCE: AQ 2019.40  
 ; CURRENT APPLICATION NUMBER: US/10/623,432  
 ; CURRENT FILING DATE: 2003-07-17  
 ; PRIOR APPLICATION NUMBER: US/10/121,740  
 ; PRIOR FILING DATE: 2002-04-11  
 ; PRIOR APPLICATION NUMBER: 60/283,902  
 ; PRIOR FILING DATE: 2002-03-11  
 ; PRIOR APPLICATION NUMBER: 60/363,072  
 ; PRIOR FILING DATE: 2001-04-16  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 650  
 ; TYPE: DNA  
 ; ORGANISM: Muscodor roseus  
 US-10-623-432-4

Query Match 40.1%; Score 124.2; DB 17; Length 650;  
 Best Local Similarity 71.4%; Pred. No. 1.3e-34;  
 Matches 222; Conservative 0; Mismatches 78; Indels 11; Gaps 4;

QY 1 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCGAATCTTTGAACGCACA 60  
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 QY 61 TTGGGCCCCGCGAGTATTCGCGGGGCGATGCTGTTGAGGCGATTTCACCCCTCAAGCC 120  
 DB 389 TTGGGCCCCATTACATTTCTAGTGGGCGATGCTGTTGAGGCGATTTC-ACCACTTAAGCC 447  
 QY 121 CCGCGGTTTGGTGTGGGAGTGGCAAGCCCTTGCGGCAAGCCGCCCGCAATCTAGTG 180  
 DB 448 CTGTGCTTAGAGCGTTGGAGCC-----TACGGCACTGCCCGTAGCTCCCTAAAGTATG 502  
 QY 181 GCGGCTCTGCTGAGCTTCATTTGCTAGTAAACCCCTCGCACT-GGTACCGGGG 239  
 DB 503 GCGAGTTGTTTC---TACTCTAGGCGTAGTAATCTATCTCGCTCTGAGTGGTTC 558  
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RESULT 15  
 US-10-046-955-5  
 ; Sequence 5, Application US/10046955

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; Publication No. US20030129600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-10-046-955-5

Query Match      39.7%; Score 123.2; DB 15; Length 365;
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QY      179  TGGGGGTTCGCTGAGCTTCATTCGTAAGTAATAACCTCGCAACTGTAGCC--G 236
Db      232  GCACCGGTCCGCTCTCGAGGTATGGGCTTGTGTCACCCGCTCGATTAGGCGCGCGG 291
QY      237  GCGGCGCCAGCCCGTTAAACCCCACTTGAATGTTGACCTCGGATCAGTAGAATA 296
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Job time : 1263.46 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 ; Search time 4340 Seconds  
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2133.013 Million cell updates/sec

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Perfect score: 310  
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Scoring table: IDENTITY\_NUC  
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Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: em\_esthm:\*  
3: em\_estin:\*  
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5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estc1:\*  
10: gb\_estc2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	60.0	739	14	CF870552 tric024xb
2	186	60.0	755	14	CF870665 tric024xj
3	186	60.0	796	14	CB900742 tric024xb
4	186	60.0	808	14	CB900860 tric024xj

Result No.	Score	Query Match	Length	ID	Description
5	139.8	45.1	735	14	CF880267 tric081xc
6	139.8	45.1	840	14	CB907036 tric081xc
7	120.2	38.8	704	13	BQ751285 tric081xc
8	120.2	38.8	725	13	BQ752001 tric081xc
9	120.2	38.8	806	13	BQ751015 tric081xc
10	120.2	38.8	806	13	BQ751484 tric081xc
11	118.6	38.3	745	13	BQ751971 tric081xc
12	118.6	38.3	758	13	BQ751399 tric081xc
13	116	37.4	169	12	BM870292 tric081xc
14	113.6	36.6	743	13	BQ751216 tric081xc
15	112	36.1	743	13	BQ751027 tric081xc
16	110.2	35.5	225	18	BZ424439 tric081xc
17	109.2	35.2	214	10	BF251183 tric081xc
18	101.8	32.8	195	28	BZ425056 tric081xc
19	101.8	32.8	389	28	BZ424630 tric081xc
20	100.8	32.5	213	9	A1209736 tric081xc
21	100.8	32.5	318	9	A1213025 tric081xc
22	99.6	32.1	570	28	BZ293287 tric081xc
23	99.6	32.1	603	28	BZ296472 tric081xc
24	99.2	32.0	597	28	BZ293452 tric081xc
25	97.6	31.5	846	29	CNS07820 tric081xc
26	97.6	31.5	893	29	CNS07956 tric081xc
27	97.6	31.5	995	29	CNS077A08 tric081xc
28	97.6	31.5	999	29	CNS07730 tric081xc
29	97.6	31.5	1034	29	CNS07922 tric081xc
30	97.6	31.5	1094	29	CNS076RE tric081xc
31	97.6	31.5	1098	29	CNS07812 tric081xc
32	97.2	31.4	981	29	CNS0769H tric081xc
33	96.4	31.1	515	28	AZ927454 tric081xc
34	96.4	31.1	522	28	AZ927478 tric081xc
35	96.2	31.0	870	29	CNS06K29 tric081xc
36	96.2	31.0	1004	29	CNS06KCF tric081xc
37	96.2	31.0	1043	29	CNS06L0Y tric081xc
38	96	31.0	638	10	BE337372 tric081xc
39	96	31.0	969	29	CNS07D0M tric081xc
40	96	31.0	971	29	CNS07DPL tric081xc
41	96	31.0	982	29	CNS07D5J tric081xc
42	96	31.0	994	29	CNS07CXY tric081xc
43	96	31.0	1014	29	CNS07C17 tric081xc
44	96	31.0	1027	29	CNS07DYS tric081xc
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## ALIGNMENTS

RESULT 1  
LOCUS CF870552  
DEFINITION tric024xb14.b1 T.reesei mycelial culture, Version 6 October 2003  
ACCESSION CF870552  
VERSION CF870552.1 GI:38125234  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
REFERENCE Diener S.B., Dankmeyer L., Dunn-Coleman N., Houfek T.D., Mitchell T.K., van Solingen P., Teunissen P.J.M., Ward M. and Dean R.A.  
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset  
Unpublished (2003)  
Contact: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: LT-F1 primer.

## FEATURES

Location/Qualifiers  
1. .739  
/organism="Hypocrea jecorina"  
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## ORIGIN

Query Match 60.0%; Score 186; DB 14; Length 739;  
Best Local Similarity 80.9%; Pred. No. 1,1e-43;  
Matches 254; Conservative 0; Mismatches 55; Indels 5; Gaps 3;

Qy 1 AATGCGATAGTAAATGCAAAATTCAGTGAATCGAATCTTTGAACGCACA 60  
Db 43 AATGCGATAGTAAATGCAAAATTCAGTGAATCGAATCTTTGAACGCACA 102  
Qy 61 TTGGCCCGCCAGTATTTGGCGGGCATGCTGTTCGAGGTCATTCAACCTCAAGCC 120  
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Qy 121 CCGGGTTTGTGTGGGATCGCAAGCCCTTCGGCAAGCGGGCCCGGAATCTAGTG 180  
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Db 282 CCGGCAAGCCGTTAAACCCCAACTTGAATGTTGACCTCGATCAGTAGGAATA 341  
Qy 297 CCGGCTGAACCTTAA 310  
Db 342 CCGGCTGAACCTTAA 355

RESULT 2  
CF870665 755 bp mRNA linear EST 31-OCT-2003  
LOCUS tric024xb14.b1 T.reesei mycelial culture, Version 6 October 2003  
DEFINITION Hypocrea jecorina cDNA clone tric024xb14, mRNA sequence.  
ACCESSION CF870665  
VERSION CF870665.1 GI:38125347  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 755)  
AUTHORS Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D., Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and Dean, R.A.  
TITLE Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset  
JOURNAL Unpublished (2003)  
COMMENT Contact: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: LR-F1 primer.  
FEATURES  
source Location/Qualifiers  
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## ORIGIN

Query Match 60.0%; Score 186; DB 14; Length 755;  
Best Local Similarity 80.9%; Pred. No. 1,1e-43;  
Matches 254; Conservative 0; Mismatches 55; Indels 5; Gaps 3;

Qy 1 AATGCGATAGTAAATGCAAAATTCAGTGAATCGAATCTTTGAACGCACA 60  
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Qy 181 GCGGTCCTGCTGAGCTTCCATTGCTAGTAG--TAAACCTCGCAACTGTACGGGGCG 239  
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Db 342 CCGGCTGAACCTTAA 355

RESULT 3  
CB900742 796 bp mRNA linear EST 02-JUL-2003  
LOCUS tric024xb14 T.reesei mycelial culture, Version 3 april Hypocrea  
DEFINITION jecorina cDNA clone tric024xb14, mRNA sequence.  
ACCESSION CB900742  
VERSION CB900742.1 GI:30115400  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 796)  
AUTHORS Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Kelley, A.S., Weerman, H.J., Teunissen, P.J., Yao, J. and Ward, M.  
TITLE Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus Trichoderma reesei  
JOURNAL J. Biol. Chem. 278 (34), 31988-31997 (2003)  
MEDLINE 22803314  
PUBMED 12788920  
COMMENT Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
Seq primer: LR-F1 primer.  
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1. .796

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## ORIGIN

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Best Local Similarity 80.9%; Pred. No. 1,1e-43;  
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QY 61 TTGGGCCCCGAGTATCTGGCGGCGATGCTGTTCAGAGCTCATTTCAACCTCGAAC 120  
DB 160 TTGGGCCCCGAGTATCTGGCGGCGATGCTGTTCAGAGCTCATTTCAACCTCGAAC 219  
QY 121 CCCGGGTTTGTTGGGATCGGCAAGCCCTTGGCGGCAAGCCCGCCGAAATCTAGTG 180  
DB 220 CTCGCGGGGGGT-CGGCGTTGGGATCGGCGCTTCACCGGCGCCGCGAAATACAGTG 278  
QY 181 GCGGTCTGCTGAGCTTCATTTGCTAGTAG-TAAACCTCGCAACTGTAGCGGCG 239  
DB 279 GCGGTCTGCGGAGCTCTCTCGGAGTAGTTGCACTCGACCGGAGGCGCG 338  
QY 240 CGGCGAAGCGGTAA--ACCCCACTTCTGAATGTTGACTCGGATCAGTAGAATA 296  
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QY 297 CCCGCTGAACCTAA 310  
DB 399 CCCGCTGAACCTAA 412

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CB900860  
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DEFINITION jecorina cDNA clone tric024xj04, mRNA sequence.  
ACCESSION CB900860  
VERSION CB900860.1 GI:30115518  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 808)  
AUTHORS Foreman, P.K., Brown, D.B., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.D.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

JOURNAL MEDLINE 22803314  
PUBMED 12788920  
COMMENT Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
Seq primer: LT-F1 primer.  
Location/Qualifiers 1..808  
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FEATURES  
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/mol\_type="rRNA"  
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/clone\_1lb="T. reesei mycelial culture, Version 3 april"  
/note="Vector: pREP3; Site\_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

## ORIGIN

Query Match 60.0%; Score 186; DB 14; Length 808;  
Best Local Similarity 80.9%; Pred. No. 1,1e-43;  
Matches 254; Conservative 0; Mismatches 55; Indels 5; Gaps 3;  
QY 1 AATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 60  
DB 96 AATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATGATCTTTGAACGACA 155  
QY 61 TTGGGCCCCGAGTATCTGGCGGCGATGCTGTTCAGAGCTCATTTCAACCTCGAAC 120  
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QY 181 GCGGTCTGCTGAGCTTCATTTGCTAGTAG-TAAACCTCGCAACTGTAGCGGCG 239  
DB 275 GCGGTCTGCGGAGCTCTCTCGGAGTAGTTGCACTCGACCGGAGGCGCG 334  
QY 240 CGGCGAAGCGGTAA--ACCCCACTTCTGAATGTTGACTCGGATCAGTAGAATA 296  
DB 335 CGGCGAAGCGGTAAACCCCAACTCTGAATGTTGACTCGGATCAGTAGAATA 394  
QY 297 CCCGCTGAACCTAA 310  
DB 395 CCCGCTGAACCTAA 408

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CF880267  
LOCUS tric081xc18.b2 T. reesei mycelial culture, Version 6 October 2003  
DEFINITION Hypocrea jecorina cDNA clone tric081xc18, mRNA sequence.  
ACCESSION CF880267  
VERSION CF880267.1 GI:38134949  
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SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 735)  
AUTHORS Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,  
Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and  
Dean, R.A.  
Analysis of the protein processing and secretion pathways in a  
Trichoderma reesei EST dataset  
Unpublished (2003)  
CONTACT: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: LT-F1 primer.  
Location/Qualifiers 1..735  
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culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
ORIGIN

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Query Match	45.1%;	Score 139.8;	DB 14;	Length 735;
Best Local Similarity	78.0%;	Pred. No. 4,1e-30;		
Matches 192; Conservative	0;	Mismatches 52;	Indels 2;	Gaps 2;

QY	1	AAATGGCATAGTAAATGTAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA	60
Db	50	AAATGGCATAGTAAATGTAATTGCAAAATTCAGTGAATCATCGAATCTTTGAACGACA	109
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Db	110	TTGCGCCCGCCAGATATTTCGGCGGGCAGTGCCTGTTCGAGCGTCATTTCAACCTCGAAGCC	169
QY	121	CCGCGGCTTTGATGTTGGGGATCGCGAAGCCCTTCGGCGAAGCCCGGCCCGGAAATCTAATG	180
Db	170	CTCTCCGGGGGGT-CGGTCTTTGGGGGATCGGCCCCCTACCGGGCCGCCCCCGAAATACAGNG	228
QY	181	GCGGTCCTCGTCAGACGTTCCATTCGATG-TAGTAAACCTTCGCAACTGTGACGCGCG	239
Db	229	GCGGTCCTCGTCAGACGTTCTTCGGCGAGTACTTGACACTTCACCCGAGCGCGCG	288
QY	240	CGGCGCA	245
Db	289	CGGCGCA	294

RESULT 6	CB907036	840 bp	mRNA	linear	EST 02-JUL-2003
LOCUS	CB907036				
DEFINITION	tritic081xc18 T.reesei mycelial culture, Version 3 april Hypocrea jecorina cDNA clone tritic081xc18, mRNA sequence.				
ACCESSION	CB907036				

VERSION	CB907036.1	GI:30121694
KEYWORDS	EST.	
SOURCE	Hypocrea jecorina (anamorph: Trichoderma reesei)	
ORGANISM	Hypocrea jecorina	

REFERENCE  
AUTHORS  
1 (bases 1 to 840)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener

TITLE	JOURNAL	YEAR	VOLUME	PAGE	DOI
Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus <i>Trichoderma reesei</i>	J. Biol. Chem.	278 (34)	31988-31997	(2003)	

PUBMED 12788920  
Contact: Pamela K. Foreman

```

925 Page Mill Road Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 821-7817
Email: f10reman@engencor.com
Seg primer: UT-PI primer.
Location/Qualifiers
1. .840
source
FEATURES

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FEATURES
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    location/Qualifiers
    1. 840
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        /note="Vector: pK6P3; Site_1: Not I/Sal I; Mycelial

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culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

Query Match	45.1%	Score 139.8;	DB 14;	Length 840;
Best Local Similarity	78.0%	Pred. No. 4-4e-30;		
Matches 192; Conservative	0;	Mismatches 52;	Indels 2;	Gaps 2;

[illegible]

RESULT 7					
B0751285					
LOCUS					
DEFINITION					
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	EST651846	DSCT	Colletotrichum trifolii	cdNA clone pDSCT4-17,	mRNA
	sequence.				
	seq=100c				

ACCESSION	BQ751285
VERSION	BQ751285.1
KEYWORDS	GI:21906690
SOURCE	EST.
ORGANISM	<i>Colletotrichum trifolii</i>
	<i>Colletotrichum trifolii</i>

REFERENCE  
AUTHORS  
Sordariomycetes intercalat sedis; Phyllostoraales; Phyllostoraaceae  
mitosporic Phyllostoraaceae; Colletotrichum.  
1 (bases 1 to 704)  
Samad, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T.

JOURNAL Unpublished (2002)  
COMMENT Other\_ESTS: EST631847

One Barclay Street  
495 Bortland Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 612 640 6060

TIGR sequence name: MTSAD17TV More information is available at  
www.medicago.org

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FEATURES
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                /lab_host="DMSalpa"
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                /note="vector: pBluescript SK+; Site_1: EcoRI, Site_2:
                EcoRI, isolate: 2sp2 ; cDNA was prepared from polyA+
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enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce *E. coli* Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pluescript SK+. Aliquots of the ligation were used to transform *E. coli* DH5alpha which were plated onto medium with X-gal for selection of recombinants."

## ORIGIN

Query Match 38.8%; Score 120.2; DB 13; Length 704;  
Best Local Similarity 74.2%; Pred. No. 2.4e-24;  
Matches 210; Conservative 0; Mismatches 58; Indels 15; Gaps 4;

QY 33 AGTAAATCATGAAATCTTTGAACGACATTTGGCCCGCATATTCTGGCGGATGCT 92  
DB 1 AGTAAATCATGAAATCTTTGAACGACATTTGGCCCGCATATTCTGGCGGATGCT 60  
QY 93 GTTCAGCGGTATTTCAACCTCAAGCCCGGGTTGTGTGGGAGATCGGCAAGCCCT 152  
DB 61 GTTCAGCGGTATTTCAACCTCAAGCACC-----GCTTGGCGGTGGGCTTCCA 110  
QY 153 TCGCGCAAGCCGCGCCGAAATCTAGTGGCGGTCTGCG-TGCAGCTTCATTTGCGTAGTA 211  
DB 111 CGGCTGAGTGGGGCCCTCAAGACAGTGGCGGACCTTGGCGGAGCTCTTTGCGTAGTA 170  
QY 212 GTAAAACCTTCGCAACTGTGA--CGCGGCGGCGCAAGCCGTTAAACCCCACTTCT-- 267  
DB 171 ACATACCACTTCGCAAGCCGCGGACCTCTCTCGTTAAACCCCACTTCTTAA 230  
QY 268 GAATGTGACCTCGGATCAGTAGAATACCCGCTGAACCTTAA 310  
DB 231 CAAGTTGACCTCGGATCAGTAGAATACCCGCTGAACCTTAA 273

RESULT 8  
LOCUS B0752001 725 bp mRNA linear EST 18-JUL-2002  
DEFINITION EST632564 DSCT Colletotrichum trifolii cDNA clone pDSCT9-22, mRNA  
SEQUENCE.  
ACCESSION B0752001  
VERSION B0752001.1 GI:21907406  
KEYWORDS EST.  
SOURCE Colletotrichum trifolii  
ORGANISM Colletotrichum trifolii  
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Phyllochales; Phyllochoreae;  
mitosporic Phyllochoreae; Colletotrichum.  
1 (bases 1 to 725)  
Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,  
Cheung,F. and Fraser,C.M.  
ESTs from mycelia of Colletotrichum trifolii race 1  
Unpublished (2002)  
Other ESTs: EST632563  
Contact: Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debby@puccini.crl.umn.edu  
TIGR sequence name: MTS412TV More information is available at:  
www.medicago.org  
Seq primer: (gta ACA CGA CTC ACT ACA 999 C).  
Location/Qualifiers

FEATURES  
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/tissue\_type="mycelia"

/dev stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."  
/lab\_host="DH5alpha"  
/clone\_id="DSCT"  
/note="Vector: pluescript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 26p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce *E. coli* Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pluescript SK+. Aliquots of the ligation were used to transform *E. coli* DH5alpha which were plated onto medium with X-gal for selection of recombinants."

## ORIGIN

Query Match 38.8%; Score 120.2; DB 13; Length 725;  
Best Local Similarity 74.2%; Pred. No. 2.4e-24;  
Matches 210; Conservative 0; Mismatches 58; Indels 15; Gaps 4;

QY 33 AGTAAATCATGAAATCTTTGAACGACATTTGCGCCGCAATATTCTGGCGGATGCT 92  
DB 1 AGTAAATCATGAAATCTTTGAACGACATTTGCGCCGCAATATTCTGGCGGATGCT 60  
QY 93 GTTCAGCGGTATTTCAACCTCAAGCCCGGGTTGTGTGGGAGATCGGCAAGCCCT 152  
DB 61 GTTCAGCGGTATTTCAACCTCAAGCACC-----GCTTGGCGGTGGGCTTCCA 110  
QY 153 TCGCGCAAGCCGCGCCGAAATCTAGTGGCGGTCTGCG-TGCAGCTTCATTTGCGTAGTA 211  
DB 111 CGGCTGAGTGGGGCCCTCAAGACAGTGGCGGACCTTGGCGGAGCTCTTTGCGTAGTA 170  
QY 212 GTAAAACCTTCGCAACTGTGA--CGCGGCGGCGCAAGCCGTTAAACCCCACTTCT-- 267  
DB 171 ACATACCACTTCGCAAGCCGCGGACCTCTCTCGTTAAACCCCACTTCTTAA 230  
QY 268 GAATGTGACCTCGGATCAGTAGAATACCCGCTGAACCTTAA 310  
DB 231 CAAGTTGACCTCGGATCAGTAGAATACCCGCTGAACCTTAA 273

RESULT 9  
LOCUS B0751015 806 bp mRNA linear EST 18-JUL-2002  
DEFINITION EST631578 DSCT Colletotrichum trifolii cDNA clone pDSCT2-7, mRNA  
SEQUENCE.  
ACCESSION B0751015  
VERSION B0751015.1 GI:21906420  
KEYWORDS EST.  
SOURCE Colletotrichum trifolii  
ORGANISM Colletotrichum trifolii  
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Phyllochales; Phyllochoreae;  
mitosporic Phyllochoreae; Colletotrichum.  
1 (bases 1 to 806)  
Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,  
Cheung,F. and Fraser,C.M.  
ESTs from mycelia of Colletotrichum trifolii race 1  
Unpublished (2002)  
Other ESTs: EST631577  
Contact: Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debby@puccini.crl.umn.edu  
TIGR sequence name: MTSAB07TV More information is available at:  
www.medicago.org  
Seq primer: (gta ACA CGA CTC ACT ACA 999 C).  
Location/Qualifiers

## FEATURES

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## ORIGIN

Query Match 38.8%; Score 120.2; DB 13; Length 806;  
 Best Local Similarity 74.2%; Pred. No. 2.5e-24;  
 Matches 210; Conservative 0; Mismatches 58; Indels 15; Gaps 4;

QY 33 AGTGAATCATGAAATCTTTGAAGCAGCATTCGCGCCGACATTCCTGGCGGAGCCT 92  
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 QY 93 GTTGAGGCGTATTTCAACCTCAAGCCCGGGTTGGTGGGATGGCAAGCCT 152  
 DB 61 GTTGAGGCGTATTTCAACCTCAAGCACC-----GTTGGGTTGGGCGTTTCCA 110  
 QY 153 TGGCGGAGCGGCGCCGAAATCTAGTGGCGGTCTCGC-TGCAGCTTCATTTGGTATGA 211  
 DB 111 CGGCTGACGTGGGCGCTCAAGACAGTGGGAGCCTCTGGGAGCCTCTTTGGTATGA 170  
 QY 212 GTTAAACCTCTGCAACTGTGA--CGCGGCGGCGCAAGCGGTAAACCCCAATTCT-- 267  
 DB 171 ACATACACACTCGACCGGAGCGGAGGACCTCTGCGGTAAACCCCAATTCTTA 230  
 QY 268 GAATGTTGACCTCGGATCAGTAGAATACCCGCTGAATTAA 310  
 DB 231 CAAGGTTGACCTCGGATCAGTAGAATACCCGCTGAATTAA 273

RESULT 10 806 bp mRNA linear EST 18-JUL-2002  
 BQ751484  
 LOCUS EST632047 DSCR Colletotrichum trifolii cDNA clone pDST5-48, mRNA  
 DEFINITION  
 ACCESSION BQ751484  
 VERSION BQ751484.1 GI:21906889  
 KEYWORDS EST.  
 SOURCE Colletotrichum trifolii  
 ORGANISM Colletotrichum trifolii  
 Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Mitosporic Phyllachoraceae; Colletotrichum.  
 1 (bases 1 to 806)  
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,  
 Cheung,F. and Fraser,C.M.  
 ESTs from mycelia of Colletotrichum trifolii race 1  
 Unpublished (2002)  
 Other ESTs: EST632046  
 Contact: Deborah A. Samac  
 Department of Plant Pathology  
 University of Minnesota  
 495 Boring Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENTFEATURES  
source

Tel: 612 625 1243  
 Fax: 651 649 5058  
 Email: debbys@uccini.crl.umn.edu  
 TIGR sequence name: MTSAB48TV More information is available at:  
 www.medicago.org  
 Seq primer: (GRA ATA CGA CTC ACT ATA GGG C).  
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 /lab\_host="DH5alpha"  
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 /note="Vector: pBluescript SK+, Site 1: EcoRI; Site 2: EcoRI; isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gill from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

## ORIGIN

Query Match 38.8%; Score 120.2; DB 13; Length 806;  
 Best Local Similarity 74.2%; Pred. No. 2.5e-24;  
 Matches 210; Conservative 0; Mismatches 58; Indels 15; Gaps 4;

QY 33 AGTGAATCATGAAATCTTTGAAGCAGCATTCGCGCCGACATTCCTGGCGGAGCCT 92  
 DB 1 AGTGAATCATGAAATCTTTGAAGCAGCATTCGCGCCGACATTCCTGGCGGAGCCT 60  
 QY 93 GTTGAGGCGTATTTCAACCTCAAGCCCGGGTTGGTGGGATGGCAAGCCT 152  
 DB 61 GTTGAGGCGTATTTCAACCTCAAGCACC-----GTTGGGTTGGGCGTTTCCA 110  
 QY 153 TGGCGGAGCGGCGCCGAAATCTAGTGGCGGTCTCGC-TGCAGCTTCATTTGGTATGA 211  
 DB 111 CGGCTGACGTGGGCGCTCAAGACAGTGGGAGCCTCTGGGAGCCTCTTTGGTATGA 170  
 QY 212 GTTAAACCTCTGCAACTGTGA--CGCGGCGGCGCAAGCGGTAAACCCCAATTCT-- 267  
 DB 171 ACATACACACTCGACCGGAGCGGAGGACCTCTGCGGTAAACCCCAATTCTTA 230  
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 DB 231 CAAGGTTGACCTCGGATCAGTAGAATACCCGCTGAATTAA 273

RESULT 11 745 bp mRNA linear EST 18-JUL-2002  
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 LOCUS EST632534 DSCR Colletotrichum trifolii cDNA clone pDST9-3, mRNA  
 DEFINITION  
 ACCESSION BQ751971  
 VERSION BQ751971  
 KEYWORDS EST.  
 SOURCE Colletotrichum trifolii  
 ORGANISM Colletotrichum trifolii  
 Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Mitosporic Phyllachoraceae; Colletotrichum.  
 1 (bases 1 to 745)  
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,  
 Cheung,F. and Fraser,C.M.

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

FEATURES  
SOURCE

ESTs from mycelia of *Colletotrichum trifolii* race 1  
Unpublished (2002)  
Contact: Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlang Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debby@pucini.crl.umn.edu  
TIGR sequence name: MTS103TV More information is available at:  
www.medicago.org  
Seq primer: (gta Aca CGA CTC Act Aca 999 C) .  
Location/Qualifiers  
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ORIGIN

Query Match 38.3%; Score 118.6; DB 13; Length 745;  
Best Local Similarity 73.9%; Pred. No. 7.2e-24;  
Matches 209; Conservative 0; Mismatches 59; Indels 15; Gaps 4;

33 AGTGAATCATGAACTTTTGAACGACATGGCGGCGGATTTCTGGGGGATGCT 92  
1 AGTGAATCATGAACTTTTGAACGACATGGCGGCGGATTTCTGGGGGATGCT 60  
93 GTTGAAGCGATTTCAACCTTCAAGCCCGGGTTTGGTGGGATCGGCAAGCCT 152  
61 GTTGAAGCGATTTCAACCTTCAAGC-----GTTGGCGTTGGGGCTTCA 110  
153 TCGGGCAAGCGGCGGAAATCTAGTGGCGGCTCGC-TGCACTTCATTTGGTAGTA 211  
111 CGGCTGACGTGGGCGCTCAAGACAGTGGCGGACCTCGCGAGCGCTCTTTGGGTAGTA 170  
212 GTAACACCTTCGCACTGTA--CGCGGCGGCGCAAGCGCTTAAACCCCACTCT-- 267  
171 ACATACCACTTCGCACTGTA--CGCGGCGGCGCAAGCGCTCTTGGGTAGTA 230  
268 GAATGTTGACCTCGGATCAGTAGAATACCGGCTGAACCTTAA 310  
231 CAAGTTGACCTCGGATCAGTAGAATACCGGCTGAACCTTAA 273

RESULT 12  
BO751399 758 bp mRNA linear EST 18-JUL-2002  
LOCUS EST613962 DSC7 Colletotrichum trifolii cDNA clone pDSC7A-95, mRNA  
DEFINITION  
ACCESSION BO751399  
VERSION BO751399.1 GI:21906804  
KEYWORDS EST.  
SOURCE Colletotrichum trifolii  
ORGANISM Colletotrichum trifolii

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
SOURCE

Eukaryota: Fungi: Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;  
mitosporic Phyllachoraceae; Colletotrichum.  
1 (bases 1 to 758)  
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T.,  
Cheung, F., and Fraser, C.M.  
ESTs from mycelia of *Colletotrichum trifolii* race 1  
Unpublished (2002)  
Other ESTs: EST613961  
Contact: Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlang Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debby@pucini.crl.umn.edu  
TIGR sequence name: MTSAD95TV More information is available at:  
www.medicago.org  
Seq primer: (gta Aca CGA CTC Act Aca 999 C) .  
Location/Qualifiers  
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ORIGIN

Query Match 38.3%; Score 118.6; DB 13; Length 758;  
Best Local Similarity 73.9%; Pred. No. 7.3e-24;  
Matches 209; Conservative 0; Mismatches 59; Indels 15; Gaps 4;

33 AGTGAATCATGAACTTTTGAACGACATGGCGGCGGATTTCTGGGGGATGCT 92  
1 AGTGAATCATGAACTTTTGAACGACATGGCGGCGGATTTCTGGGGGATGCT 60  
93 GTTGAAGCGATTTCAACCTTCAAGCCCGGGTTTGGTGGGATCGGCAAGCCT 152  
61 GTTGAAGCGATTTCAACCTTCAAGC-----GTTGGCGTTGGGGCTTCA 110  
153 TCGGGCAAGCGGCGGAAATCTAGTGGCGGCTCGC-TGCACTTCATTTGGTAGTA 211  
111 CGGCTGACGTGGGCGCTCAAGACAGTGGCGGACCTCGCGAGCGCTCTTTGGGTAGTA 170  
212 GTAACACCTTCGCACTGTA--CGCGGCGGCGCAAGCGCTTAAACCCCACTCT-- 267  
171 ACATACCACTTCGCACTGTA--CGCGGCGGCGCAAGCGCTCTTGGGTAGTA 230  
268 GAATGTTGACCTCGGATCAGTAGAATACCGGCTGAACCTTAA 310  
231 CAAGTTGACCTCGGATCAGTAGAATACCGGCTGAACCTTAA 273

RESULT 13  
BM870292 169 bp mRNA linear EST 06-MAY-2003  
LOCUS BM870292

DEFINITION mgns009xj23f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgns009xj23 5', mRNA sequence.

ACCESSION BM870292

VERSION BM870292.2 GI:30404719

KEYWORDS EST.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 169)  
Ebbold, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatterai, K. and Dean, R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe grisea

TITLE Unpublished (2002)

JOURNAL On Mar 7, 2002 this sequence version replaced gi:19237974.

COMMENT Contact: Ebbold DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 4831  
Email: d-ebbold@tamu.edu  
Chromatogram file of this sequence is available, see contact person/Best nr hit (April. 22, 2003) gb|AL79278.1| unknown  
[Saccharomyces cerevisiae] 79 1e-14

PCR primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgns009 row: J column: 23  
Seq primer: T3.

FEATURES  
source  
1..169  
location/Qualifiers  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgns009xj23"  
/sex="Mati-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_idb="Magnaporthe grisea NS Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Nitrogen starvation library. Cells were inoculated into minimal medium and grown for two days with shaking (150 rpm) at room temperature. Culture was harvested, blended, inoculated into minimal medium as above for 24 h. Cells were harvested, washed with water and inoculated into minimal medium base lacking nitrogen source for 6 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

ORIGIN  
Query Match 37.4%; Score 116; DB 12; Length 169;  
Best Local Similarity 96.0%; Pred. No. 2e-23;  
Matches 115; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 AATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATGAACTTTGAAGCACA 60  
Db 39 AATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATGAACTTTGAAGCACA 98

QY 61 TTGGCGCCCGCAATTTCTGGCGCGCATGCGCTTTGAGGCGATTTCAACCTCAAGC 120  
Db 99 TTGCGCGCCCGCAATTTCTGGCGCGCATGCGCTTTGAGGCGATTTCAACCTCAAGC 158

QY 121 CCGG 124  
Db 159 TCGG 162

RESULT 14  
B0752136  
LOCUS B0752136

DEFINITION 774 bp mRNA linear EST 18-JUL-2002  
EST632699 DSCOT Colletotrichum trifolii cDNA clone pDSC10-23, mRNA sequence.

ACCESSION B0752136

VERSION B0752136.1 GI:21907541

KEYWORDS EST.

SOURCE Colletotrichum trifolii

ORGANISM Colletotrichum trifolii  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.

REFERENCE 1 (bases 1 to 774)  
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T., Chung, F. and Fraser, C.M.  
ESTs from mycelia of Colletotrichum trifolii race 1

TITLE Unpublished (2002)

JOURNAL Other ESTs: EST632698

COMMENT Contact: Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debby@puccini.crl.umn.edu  
TIGR sequence name: MTSAMJ23TV More information is available at: www.medicago.org  
Seq primer: (5' to 3') Aca Cgc Act Aca ggg C).

FEATURES  
source  
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location/Qualifiers  
/organism="Colletotrichum trifolii"  
/mol\_type="mRNA"  
/strain="race 1"  
/db\_xref="taxon:5466"  
/clone="pDSC10-23"  
/tissue\_type="mycelia"  
/dev\_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (curin minimal medium containing 2% glucose)."  
/lab\_host="DH5alpha"  
/clone\_idb="DSCOT"  
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: EcoRI; isolate: 28p2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN  
Query Match 36.6%; Score 113.6; DB 13; Length 774;  
Best Local Similarity 73.4%; Pred. No. 2.2e-22;  
Matches 204; Conservative 0; Mismatches 59; Indels 15; Gaps 4;

38 ATCATCGAATCTTTGAACGCAATTTGGCGCGCGCAAGTAATTCGCGGCGAATGCTTGG 97  
Db 5 ATTATCGAATCTTTGAACGCAATTTGGCGCGCGCAAGTAATTCGCGGCGAATGCTTGG 64

QY 98 AGCGTCATTTCAACCTCAAGCCCCCGGGTTGTGTGGGATCGCAAGCCCTTCGG 157  
Db 65 AGCGTCATTTCAACCTCAAGCACC-----GCTTGGCGTTGGGCTTCCAGCGCT 114

QY 158 CAAGCGCGCGCGCAATTTAGTGGCGGCTTCGC-TGAGCTTCCATTGCGTAGTAATA 216  
Db 115 GACGTGGCGCTCAAGACAGTGGCGGAGCCTTCGCGAGCGCTCTTGGTAGTAATA 174

QY 217 ACCCTGCACTGTA--CGCGGCGGCGCAAGCCGTTAAACCCCACTTCT--GAATG 272  
 DB 175 CCACCTGCCACCGGAGCCCGGAGGCACTCTCCGCTGTAACCCCAATTTTCAAGG 234  
 QY 273 TTGACCTCGATCAGTAGAATATACCGCTGAACCTTAA 310  
 DB 235 TTGACCTCGATCAGTAGAATATACCGCTGAACCTTAA 272

## RESULT 15

B0751027

743 bp mRNA linear EST 18-JUL-2002

LOCUS EST631590 DSCF Colletotrichum trifolii cDNA clone pDSCF2-20, mRNA

DEFINITION

sequence.

ACCESSION

B0751027

VERSION

B0751027.1 GI:21906432

KEYWORDS

EST.

SOURCE

Colletotrichum trifolii

ORGANISM

Colletotrichum trifolii

REFERENCE

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

AUTHORS

Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;

1 (bases 1 to 743)

mitosporic Phyllachoraceae; Colletotrichum.

Samad, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T.,

Cheung, F. and Fraser, C.M.

ESTs from mycelia of Colletotrichum trifolii race 1

Unpublished (2002)

Other ESTs: EST631589

Contact: Deborah A. Samad

Department of Plant Pathology

University of Minnesota

495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

Tel: 612 625 1243

Fax: 612 625 1243

Email: debby@puccini.crl.umn.edu

TIGR sequence name: MTSAB20TV More information is available at:

www.medicago.org

Seq primer: (GTA ATA CGA CTC ACT ATA ggg C).

Location/Qualifiers

1..743

/organism="Colletotrichum trifolii"

/mol\_type="mRNA"

/strain="race 1"

/db\_xref="taxon:5466"

/clone="pDSCF2-20"

/issue\_type="mycelia"

/dev\_stage="young, actively growing mycelia (3 days after

inoculation) grown in liquid culture (cutin minimal medium

containing 2% glucose)."

/lab\_host="DH5alpha"

/clone\_lib="DSCF"

/note="Vector: pBluescript SK+; Site\_1: EcoRI; Site\_2:

EcoRI; isolate: 2sp2; cDNA was prepared from polyA+

enriched RNA. The cDNA was ligated into Lambda gIII from

Stratagene and packaged using Gigapack packaging extracts.

An aliquot of the amplified library was used to transduce

E. coli Y1090 and phage DNA was purified from a liquid

lysate. The cDNA inserts were gel purified after EcoRI

digestion and ligated into pBluescript SK+. Aliquots of

the ligation were used to transform E. coli DH5alpha which

were plated onto medium with X-gal for selection of

recombinants."

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recombinants."

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 Job time : 4343.33 secs

DB 65 AGCGTCATTTCAACCCCTCAAGCACC-----GCTGGCGTTGGGGCTTCCACGGCT 114  
 QY 158 CAAGCCGCCCCGAATCTAGTGGCGGTCTGCG-TGAGCTTCATTGCGTAGTAGTAA 216  
 DB 115 GACGTGGGCCCTCAAGACAGTGGCGGACCTCCGCGAGCCTCTTGGCGTAGTAACTA 174  
 QY 217 ACCCTGCACTGTA--CGCGGCGGCGCAAGCGTTAAACCCCACTTCT--GAATG 272  
 DB 175 CCACCTGCCACCGGAGCCCGGAGGCACTCTCGCTGAACCCCAATTTTCAAGG 234  
 QY 273 TTGACCTCGATCAGTAGAATATACCGCTGAACCTTAA 310  
 DB 235 TTGACCTCGATCAGTAGAATATACCGCTGAACCTTAA 272

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 05:20:41 ; Search time 1575.63 Seconds

(without alignments)  
8527.610 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310

Sequence: 1 aaatgcgataagtaagtga.....sgaataccgcgtgaactaa 310

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1164953

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : GenEmbl1.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_scs.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vr.\*

15: em\_da.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_scs.\*

28: em\_un.\*

29: em\_vr.\*

30: em\_hcg\_hum.\*

31: em\_hcg\_inv.\*

32: em\_hcg\_other.\*

33: em\_hcg\_mus.\*

34: em\_hcg\_pln.\*

35: em\_hcg\_rnd.\*

36: em\_hcg\_mam.\*

37: em\_hcg\_vrt.\*

38: em\_sy.\*

39: em\_hcgo\_hum.\*

40: em\_hcgo\_mus.\*

41: em\_hcgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	6 AR206401	AR206401 Sequence
2	310	100.0	310	6 BD083592	BD083592 Nucleic a
3	310	100.0	310	8 AF117922	AF117922 Gdbbere1
4	232	74.8	351	8 AF162903	AF162903 Fusarium
5	232	74.8	556	8 AF455422	AF455422 Gdbbere1
6	232	74.8	556	8 AF455460	AF455460 Gdbbere1
7	232	74.8	558	8 PFUORNA	PFUORNA
8	232	74.8	558	8 PFUORNA	PFUORNA
9	232	74.8	562	8 AY237110	AY237110 Fusarium
10	232	74.8	569	8 AF452163	AF452163 Pychium u
11	232	74.8	596	8 AF291061	AF291061 Sequence
12	232	74.8	2293	6 AR168094	AR168094 Sequence
13	228	73.5	534	8 PFU34557	PFU34557 Fusarium fu
14	228	73.5	534	8 PFU34558	PFU34558 Fusarium pr
15	226	72.9	502	8 AF165873	AF165873 Gdbbere1
16	216	69.7	521	8 FSU61691	FSU61691 Fusarium sp
17	181	58.4	531	8 AF158303	AF158303 Fusarium
18	181	58.4	540	8 AF158304	AF158304 Fusarium
19	177	57.1	534	8 FSU61670	FSU61670 Fusarium an
20	177	57.1	534	8 FSU61693	FSU61693 Fusarium sp
21	165	53.2	522	8 FCU61678	FCU61678 Fusarium co
22	158	51.0	541	8 AF158307	AF158307 Fusarium
23	158	51.0	541	8 AF158309	AF158309 Fusarium
24	158	51.0	559	8 FDLARNA	FDLARNA
25	155	50.0	535	8 FAU34573	FAU34573 Fusarium ac
26	154	49.7	535	8 FDU34572	FDU34572 Fusarium dl
27	143	46.1	471	8 AF150468	AF150468 Neccria h
28	139	44.8	534	8 FSU61692	FSU61692 Fusarium sp
29	134	43.2	349	8 AF162897	AF162897 Fusarium
30	134	43.2	527	8 FSU61687	FSU61687 Fusarium gl
31	134	43.2	529	8 AF158312	AF158312 Fusarium
32	134	43.2	557	8 FNYGRNA	FNYGRNA
33	131	42.3	534	8 FP034574	FP034574 Fusarium ny
34	130	41.9	421	8 AF430128	AF430128 Fusarium ph
35	130	41.9	421	8 AF430129	AF430129 Fusarium
36	130	41.9	533	8 FNU34568	FNU34568 Fusarium ny
37	130	41.9	533	8 FNU34575	FNU34575 Fusarium ud
38	130	41.9	540	8 AF158302	AF158302 Fusarium
39	130	41.9	575	8 AF261662	AF261662 Fusarium
40	118	38.1	532	8 FSU34560	FSU34560 Fusarium th
41	118	38.1	543	8 FB034581	FB034581 Fusarium bu
42	118	38.1	1460	8 AF310976	AF310976 Fusarium
43	118	38.1	1460	8 AF310977	AF310977 Fusarium
44	117	37.7	538	8 FSU61695	FSU61695 Fusarium sp
45	117	37.7	1458	8 AF310981	AF310981 Fusarium

# ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	310 bp	DNA	linear	PAT 20-JUN-2002
AR206401	Sequence 7 from patent US 6372430.	AR206401				
AR206401	GI:21504992	AR206401.1				
UNKNOWN.	Unknown.	Unknown.				
Unclassified.	Unclassified.	Unclassified.				
REFERENCE	1 (bases 1 to 310)	1 (bases 1 to 310)				
AUTHORS	Morrison,C.J., Reiss,E., Aldorevich,L. and Choi,J.Soo.	Morrison,C.J., Reiss,E., Aldorevich,L. and Choi,J.Soo.				
TITLE	Nucleic acids for detecting Aspergillus species and other filamentous fungi	Nucleic acids for detecting Aspergillus species and other filamentous fungi				
JOURNAL	Patent: US 6372430-A 7 16-APR-2002;	Patent: US 6372430-A 7 16-APR-2002;				

FEATURES	source	Location/Qualifiers
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		/organism="unknown"
		/mol_type="unassigned DNA"
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Best Local Similarity	100.0%; Pred. No. 2.7e-171;	
Matches 310; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	AAATGCGATAAGTATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
DB	1	AAATGCGATAAGTATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAAGCACA 60
QY	61	TTGGGCCCCCGACGATTTTGGCGGGGCATGCTGTTGCGCGCTCATTTCAACCTTCAGCC 120
DB	61	TTGGGCCCCCGACGATTTTGGCGGGGCATGCTGTTGCGCGCTCATTTCAACCTTCAGCC 120
QY	121	CCCGGGTTTGGTGTGGGATCGGCAACCCCTTGCGGAGCCCGGCCCGGAAATCTAGTG 180
DB	121	CCCGGGTTTGGTGTGGGATCGGCAACCCCTTGCGGAGCCCGGCCCGGAAATCTAGTG 180
QY	181	GCGGTCTGCTGACGCTTCATTTGCGTAGTAAACCTTCGCAACTGTACCGCGCGC 240
DB	181	GCGGTCTGCTGACGCTTCATTTGCGTAGTAAACCTTCGCAACTGTACCGCGCGC 240
QY	241	GGCCGACGCGTTAAACCCCACTTCGAAATTTGACCTCGGATCAGTAGGAATACCG 300
DB	241	GGCCGACGCGTTAAACCCCACTTCGAAATTTGACCTCGGATCAGTAGGAATACCG 300
QY	301	CTGAACCTAA 310
DB	301	CTGAACCTAA 310
RESULT 2		
LOCUS	BD083592	
DEFINITION	BD083592	310 bp DNA linear PAT 27-AUG-2002
ACCESSION	BD083592	Nucleic acids for detecting Aspergillus species and other filamentous fungi1.
VERSION	BD083592.1	GI:22629202
KEYWORDS	JP 2001525665-A/7.	
SOURCE	Gibberella fujikuroi	
ORGANISM	Gibberella fujikuroi	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.	
AUTHORS	1 (bases 1 to 310)	
TITLE	Morrison,C.J., Reise,E., Aidorevich,L. and Choi,J.S.	
JOURNAL	Nucleic acids for detecting Aspergillus species and other filamentous fungi	
COMMENT	Patent: JP 2001525665-A 7 11-DEC-2001;	
	THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY	
	THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES	
	SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O	
	CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND	
	PREVENTION TECHNOLOGY TRANSFER OFFICE	
	OS Fusharui moniiforme	
	PN JP 2001525665-A/7	
	PD 11-DEC-2001	
	PF 01-MAY-1998 JP 1998548275	
	PR 02-MAY-1997 US 60/045400	
	PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO	
	PC CHOI	
	CC C1201/68	
	CC Strandedness: Single;	
	CC Topology: linear;	
	CC Key	
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	/mol_type="genomic DNA"	

ORIGIN	/db_xref="taxon:5127"			
Query Match	100.0%;	Score 310;	DB 6;	Length 310;
Best Local Similarity	100.0%;	Pred. No. 2,7e-171;		
Matches 310;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AAATGCCAATAGTATGTGAATTTGCCAAATTCAGTGAATCATCGAATCTTTGAACGCACA	60	
DB	1	AAATGCCAATAGTATGTGAATTTGCCAAATTCAGTGAATCATCGAATCTTTGAACGCACA	60	
QY	61	TTGGCGCCCGCAGATATCTGGCGGGCATGCGCTGTTCGAGCGTCATTTCAACCTCAAGCC	120	
DB	61	TTGGCGCCCGCAGATATCTGGCGGGCATGCGCTGTTCGAGCGTCATTTCAACCTCAAGCC	120	
QY	121	CCCGGGTTTGGTGTGGGGATCGGCAAGCCCTTTCGGGCAAGCCGGCCCGGAATCTAGTG	180	
DB	121	CCCGGGTTTGGTGTGGGGATCGGCAAGCCCTTTCGGGCAAGCCGGCCCGGAATCTAGTG	180	
QY	181	GCAGTCTTCGTGCGACGCTTCATTTCCGTAAGTAATAAACCTTCGACACTGGTACGCGGCG	240	
DB	181	GCAGTCTTCGTGCGACGCTTCATTTCCGTAAGTAATAAACCTTCGACACTGGTACGCGGCG	240	
QY	241	GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTGTGACCTGGATCAGGTAGGAATACCG	300	
DB	241	GGCCAAAGCCGTTAAACCCCAACTTCTGAATGTGTGACCTGGATCAGGTAGGAATACCG	300	
QY	301	CTGAACCTTAA 310		
DB	301	CTGAACCTTAA 310		
RESULT 3				
LOCUS	AF117922	310 bp	DNA	linear
DEFINITION	Gibberella fujikuroi ATCC 38519 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence.			
ACCESSION	AF117922			
VERSION	AF117922.1	GI:8570108		
KEYWORDS				
SOURCE				
ORGANISM	Gibberella fujikuroi			
	Bukariyota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.			
REFERENCE	1. Choi,J.S., Westernman,J.M. and Morrison,C.J. Rapid differentiation of filamentous fungi using species-specific DNA probes			
AUTHORS	Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)			
JOURNAL	2. (bases 1 to 310)			
REFERENCE	Choi,J.S., Westernman,J.M. and Morrison,C.J.			
AUTHORS	Direct Submission			
JOURNAL	Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA 30333, USA			
FEATURES				
source	1. 310 Location/Qualifiers			
	/organism="Gibberella fujikuroi"			
	/mol_type="genomic DNA"			
	/strain="ATCC 38519"			
	/db_xref="ATCC:38519"			
	/db_xref="taxon:5127"			
	<1..159			
rRNA	/product="5.8S ribosomal RNA"			
	159..272			
misc_RNA	/product="internal transcribed spacer 2"			
	/note="ITS2"			
rRNA	273..>310			
	/product="26S ribosomal RNA"			
ORIGIN				
Query Match	100.0%;	Score 310;	DB 8;	Length 310;



Best Local Similarity 100.0%; Pred. No. 2,7e-171;  
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGCGTAATGATATGGAATTTGCAAAATTCAGTATCATTCGAATCTTTGAAGCGCA 60  
Db 1 AATGCGTAATGATATGGAATTTGCAAAATTCAGTATCATTCGAATCTTTGAAGCGCA 60  
QY 61 TTGCGCCCGCCAGTATCTGGCGGGCATGCGCTTTCAGAGCGTCAATTCACCCCTCAAGCC 120  
Db 61 TTGCGCCCGCCAGTATCTGGCGGGCATGCGCTTTCAGAGCGTCAATTCACCCCTCAAGCC 120  
QY 121 CCCGGGTTTGTGTGGGATTCGGCAAGCCCTTGGCGGAGCCCGCCCGGAATCTAGTG 180  
Db 121 CCCGGGTTTGTGTGGGATTCGGCAAGCCCTTGGCGGAGCCCGCCCGGAATCTAGTG 180  
QY 181 GCGGCTGTGCTGACGCTTCATTCGTGTAGTAAACCTTCGCACTGTGTACGGGGCGC 240  
Db 181 GCGGCTGTGCTGACGCTTCATTCGTGTAGTAAACCTTCGCACTGTGTACGGGGCGC 240  
QY 241 GGGCAAGCGGTTAAACCCCAACTCTGAATGTTGACCTCGGATCAGGTAGGAATACCG 300  
Db 241 GGGCAAGCGGTTAAACCCCAACTCTGAATGTTGACCTCGGATCAGGTAGGAATACCG 300  
QY 301 CTGAACCTTAA 310  
Db 301 CTGAACCTTAA 310

RESULT 4  
AF162903 351 bp DNA linear PLN 04-AUG-1999  
LOCUS AF162903  
DEFINITION Fusarium proliferatum 5.8S ribosomal RNA gene, partial sequence;  
internal transcribed spacer 2, complete sequence; and 28S ribosomal  
RNA gene, partial sequence.  
ACCESSION AF162903  
VERSION AF162903.1 GI:5690392  
KEYWORDS  
SOURCE  
ORGANISM Fusarium proliferatum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Nectriaceae; Gibberella; Gibberella  
fujiikuroi complex.  
AUTHORS Min, B.R.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji  
Dong, Chong Ro-Gu, Seoul 110-743, Korea  
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/strain="6787"  
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rRNA  
129..293  
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misc\_RNA  
129..293  
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294..351  
/product="28S ribosomal RNA"  
ORIGIN  
Query Match 74.8%; Score 232; DB 8; Length 351;  
Best Local Similarity 99.6%; Pred. No. 3.4e-125;  
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 AATTAGTGAATCATGATCTTTGACGACATTCGCGCGCGAGTATTCGCGGGCA 87  
Db 49 AATTAGTGAATCATGATCTTTGACGACATTCGCGCGCGAGTATTCGCGGGCA 108  
QY 88 TGCCGTTCGAGCGTCAATTCACACCTCAAGCCCGGGTTGTGTTGGGATCGGCA 147  
Db 109 TGCCGTTCGAGCGTCAATTCACACCTCAAGCCCGGGTTGTGTTGGGATCGGCA 168

QY 148 GCCCTTCGCGCAAGCCGCGCCGGAATCTAGTGGCGGTCTCGTCGACGCTTCATTCGCT 207  
Db 169 GCCCTTCGCGCAAGCCGCGCCGGAATCTAGTGGCGGTCTCGTCGACGCTTCATTCGCT 228  
QY 208 AGTAGTAAACCTTCGCACTGTGTACGGCGGGCCAGACCGTTAAACCCCACTTCT 267  
Db 229 AGTAGTAAACCTTCGCACTGTGTACGGCGGGCCAGACCGCGTTAAACCCCACTTCT 288  
QY 268 GAATGTTGACCTCGGATCAGTAGGAATACCGCTGAACCTTAA 310  
Db 289 GAATGTTGACCTCGGATCAGTAGGAATACCGCTGAACCTTAA 331

RESULT 5  
AF455422 556 bp DNA linear PLN 16-JUN-2003  
LOCUS AF455422  
DEFINITION  
AF455422 556 bp DNA linear PLN 16-JUN-2003  
Gibberella fujiikuroi isolate w518 small subunit ribosomal RNA  
gene, partial sequence; internal transcribed spacer 1, 5.8S  
ribosomal RNA gene and internal transcribed spacer 2, complete  
sequence; and large subunit ribosomal RNA gene, partial sequence.  
AF455422  
AF455422.1 GI:21666850  
KEYWORDS  
SOURCE  
ORGANISM  
Gibberella fujiikuroi (anamorph: Fusarium fujiikuroi)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Nectriaceae; Gibberella; Gibberella  
fujiikuroi complex.  
AUTHORS Buzina, W., Braun, H., Freudenrich, K., Lackner, A. and  
Stemberger, H.  
TITLE Fungal biodiversity as found in nasal mucus  
REFERENCE Med. Mycol. 41 (2), 149-161 (2003)  
2 (bases 1 to 556)  
Buzina, W., Braun, H., Freudenrich, K., Lackner, A. and  
Stemberger, H.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-2001) Laboratory for Mycology and Molecular  
Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Graz A  
8036, Austria  
FEATURES  
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1..556  
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49..247  
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rRNA  
248..353  
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354..518  
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519..556  
/product="large subunit ribosomal RNA"  
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Query Match 74.8%; Score 232; DB 8; Length 556;  
Best Local Similarity 99.6%; Pred. No. 3.4e-125;  
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 AATTAGTGAATCATGATCTTTGACGACATTCGCGCGCGAGTATTCGCGGGCA 87  
Db 274 AATTAGTGAATCATGATCTTTGACGACATTCGCGCGCGAGTATTCGCGGGCA 333  
QY 88 TGCCGTTCGAGCGTCAATTCACACCTCAAGCCCGGGTTGTGTTGGGATCGGCA 147  
Db 334 TGCCGTTCGAGCGTCAATTCACACCTCAAGCCCGGGTTGTGTTGGGATCGGCA 393  
QY 148 GCCCTTCGCGCAAGCCGCGCCGGAATCTAGTGGCGGTCTCGTCGACGCTTCATTCGCT 207  
Db 394 GCCCTTCGCGCAAGCCGCGCCGGAATCTAGTGGCGGTCTCGTCGACGCTTCATTCGCT 453

QY 208 AGTAGTAAACCTCGCACTGTACGGGGGGGCGCAAGCCGTTAAACCCCACTTCT 267  
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 Db 454 AGTAGTAAACCTCGCACTGTACGGGGGGGCGCAAGCCGTTAAACCCCACTTCT 513  
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 QY 268 GAATGTTGACCTCGATCAGTAGAATAATCCCGCTGAATTTAA 310  
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 Db 514 GAATGTTGACCTCGATCAGTAGAATAATCCCGCTGAATTTAA 556  
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 RESULT 6  
 AF455460  
 LOCUS  
 DEFINITION  
 556 bp DNA linear PLN 16-JUN-2003  
 Gibberella fujikuroi isolate wb355 small subunit ribosomal RNA  
 gene, partial sequence; internal transcribed spacer 1, 5.8S  
 ribosomal RNA gene and internal transcribed spacer 2, complete  
 sequence; and large subunit ribosomal RNA gene, partial sequence.  
 AF455460  
 ACCESSION  
 VERSION  
 KEYWORDS  
 AF455460.1 GI:21666892  
 SOURCE  
 ORGANISM  
 Gibberella fujikuroi (anamorph: Fusarium fujikuroi)  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella  
 fujikuroi complex.  
 1 (bases 1 to 556)  
 Buzina, W., Braun, H., Freudenrichs, K., Lackner, A. and  
 Stammeberger, H.  
 Fungal biodiversity as found in nasal mucus  
 Med. Mycol. 41 (2), 149-161 (2003)  
 2 (bases 1 to 556)  
 Buzina, W., Braun, H., Freudenrichs, K., Lackner, A. and  
 Stammeberger, H.  
 Direct Submission  
 Submitted (04-DEC-2001) Laboratory for Mycology and Molecular  
 Biology, ENT-University Hospital, Auenbruggerplatz 26-28, Graz A  
 8036, Austria  
 FEATURES  
 source  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /isolate="wb355"  
 /db\_xref="taxon:5127"  
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 misc\_RNA  
 49..247  
 /product="internal transcribed spacer 1"  
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 248..353  
 /product="5.8S ribosomal RNA"  
 misc\_RNA  
 354..518  
 /product="internal transcribed spacer 2"  
 rRNA  
 519..>556  
 /product="large subunit ribosomal RNA"  
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 Query Match 74.8%; Score 232; DB 8; Length 556;  
 Best Local Similarity 99.6%; Pred. No. 3,4e-125;  
 Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 28 AATTCAGTGAATCGAATCTTTGAAGCAGCATGGCCGCGCAGTATCTGGCGGCA 87  
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 Db 274 AATTCAGTGAATCGAATCTTTGAAGCAGCATGGCCGCGCAGTATCTGGCGGCA 333  
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 QY 88 TGGCTGTTGAGGGTCAATTTCAACCCCTCAGCCCGGGTTTGTTGGGATCGGCA 147  
 |||||  
 Db 334 TGGCTGTTGAGGGTCAATTTCAACCCCTCAGCCCGGGTTTGTTGGGATCGGCA 393  
 |||||  
 QY 148 GCCCTGGCGCAAGCCGCGCCGCAATCTAGTGGCGTCTCGCTGACGCTTCATTGCGT 207  
 |||||  
 Db 394 GCCCTGGCGCAAGCCGCGCCGCAATCTAGTGGCGTCTCGCTGACGCTTCATTGCGT 453  
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 QY 208 AGTAGTAAACCTCGCACTGTACGGGGGGGCGCAAGCCGTTAAACCCCACTTCT 267  
 |||||

Db 454 AGTAGTAAACCTCGCACTGTACGGGGGGGCGCAAGCCGTTAAACCCCACTTCT 513  
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 QY 268 GAATGTTGACCTCGATCAGTAGAATAATCCCGCTGAATTTAA 310  
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 Db 514 GAATGTTGACCTCGATCAGTAGAATAATCCCGCTGAATTTAA 556  
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 RESULT 7  
 FFURRNA  
 LOCUS  
 DEFINITION  
 558 bp DNA linear PLN 14-JUN-2001  
 Fusarium fujikuroi 18S rRNA gene (partial), 5.8S rRNA gene, 28S  
 rRNA gene (partial), internal transcribed spacer 1 (ITS1) and  
 internal transcribed spacer 2 (ITS2).  
 X94176.1 X93900  
 X94176.1 GI:1122868  
 18S ribosomal RNA; 18S rRNA gene, 28S ribosomal RNA; 28S rRNA gene,  
 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;  
 internal transcribed spacer 2; ITS1, ITS2.  
 Gibberella fujikuroi (anamorph: Fusarium fujikuroi)  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella  
 fujikuroi complex.  
 1  
 Maalwijk, C., de Koning, J.R.A., Baayen, R.P. and Gams, W.  
 Discordant groupings of Fusarium spp. from sections Elegans,  
 liseola and Diamina a based on ribosomal ITS1 and ITS2 sequences  
 Mycologia 88, 361-368 (1996)  
 2 (bases 1 to 558)  
 Maalwijk, C.  
 Direct Submission  
 Submitted (08-DEC-1995) C. Maalwijk, Research Inst. for Plant  
 Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS  
 On Jun 15, 2001 this sequence version replaced gi:1103564.  
 Overlaps with X78260.  
 COMMENT  
 ORIGIN  
 source  
 Location/Qualifiers  
 1..558  
 /organism="Gibberella fujikuroi"  
 /mol\_type="genomic DNA"  
 /strain="CBS 221.76"  
 /specific\_host="rice"  
 /db\_xref="taxon:5127"  
 1..30  
 /gene="18S rRNA"  
 <1..30  
 /gene="18S rRNA"  
 /product="18S ribosomal RNA"  
 misc\_feature  
 31..177  
 /note="internal transcribed spacer 1, ITS1"  
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 178..335  
 /gene="5.8 rRNA"  
 rRNA  
 178..335  
 /gene="5.8 rRNA"  
 /product="5.8 ribosomal RNA"  
 misc\_feature  
 336..500  
 /note="internal transcribed spacer 2, ITS2"  
 gene  
 501..558  
 /gene="28S rRNA"  
 rRNA  
 501..>558  
 /gene="28S rRNA"  
 /product="28S ribosomal RNA"  
 ORIGIN  
 Query Match 74.8%; Score 232; DB 8; Length 558;  
 Best Local Similarity 99.6%; Pred. No. 3,4e-125;  
 Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 28 AATTCAGTGAATCGAATCTTTGAAGCAGCATGGCCGCGCAGTATCTGGCGGCA 87  
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 Db 256 AATTCAGTGAATCGAATCTTTGAAGCAGCATGGCCGCGCAGTATCTGGCGGCA 315  
 |||||  
 QY 88 TGGCTGTTGAGGGTCAATTTCAACCCCTCAGCCCGGGTTTGTTGGGATCGGCA 147  
 |||||

Db 316 TGCCCTGTCGAGCGTCATTTCACACCCCTCAAGCCCCGGGTTGTGTTGGAGTCGGCA 375  
Qy 148 GCCCTTGGGCAAGCGCGCCCGGAATCTAGTGGGGCTCTGCTGACCTTCATTTGGGT 207  
Db 376 GCCCTTGGGCAAGCGCGCCCGGAATCTAGTGGGGCTCTGCTGACCTTCATTTGGGT 435  
Qy 208 AGTAGTAAACCCCTCGCACTGTGTACGGCGCGGCCCAAGCCGTTAAACCCCACTTCT 267  
Db 436 AGTAGTAAACCCCTCGCACTGTGTACGGCGCGGCCCAAGCCGTTAAACCCCACTTCT 495  
Qy 268 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 310  
Db 496 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 538  
RESULT 8  
PPORRNA 558 bp DNA linear PLN 14-JUN-2001  
LOCUS Fusarium proliferatum 18S rRNA gene (partial), 5.8S rRNA gene, 28S  
DEFINITION rRNA gene (partial), internal transcribed spacer 1 (ITS1) and  
internal transcribed spacer 2 (ITS2).  
ACCESSION X94171.1 GI:1122873  
VERSION X94171.1 X93904  
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;  
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;  
internal transcribed spacer 2; ITS1; ITS2.  
SOURCE Fusarium proliferatum  
ORGANISM Fusarium proliferatum  
REFERENCE 1  
AUTHORS Maalwijk, C., de Koning, J.R.A., Baayen, R.P. and Gams, W.  
TITLE Discordant groupings of Fusarium spp. from sections *Elegans*,  
JOURNAL Liseola and *Diamina* a based on ribosomal ITS1 and ITS2 sequences  
REFERENCE Mycologia 88, 361-368 (1996)  
AUTHORS Maalwijk, C.  
TITLE Direct Submission  
JOURNAL Submitted (08-DEC-1995) C. Maalwijk, Research Inst. for Plant  
COMMENT Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS  
On Jun 15, 2001 this sequence version replaced gi:1103572.  
OVERLAPS with X78260.  
FEATURES  
source location/Qualifiers  
1..558  
/organism="Fusarium proliferatum"  
/mol\_type="genomic DNA"  
/strain="CBS 217.76"  
/specific\_host="Cattleya"  
/db\_xref="taxon:42674"  
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/gene="18S rRNA"  
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/gene="18S rRNA"  
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misc\_feature 31..177  
/note="internal transcribed spacer 1, ITS1"  
178..335  
/gene="5.8 rRNA"  
178..335  
/gene="5.8 rRNA"  
misc\_feature 336..500  
/product="5.8 ribosomal RNA"  
/note="internal transcribed spacer 2, ITS2"  
501..558  
/gene="28S rRNA"  
501..558  
/gene="28S rRNA"  
/product="28S ribosomal RNA"  
ORIGIN  
Query Match 74.8%; Score 232; DB 8; Length 558;  
Best Local Similarity 99.6%; Pred. No. 3.4e-125;

Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 28 AATTCAGTGAATCATTCGAATTTTGAACGCACTTGGCCCGCAGATTTCTGGCGGCA 87  
Db 256 AATTCAGTGAATCATTCGAATTTTGAACGCACTTGGCCCGCAGATTTCTGGCGGCA 315  
Qy 88 TGCCGTTTCGAGCGTCATTTCACACCCCTCAAGCCCCGGGTTGTGTTGGAGTCGGCA 147  
Db 316 TGCCGTTTCGAGCGTCATTTCACACCCCTCAAGCCCCGGGTTGTGTTGGAGTCGGCA 375  
Qy 148 GCCCTTGGGCAAGCGCGCCCGGAATCTAGTGGGGCTCTGCTGACCTTCATTTGGGT 207  
Db 376 GCCCTTGGGCAAGCGCGCCCGGAATCTAGTGGGGCTCTGCTGACCTTCATTTGGGT 435  
Qy 208 AGTAGTAAACCCCTCGCACTGTGTACGGCGCGGCCCAAGCCGTTAAACCCCACTTCT 267  
Db 436 AGTAGTAAACCCCTCGCACTGTGTACGGCGCGGCCCAAGCCGTTAAACCCCACTTCT 495  
Qy 268 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 310  
Db 496 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 538  
RESULT 9  
AY237110 562 bp DNA linear PLN 09-APR-2003  
LOCUS Fusarium sp. 03001 18S ribosomal RNA gene, partial sequence;  
DEFINITION internal transcribed spacer 1, 5.8 ribosomal RNA gene and internal  
transcribed spacer 2, complete sequence; and 28S ribosomal RNA  
gene, partial sequence.  
ACCESSION AY237110.1 GI:29691499  
VERSION AY237110.1  
KEYWORDS Fusarium sp. 03001  
SOURCE Fusarium sp. 03001  
ORGANISM Fusarium sp. 03001  
REFERENCE 1  
AUTHORS Atunian, M.R. and Heiang, T.  
TITLE Direct Submission  
JOURNAL Submitted (14-FEB-2003) Environmental Biology, University of  
Guelph, Guelph, ON N1G 2W1, Canada  
FEATURES  
source location/Qualifiers  
1..562  
/organism="Fusarium sp. 03001"  
/mol\_type="genomic DNA"  
/isolate="03001"  
/db\_xref="taxon:227081"  
<1..40  
/product="18S ribosomal RNA"  
41..186  
/product="internal transcribed spacer 1"  
187..345  
/product="5.8 ribosomal RNA"  
346..510  
/product="internal transcribed spacer 2"  
511..562  
/product="28S ribosomal RNA"  
ORIGIN  
Query Match 74.8%; Score 232; DB 8; Length 562;  
Best Local Similarity 99.6%; Pred. No. 3.4e-125;  
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 28 AATTCAGTGAATCATTCGAATTTTGAACGCACTTGGCCCGCAGATTTCTGGCGGCA 87  
Db 266 AATTCAGTGAATCATTCGAATTTTGAACGCACTTGGCCCGCAGATTTCTGGCGGCA 325  
Qy 88 TGCCGTTTCGAGCGTCATTTCACACCCCTCAAGCCCCGGGTTGTGTTGGAGTCGGCA 147  
Db 326 TGCCGTTTCGAGCGTCATTTCACACCCCTCAAGCCCCGGGTTGTGTTGGAGTCGGCA 385  
Qy 148 GCCCTTGGGCAAGCGCGCCCGGAATCTAGTGGGGCTCTGCTGACCTTCATTTGGGT 207

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Db      386 GCCCTGGCGCAGCGCGCGCCCGGAATTAAGTGGCGGCTGCTGCACTTCCTTCCT 445
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Qy      208 AGTAGTAAACCTCTGCACTGTGACGGCGCGCCAGCCGTTAAACCCCACTTCT 267
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Db      446 AGTAGTAAACCTCTGCACTGTGACGGCGCGCCAGCCGTTAAACCCCACTTCT 505
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Qy      268 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 310
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Db      506 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 548
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RESULT 10
AF452163
LOCUS      Pythium ultimum var. sporangiferum isolate 308276R 18S ribosomal
DEFINITION
ACCESSION  AF452163
VERSION     AF452163
KEYWORDS   Pythium ultimum var. sporangiferum
SOURCE      Pythium ultimum var. sporangiferum
ORGANISM   Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Pythium.
REFERENCE   1 (bases 1 to 569)
            Moorman,G.W., Geisler,D.M., Kang,S. and Kim,S.
            Pythium species and a population identification using DNA markers
            Unpublished
            2 (bases 1 to 569)
            Moorman,G.W., Geisler,D.M., Kang,S. and Kim,S.
            Direct Submission
            Submitted (26-NOV-2001) Plant Pathology, Pennsylvania State
            University, 210 Buckhout Laboratory, University Park, PA 16802, USA
            Location/Qualifiers
            source          1..569
                           /organism="Pythium ultimum var. sporangiferum"
                           /mol_type="genomic DNA"
                           /variey="sporangiferum"
                           /isolate="308276R"
                           /db_xref="taxon:115421"
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                           /product="18S ribosomal RNA"

ORIGIN
Query Match      74.8%; Score 232; DB 8; Length 569;
Best Local Similarity 99.6%; Pred. No. 3.4e-125;
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      28  AATTCAGTGAATCATCGAATCTTTGAAGCAGCATTTGCGCCGACATTTCTGGCGGCA 87
      |||
Db      273 AATTCAGTGAATCATCGAATCTTTGAAGCAGCATTTGCGCCGACATTTCTGGCGGCA 332
      |||
Qy      88  TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCCGGGTTGGTGGGATCGGCA 147
      |||
Db      333 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCCGGGTTGGTGGGATCGGCA 392
      |||
Qy      148 GCCCTTGGCGAAGCGCGCCCGGAATCTAGTGGCGGCTCTCGCTGACGCTTCCATTTGCC 207
      |||
Db      393 GCCCTTGGCGAAGCGCGCCCGGAATCTAGTGGCGGCTCTCGCTGACGCTTCCATTTGCC 452
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Qy      208 AGTAGTAAACCTCTGCACTGTGACGGCGCGCCAGCCGTTAAACCCCACTTCT 267
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Db      453 AGTAGTAAACCTCTGCACTGTGACGGCGCGCCAGCCGTTAAACCCCACTTCT 512
      |||
Qy      268 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 310
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Db      513 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 555
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RESULT 11
AF291061
LOCUS      Fusarium proliferatum NRRL 31071 18S ribosomal RNA, partial
DEFINITION

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sequence; internal transcribed spacer 1, 5.8S ribosomal RNA, and
internal transcribed spacer 2, complete sequence; 28S ribosomal
RNA, partial sequence.
AF291061
AF291061.1 GI:15637128
ACCESSION
VERSION
KEYWORDS
SOURCE      Fusarium proliferatum
ORGANISM   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella
            fujikuroi complex.
            1 (bases 1 to 596)
            Kwon,S.-I., van Dohn,C.D. and Anderson,A.J.
            Gene sequence analysis of an opportunistic wheat pathogen, an
            isolate of Fusarium proliferatum
            Can. J. Bot. 79 (9), 1115-1121 (2001)
            2 (bases 1 to 596)
            Kwon,S.-I. and Anderson,A.J.
            Direct Submission
            Submitted (31-JUL-2000) Biology, Utah State University, Logan, UT
            84322-5305, USA
            Location/Qualifiers
            source          1..596
                           /organism="Fusarium proliferatum"
                           /mol_type="genomic DNA"
                           /strain="NRRL 31071"
                           /specific_host="Triticum aestivum cv. Super Dwarf"
                           /db_xref="taxon:42674"
                           <1..596
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                           spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
                           2, 28S ribosomal RNA"

ORIGIN
Query Match      74.8%; Score 232; DB 8; Length 596;
Best Local Similarity 99.6%; Pred. No. 3.4e-125;
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      28  AATTCAGTGAATCATCGAATCTTTGAAGCAGCATTTGCGCCGACATTTCTGGCGGCA 87
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Db      294 AATTCAGTGAATCATCGAATCTTTGAAGCAGCATTTGCGCCGACATTTCTGGCGGCA 353
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Qy      88  TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCCGGGTTGGTGGGATCGGCA 147
      |||
Db      354 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCCGGGTTGGTGGGATCGGCA 413
      |||
Qy      148 GCCCTTGGCGAAGCGCGCCCGGAATCTAGTGGCGGCTCTCGCTGACGCTTCCATTTGCC 207
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Db      414 GCCCTTGGCGAAGCGCGCCCGGAATCTAGTGGCGGCTCTCGCTGACGCTTCCATTTGCC 473
      |||
Qy      208 AGTAGTAAACCTCTGCACTGTGACGGCGCGCCAGCCGTTAAACCCCACTTCT 267
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Db      474 AGTAGTAAACCTCTGCACTGTGACGGCGCGCCAGCCGTTAAACCCCACTTCT 533
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Qy      268 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 310
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Db      534 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 576
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RESULT 12
AR168094
LOCUS      Sequence 1 from patent US 6287800.
DEFINITION
ACCESSION  AR168094
VERSION     AR168094.1 GI:17903914
KEYWORDS
SOURCE      Unknown.
ORGANISM   Unclassified.
            1 (bases 1 to 2293)
            Gallazzo,J.L. and Lee,M.D.
            Production of high titers of gibberellins, GA4 and GA7, by
            Gibberella fujikuroi strain LTB-1027

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JOURNAL Patent: US 6287800-A 1 11-SEP-2001;  
 FEATURES Location/Qualifiers  
 source 1..2293  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 74.8%; Score 232; DB 6; Length 2293;  
 Best Local Similarity 99.6%; Pred. No. 3.6e-123;  
 Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 AATTCAGTAATCATCATCTTTTGAACGACATTTGCCCGCCAGATATTCGTGGCGGCA 87  
 Db 1999 AATTCAGTAATCATCATCTTTTGAACGACATTTGCCCGCCAGATATTCGTGGCGGCA 2058  
 Qy 88 TGCCTGTTGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGTGTGGGGATCGGCA 147  
 Db 2059 TGCCTGTTGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGTGTGGGGATCGGCA 2118  
 Qy 148 GCCCTTGGGCAAGCGCGCCCGGAATCTAGTGGCGGCTGTGCTGCAGCTTCCATTGCGT 207  
 Db 2119 GCCCTTGGGCAAGCGCGCCCGGAATCTAGTGGCGGCTGTGCTGCAGCTTCCATTGCGT 2178  
 Qy 208 AGTAGTAAACCTTCGCAACTGTACGGCGCGCGCCCAAGCCGTTAAACCCCACTTCT 267  
 Db 2179 AGTAGTAAACCTTCGCAACTGTACGGCGCGCGCCCAAGCCGTTAAACCCCACTTCT 2238  
 Qy 268 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 310  
 Db 2239 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAACCTTAA 2281

## RESULT 13

FPU34557 534 bp DNA linear PLN 15-JUL-1998  
 LOCUS Fusarium fujikuroi internal transcribed spacer RNA.  
 DEFINITION U34557  
 ACCESSION U34557  
 VERSION U34557.1 GI:1808928

## KEYWORDS

## SOURCE

## ORGANISM

Gibberella fujikuroi  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella  
 fujikuroi complex.

## REFERENCE

## AUTHORS

## TITLE

O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.  
 Two divergent intragenomic rDNA ITS2 types within a monophyletic  
 lineage of the fungus *Fusarium* are nonorthologous

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.  
 Molecular systematics and phylogeography of the *Gibberella*  
*fujikuroi* species complex

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.  
 Direct Submission  
 Submitted (21-AUG-1995) Kerry O'Donnell, NCAUR, USDA, 1815 N.  
 University St., Peoria, IL 61604, USA

## FEATURES

## source

## ORIGIN

Query Match 73.5%; Score 228; DB 8; Length 534;  
 Best Local Similarity 99.6%; Pred. No. 7.9e-123;

Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 AATTCAGTAATCATCATCTTTTGAACGACATTTGCCCGCCAGATATTCGTGGCGGCA 87  
 Db 256 AATTCAGTAATCATCATCTTTTGAACGACATTTGCCCGCCAGATATTCGTGGCGGCA 315  
 Qy 88 TGCCTGTTGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGTGTGGGGATCGGCA 147  
 Db 316 TGCCTGTTGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGTGTGGGGATCGGCA 375  
 Qy 148 GCCCTTGGGCAAGCGCGCCCGGAATCTAGTGGCGGCTGTGCTGCAGCTTCCATTGCGT 207  
 Db 376 GCCCTTGGGCAAGCGCGCCCGGAATCTAGTGGCGGCTGTGCTGCAGCTTCCATTGCGT 435  
 Qy 208 AGTAGTAAACCTTCGCAACTGTACGGCGCGCGCCCAAGCCGTTAAACCCCACTTCT 267  
 Db 436 AGTAGTAAACCTTCGCAACTGTACGGCGCGCGCCCAAGCCGTTAAACCCCACTTCT 495  
 Qy 268 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAAC 306  
 Db 496 GAATGTTGACCTCGGATCAGTAGGAATACCCGCTGAAC 534

## RESULT 14

FPU34558 534 bp DNA linear PLN 15-JUL-1998  
 LOCUS Fusarium proliferatum NRRL 22944 internal transcribed spacer RNA.  
 DEFINITION U34558  
 ACCESSION U34558  
 VERSION U34558.1 GI:1808934

## KEYWORDS

## SOURCE

## ORGANISM

Fusarium proliferatum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella  
 fujikuroi complex.

## REFERENCE

## AUTHORS

## TITLE

O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.  
 Two divergent intragenomic rDNA ITS2 types within a monophyletic  
 lineage of the fungus *Fusarium* are nonorthologous

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.  
 Molecular systematics and phylogeography of the *Gibberella*  
*fujikuroi* species complex

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.  
 Direct Submission  
 Submitted (21-AUG-1995) Kerry O'Donnell, NCAUR, USDA, 1815 N.  
 University St., Peoria, IL 61604, USA

## FEATURES

## source

## ORIGIN

Query Match 73.5%; Score 228; DB 8; Length 534;  
 Best Local Similarity 99.6%; Pred. No. 7.9e-123;  
 Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 AATTCAGTAATCATCATCTTTTGAACGACATTTGCCCGCCAGATATTCGTGGCGGCA 87  
 Db 256 AATTCAGTAATCATCATCTTTTGAACGACATTTGCCCGCCAGATATTCGTGGCGGCA 315  
 Qy 88 TGCCTGTTGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGTGTGGGGATCGGCA 147  
 Db 316 TGCCTGTTGAGCGTCATTTCAACCTTCAAGCCCCGGGTTGTGTGGGGATCGGCA 375

QY 148 GCCCTTGCGGACACCGGCCCCGAAATCTAGTGGCGGTCTGCTGCGAGCTTCCATTGGCT 207  
 Db 376 GCCCTTGCGGACACCGGCCCCGAAATCTAGTGGCGGTCTGCTGCGAGCTTCCATTGGCT 435  
 QY 208 AGTAGTAAACCCCTCGCAACTGTAGCGGGCGGCCAAGCCGTTAAACCCCACTTCT 267  
 Db 436 AGTAGTAAACCCCTCGCAACTGTAGCGGGCGGCCAAGCCGTTAAACCCCACTTCT 495  
 QY 268 GAATGTTGACCTCGATCAGTAGAATATACCCGCTGAC 306  
 Db 496 GAATGTTGACCTCGATCAGTAGAATATACCCGCTGAC 534

RESULT 15  
 AF165873 502 bp DNA linear PLN 18-JUL-1999  
 LOCUS  
 DEFINITION  
 Gibberella fujikuroi internal transcribed spacer 1, 5.8S ribosomal  
 RNA gene and internal transcribed spacer 2, complete sequence; and  
 28S ribosomal RNA gene, partial sequence.  
 AF165873  
 AF165873.1 GI:5524730

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Gibberella fujikuroi  
 Gibberella fujikuroi  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella  
 fujikuroi complex.  
 1 (bases 1 to 502)  
 Iwen, P.C., Henry, T. and Hinrichs, S.H.  
 Sequence analysis of the internal transcribed spacer regions of  
 Fusarium species most commonly associated with human invasive  
 disease  
 Unpublished  
 2 (bases 1 to 502)  
 Iwen, P.C., Henry, T. and Hinrichs, S.H.  
 Direct Submission  
 Submitted (07-JUL-1999) Pathology and Microbiology, University of  
 Nebraska Medical Center, 986485 Nebraska Medical Center, Omaha, NE  
 68198-6495, USA

FEATURES  
 source  
 location/Qualifiers  
 1..502  
 /organism="Gibberella fujikuroi"  
 /mol\_type="genomic DNA"  
 /strain="ATCC48843"  
 /variety="intermedium"  
 /db\_xref="ATCC:48843"  
 /db\_xref="taxon:5127"  
 /note="anamorph: Fusarium moniliforme"  
 1..147  
 /product="internal transcribed spacer 1"  
 /note="ITS1"  
 148..304  
 /product="5.8S ribosomal RNA"  
 305..470  
 /product="internal transcribed spacer 2"  
 471..502  
 /product="28S ribosomal RNA"

misc\_RNA  
 rRNA  
 misc\_RNA  
 rRNA

ORIGIN  
 Query Match 72.9%; Score 226; DB 8; Length 502;  
 Best Local Similarity 99.6%; Pred. No. 1,2e-121;  
 Matches 276; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATGATCTTTGAACGACATTCGCCGCCAGTATTTCTGGCGGCA 87  
 Db 226 AATTCAGTGAATCATGATCTTTGAACGACATTCGCCGCCAGTATTTCTGGCGGCA 285  
 QY 88 TGCCCTGTTGAGCGTCAATTTCAACCTCAAGCCCCGGGTTGGTGTGGGAGATCGGCA 147  
 Db 286 TGCCCTGTTGAGCGTCAATTTCAACCTCAAGCCCCGGGTTGGTGTGGGAGATCGGCA 345  
 QY 148 GCCCTTGCGGACACCGGCCCCGAAATCTAGTGGCGGTCTGCTGCGAGCTTCCATTGGCT 207

Db 346 GCCCTTGCGGACACCGGCCCCGAAATCTAGTGGCGGTCTGCTGCGAGCTTCCATTGGCT 405  
 QY 208 AGTAGTAAACCCCTCGCAACTGTAGCGGGCGGCCAAGCCGTTAAACCCCACTTCT 267  
 Db 406 AGTAGTAAACCCCTCGCAACTGTAGCGGGCGGCCAAGCCGTTAAACCCCACTTCT 465  
 QY 268 GAATGTTGACCTCGATCAGTAGAATATACCCGCTGAC 304  
 Db 466 GAATGTTGACCTCGATCAGTAGAATATACCCGCTGAC 502

Search completed: October 1, 2004, 09:56:24  
 Job time : 1578.63 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:41:36 ; Search time 259.73 Seconds  
(without alignments)  
5070.430 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310  
Sequence: 1 aaatcgcatgaagtaatgtga.....ggaataccgcgtgaactaa 310

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 212409041 residues

Word size : 10

Total number of hits satisfying chosen parameters: 596607

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310	100.0	310	2 AAV70851	Aav70851 Internal
2	232	74.8	2293	4 AAS16211	Aas16211 Fungus ge
3	228	73.5	534	7 ACC50001	Acc50001 Internal
4	117	37.7	502	3 AAA61893	Aaa61893 Fusarium
5	99	31.9	647	6 ABV78700	Abv78700 C. crass
6	95	30.6	661	6 ABV78721	Abv78721 C. sinen
7	94	30.3	504	2 AAV70851	Aav70851 Internal
8	94	30.3	504	2 AAV62591	Aav62591 Fusarium
9	94	30.3	504	2 AAV59028	Aav59028 F. culmor
10	94	30.3	504	4 AAS08426	Aas08426 Internal
11	94	30.3	521	7 ACC50000	Acc50000 Internal
12	94	30.3	522	7 ACC49999	Acc49999 Internal
13	94	30.3	522	7 ACC50002	Acc50002 Internal
14	94	30.3	545	2 AAV62593	Aav62593 Fusarium
15	94	30.3	545	2 AAV59030	Aav59030 F. monili
16	94	30.3	546	2 AAV62596	Aav62596 Fusarium
17	94	30.3	546	2 AAV59007	Aav59007 F. poae
18	92	29.7	382	3 AAA72783	Aaa72783 5.8S rRNA
19	79	25.5	155	3 AAF10640	Aaf10640 Fusarium
20	79	25.5	319	2 AAV70850	Aav70850 Internal
21	67	21.6	389	3 AAZ92490	Aaz92490 Rhizocton
22	67	21.6	569	2 AAT65101	Aat65101 T. harzia
23	67	21.6	569	2 AAT65099	Aat65099 T. harzia

24	67	21.6	582	2 AAT65100	Aat65100 T. harzia
25	66	21.3	561	2 AAV59009	Aav59009 F. avenac
26	66	21.3	659	6 ABV78724	Abv78724 C. sinen
27	55	17.7	353	2 AAT05402	Aat05402 Fusarium
28	52	16.8	503	2 AAT05401	Aat05401 Fusarium
29	52	16.8	503	2 AAV62592	Aav62592 Fusarium
30	52	16.8	503	2 AAV59029	Aav59029 F. gramin
31	46	14.8	545	2 AAT05403	Aat05403 Microdoch
32	43	13.9	537	3 AAZ91725	Aaz91725 Rosellini
33	42	13.5	343	2 AAV70871	Aav70871 Internal
34	42	13.5	344	2 AAV70870	Aav70870 Internal
35	42	13.5	553	3 AAZ91726	Aaz91726 Rosellini
36	41	13.2	377	6 ABA94559	Ab94559 Truncated
37	41	13.2	377	6 ABA94564	Ab94564 Consensus
38	41	13.2	377	6 ABA94561	Ab94561 Truncated
39	41	13.2	389	3 AAA72781	Aaa72781 5.8S rRNA
40	41	13.2	415	4 AAF75169	Aaf75169 Consensus
41	41	13.2	415	4 AAF75170	Aaf75170 Consensus
42	41	13.2	415	4 AAZ22436	Aaz22436 Internal
43	41	13.2	466	8 ADA27221	Ada27221 P. micros
44	41	13.2	466	8 ADA27221	Ada27221 P. micros
45	41	13.2	515	8 ACA62941	Aca62941 P. glomer

## ALIGNMENTS

RESULT 1  
ID AAV70851 standard; DNA; 310 BP.  
XX  
AC AAV70851;  
XX  
DT 17-OCT-2003 (revised)  
DT 26-FEB-1999 (first entry)  
XX  
DE Internal transcribed spacer 2 (ITS2) and adjacent regions.  
XX  
KW Internal transcribed spacer 2, ITS2; probe; Aspergillus flavus; A. niger;  
KW A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Nucor rouxii;  
KW M. racemosus; M. plumbeus; M. indicus; A. fumigatus;  
KW M. circinilicoides; F. circinilicoides; Rhizopus oryzae; R. microsporus;  
KW R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;  
KW Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;  
KW Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.  
XX  
OS Gibberella fujikuroi.  
XX  
PN WO9850584-A2.  
XX  
PD 12-NOV-1998.  
XX  
PF 01-MAY-1998; 98WO-US008926.  
XX  
PR 02-MAY-1997; 97US-0045400P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Morrison CJ, Reiss E, Aidorevich L, Choi JS;  
XX WPI; 1999-034737/03.  
XX  
DR New nucleic acid probes for filamentous fungi - for detecting e.g.  
XX Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,  
XX Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix  
XX species.  
XX  
PS Claim 1; Page 12; 45pp; English.  
XX  
CC The present sequence represents an internal transcribed spacer 2 (ITS2)  
CC and adjacent regions. Probes can be derived from the present sequence  
CC which are species-specific. The specification also describes ITS2  
CC sequence-derived probes for identifying a species selected from





XX	Microchondria; fungal pathogen; ds.
XX	
OS	Faearium proliferatum.
XX	
PN	MO2003027635-A2.
XX	
PD	03-APR-2003.
XX	
PR	19-SEP-2002; 2002WO-US030311.
XX	
PR	24-SEP-2001; 2001US-00961755.
XX	
PA	(SYGN ) SYNGENTA PARTICIPATIONS AG.
XX	
P1	Beck UJ, Barnett CJ;
DR	WPI, 2003-363229/34.
XX	
PT	Detecting a fungal pathogen, useful for monitoring disease development,
PT	comprises subjecting the DNA to PCR amplification using at least one
PT	primer having sequence identity with at least 10 contiguous nucleotides
XX	of Fusarium spp.
PS	Claim 5; Page 38-39; 4app; English.
CC	This invention relates to the detection of a fungal pathogen comprising
CC	isolating DNA from a plant leaf infected with a pathogen. The methods and
CC	primers are useful for identifying fungal isolates of fungal pathogens
CC	and monitoring of disease development in plant populations. The present
CC	sequence represents an internal transcribed spacer RNA encoding sequence
SQ	Sequence 534 BP; 135 A; 149 C; 130 G; 120 T; 0 U; 0 Other;
	Query Match            73.5%; Score 228; DB 7; Length 534;
	Best Local Similarity 99.6%; Pred. No. 8.8e-111;
	Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0
OY	28 AATTCAGTGAATCATCGAATCTTTGTAACGCACATTGGCCGCCAGTATTTGGCGGCA 87
Db	256 AATTCAGTGAATCATCGAATCTTTGTAACGCACATTGGCCGCCAGTATTTGGCGGCA 315
OY	88 TGCCGTGTCGAGCGTCATTTCAACCCTCAAGCCCCGGGTTTGTTGGGGATCGGCA 147
Db	316 TGCCGTGTCGAGCGTCATTTCAACCCTCAAGCCCCGGGTTTGTTGGGGATCGGCA 375
OY	148 GCCCTTGGGGCAAGCGCGCCCGGAATCTAGTGGGGGTCTGCTCAGCTTCATTGGCT 207
Db	376 GCCCTTGGGGCAAGCGCGCCCGGAATCTAGTGGGGGTCTGCTCAGCTTCATTGGCT 435
OY	208 AGTAGTAAACCCCTCGCAACTGGTATGCGGCGCGGCAAGCGGTAAACCCCACTTCT 267
Db	436 AGTAGTAAACCCCTCGCAACTGGTATGCGGCGCGGCAAGCGGTAAACCCCACTTCT 495
OY	268 GAATGTTAAGCTCGATCAGTAGGAATPCCCGCTGAAC 306
Db	496 GAATGTTAAGCTCGATCAGTAGGAATPCCCGCTGAAC 534
RESULT 4	
AAA61893	
ID	AAA61893 standard; DNA; 502 BP.
XX	
XX	AAA61893;
XX	
DT	15-SEP-2003 (revised)
DT	14-NOV-2000 (first entry)
XX	
DE	Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.
XX	
KM	Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74463;
KM	HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
KM	acquired immunodeficiency syndrome; AIDS; AIDS-related complex;

KW		symptomatic infection; asymptomatic infection; potential HIV exposure;
KM		combination therapy; de.
XX		
OS		Fusarium sp.; MF6381.
XX		
PN		MO200036132-A1.
XX		
PD		22-JUN-2000.
XX		
PF		09-DEC-1999; 99WO-US029356.
XX		
PR		14-DEC-1998; 98US-0112168P.
XX		
PA		(MERI ) MERCK & CO INC.
XX		
PJ		Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;
PI		Dombrowski AW;
XX		
DR		WPI; 2000-431606/37.
XX		
PS		New steroid compounds are HIV integrase inhibitors used for treating HIV
PT		infection and AIDS.
XX		
XX		Disclosure: Page 14; 113pp; English.
CC		The invention relates to novel steroid compounds derived from the African
CC		soil fungus Fusarium sp. MF6381 (ATCC 74469) which act as inhibitors of
CC		HIV integrase. The invention encompasses cultures of Fusarium sp. MF6381..
CC		The invention also relates to a composition comprising a compound of the
CC		invention in combination with an AIDS antiviral agent, an immunomodulator
CC		and an anti-infective agent. The compounds of the invention may be used in
CC		the inhibition of HIV integrase and in the prevention and treatment of
CC		HIV infection. A wide range of state of HIV infection may be treated;
CC		AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex);
CC		both symptomatic and asymptomatic HIV infection; and actual or potential
CC		exposure to HIV. The compounds may be used to isolate HIV integrase
CC		mutants which are potentially useful as screening tools for antiviral
CC		compounds. The compounds may also be used to establish or determine the
CC		site at which other antivirals bind to HIV integrase (e.g., by
CC		competitive inhibition). The present sequence represents the ribosomal
CC		DNA (rDNA) internal transcribed spacer (ITS) region of Fusarium sp.
CC		MF6381, which may be used to characterize MF6381. (Updated on 15-SEP-2003
CC		to standardise OS field)
CC		
SQ		Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 U; 0 Other;
Query Match	37.7%; Score 117; DB 3; Length 502;	
Best Local Similarity	100.0%; Pred. No. 7.9e-52;	
Matches 117; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
OY	28 AATTGAGTGCATTCGATCTTTGAACGACATGGCGGCCGCAGTATTTGGCGGGCA 87	
DB	223 AATTCAGTGATCATCGATCTTTGAACGACATTTGGCGGCCGCAGTATTTGGCGGGCA 282	
OY	88 TGCGTGTTCGAGCGTATTCACCCCTCAAGCCCCGGGTTTTGTTGGGGATCGG 144	
DB	283 TGCGTGTTCGAGCGTATTCACCCCTCAAGCCCCGGGTTTTGTTGGGGATCGG 339	
RESULT 5		
ABV78700		
ID	ABV78700 standard; rRNA; 647 BP.	
AC		
XX	ABV78700;	
DT	14-JAN-2003 (first entry)	
XX		
C.	crassisporea RNA sequence #2.	
DE	Ribosome ribonucleic acid; rRNA; Cordyceps crassisporea; classification;	
KW	Cordyceps sinensis; ss.	
XX		
OS	Cordyceps crassisporea.	

```
XX
PN JP2002204696-A.
XX
FD 23-JUL-2002.
XX
PF 12-JAN-2001; 2001JP-00004805.
XX
PR 12-JAN-2001; 2001JP-00004805.
XX
PA (HEAL-) HEALTHWAY KK.
XX
PA (KANE/) KANESHIRO N.
XX
DR WPI; 2002-639075/69.
XX
PT Ribosome RNA gene base sequence of Cordyceps sinensis for classification
PT of seeds of Cordyceps sinensis.
XX
PS 2; Page 12; 33pp; Japanese.
XX
CC The invention relates to a novel base sequence which is part of a fully
CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora.
CC The base sequences can be used for the classification of Cordyceps
CC sinensis. The sequence represents a C. crassispora rRNA sequence of the
CC invention
XX
SQ Sequence 647 BP; 166 A; 178 C; 160 G; 143 T; 0 U; 0 Other;

Query Match 31.9%; Score 99; DB 6; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATGATCTTTGAACGACATTTGGCCCGCCAGATTCTGGCGGCA 87
DB 272 AATTCAGTGAATCATGATCTTTGAACGACATTTGGCCCGCCAGATTCTGGCGGCA 331
QY 88 TGCCTGTTGAGCGCTCATTTCAACCCCTCAAGCCCCCGGG 126
DB 332 TGCCTGTTGAGCGCTCATTTCAACCCCTCAAGCCCCCGGG 370

RESULT 6
ABV78721
ID ABV78721 standard; rRNA; 661 BP.
XX
AC ABV78721;
XX
DT 14-JAN-2003 (first entry)
XX
DE C. sinensis rRNA sequence #20.
XX
KM Ribosome ribonucleic acid; rRNA; Cordyceps crassispora; classification;
KM Cordyceps sinensis; ss.
XX
OS Cordyceps sinensis.
XX
PN JP2002204696-A.
XX
PD 23-JUL-2002.
XX
PF 12-JAN-2001; 2001JP-00004805.
XX
PR 12-JAN-2001; 2001JP-00004805.
XX
PA (HEAL-) HEALTHWAY KK.
XX
PA (KANE/) KANESHIRO N.
XX
DR WPI; 2002-639075/69.
XX
PT Ribosome RNA gene base sequence of Cordyceps sinensis for classification
PT of seeds of Cordyceps sinensis.
XX
PS 23; Page 24; 33pp; Japanese.
XX
```

```
CC The invention relates to a novel base sequence which is part of a fully
CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora.
CC The base sequences can be used for the classification of Cordyceps
CC sinensis. The sequence represents a C. sinensis rRNA sequence of the
CC invention
XX
SQ Sequence 661 BP; 176 A; 192 C; 168 G; 123 T; 0 U; 2 Other;

Query Match 30.6%; Score 95; DB 6; Length 661;
Best Local Similarity 100.0%; Pred. No. 3.8e-40;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATGATCTTTGAACGACATTTGGCCCGCCAGATTCTGGCGGCA 87
DB 296 AATTCAGTGAATCATGATCTTTGAACGACATTTGGCCCGCCAGATTCTGGCGGCA 355
QY 88 TGCCTGTTGAGCGCTCATTTCAACCCCTCAAGCCCC 122
DB 356 TGCCTGTTGAGCGCTCATTTCAACCCCTCAAGCCCC 390

RESULT 7
AAT05400
ID AAT05400 standard; DNA; 504 BP.
XX
AC AAT05400;
XX
DT 04-JUN-1996 (first entry)
XX
DE Fusarium culmorum internal transcribed spacer sequence.
XX
KM Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
KM Pseudocercospora herpotrichoides; Mycocepharella filijensis; PCR;
KM Mycocepharella musicola; amplification; primer; ribosomal RNA gene;
KM internal transcribed region; strain; capture; colourimetric assay;
KM isolate; development; population; random amplified polymorphic DNA; ss.
XX
OS Fusarium culmorum.
XX
PN MO9529260-A2.
XX
PD 02-NOV-1995.
XX
PF 19-APR-1995; 95WO-US004712.
XX
PR 25-APR-1994; 94US-00233608.
XX
PA (CIBA ) CIBA GEIGY AG.
XX
PI Ligon JM, Beck JU;
XX
DR WPI; 1995-383005/49.
XX
PT DNA encoding intervening transcribed sequence - used for detection of
PT plant fungal pathogens.
XX
PS Claim 1; Page 54-55; 65pp; English.
XX
CC A novel method for the detection of plant pathogenic strains of fungi
CC e.g. Septoria nodorum, S.tritici, Pseudocercospora herpotrichoides,
CC Mycocepharella filijensis, M.musicola or Fusarium spp, involves the PCR
CC amplification of sequences found in the internal transcribed region (ITS)
CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AA094359-93
CC and AAT05357-72. These primers are derived from the ITS sequences of
CC these fungi (AAT05394-T05404 and AA094398) and are strain specific. The
CC amplification products of the reactions using these primers can be used
CC with the capture primers AAT05378-93 in colourimetric assays. The primers
CC and ITS DNAs can be used for the detection of specific fungal pathogen
CC isolates and in monitoring disease development in plant populations
XX
SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;

Query Match 30.3%; Score 94; DB 2; Length 504;
```

Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAAGCCACCATTTGCCGCGGCA 87  
|||||  
DB 239 AATTCAGTGAATCATCGAATCTTTGAAGCCACCATTTGCCGCGGCA 298  
|||||

QY 88 TGCCGTTCGAGCGTCATTTCAACCCCTCAAGCCC 121  
|||||  
DB 299 TGCCGTTCGAGCGTCATTTCAACCCCTCAAGCCC 332  
|||||

RESULT 8  
AAV62591  
ID AAV62591 standard; DNA; 504 BP.  
XX  
AC AAV62591;  
XX  
DT 17-DEC-1998 (first entry)  
XX  
DE Fusarium culmorum PCR amplified ITS region consensus DNA sequence.  
XX  
KW Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;  
KW Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;  
KW Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;  
KW PCR; nucleic acid detection; ss.  
XX  
OS Fusarium culmorum.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..12  
FT /tag= a  
FT /note= "3' end of small subunit rRNA gene"  
FT misc\_feature 13..161  
FT /tag= b  
FT /note= "ITS 1"  
FT misc\_feature 162..318  
FT /tag= c  
FT /note= "5.8S rRNA gene"  
FT misc\_feature 319..472  
FT /tag= d  
FT /note= "ITS 2"  
FT misc\_feature 473..504  
FT /tag= e  
FT /note= "5' end of large subunit rRNA gene"  
FT  
XX  
XX US5814453-A.  
XX  
XX 29-SEP-1998.  
XX  
XX 02-JUL-1997; 97US-00867480.  
XX  
XX 19-APR-1995; 95WO-US004712.  
XX 15-OCT-1996; 96US-00722187.  
XX  
XX (NOVS ) NOVARTIS FINANCE CORP.  
XX  
XX Beck JI;  
XX  
XX WPI; 1998-541745/46.  
XX  
XX DNA isolated from fungal RNA, and its internal transcribed spacer  
XX sequence - used for detecting fungal pathogens in plant tissue.  
XX  
XX Claim 2; Fig 3; 56pp; English.  
XX  
XX  
XX This represents the consensus DNA sequence of the internal transcribed  
XX spacer (ITS) region that was PCR amplified from Fusarium culmorum  
XX isolates, R-5106, R-5126 and R-5146. The invention provides a DNA  
XX molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal  
XX pathogen, where the DNA molecule consists of an ITS sequence selected  
XX from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium  
XX moniliforme, Septoria avenae or Microdochium nivale. A method for

CC detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.  
CC avenaceum and M. nivale isolates is also provided. The method comprises  
CC isolating DNA from a plant leaf infected with at least one of the above  
CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by  
CC PCR using specific primers from within these sequences. The pathogen(s)  
CC are detected by visualising the amplified part of the ITS sequence  
XX  
SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;  
Query Match 30.3%; Score 94; DB 2; Length 504;  
Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAAGCCACCATTTGCCGCGGCA 87  
|||||  
DB 239 AATTCAGTGAATCATCGAATCTTTGAAGCCACCATTTGCCGCGGCA 298  
|||||

QY 88 TGCCGTTCGAGCGTCATTTCAACCCCTCAAGCCC 121  
|||||  
DB 299 TGCCGTTCGAGCGTCATTTCAACCCCTCAAGCCC 332  
|||||

RESULT 9  
AAV59028  
ID AAV59028 standard; DNA; 504 BP.  
XX  
AC AAV59028;  
XX  
DT 25-MAR-2003 (revised)  
DT 06-JAN-1999 (first entry)  
XX  
DE F. culmorum internal transcribed spacer.  
XX  
XX Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;  
KW fungal pathogen identification; infection identification; ss.  
XX  
OS Fusarium culmorum.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 13..161  
FT /tag= a  
FT /note= "ITS1"  
FT misc\_feature 319..472  
FT /tag= b  
FT /note= "ITS2"  
FT  
XX  
XX US5827695-A.  
XX  
XX 27-OCT-1998.  
XX  
XX 04-AUG-1997; 97US-00905314.  
XX  
XX 04-AUG-1997; 97US-00905314.  
XX  
XX (NOVS ) NOVARTIS FINANCE CORP.  
XX  
XX Beck JI;  
XX  
XX WPI; 1998-593995/50.  
XX  
XX Wheat pathogen internal transcribed spacer sequences - used as a basis  
XX for primers for the species-specific polymerase chain reaction detection  
XX of the pathogens.  
XX  
XX Disclosure; Col 21-22; 20pp; English.  
XX  
XX  
XX This sequence represents an internal transcribed spacer (ITS) sequence of  
XX the invention. The primer pairs, based on the ITS sequences, are used for  
XX the PCR amplification detection of wheat Microdochium and Fusarium fungal  
XX pathogens, especially M. nivale, F. graminearum, F. culmorum, F.  
XX avenaceum, F. poae, F. moniliforme or F. roseum. The two different  
XX strains of fungi show different symptoms during infection, which may or  
XX may not be due to infection. Early identification of the strain causing

CC the infection allows early, and more specific fungicidal treatment.  
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to  
 CC correct PR field.)

CC Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;

Query Match 30.3%; Score 94; DB 2; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AATTGAGTGAATCATCGAATCTTTGAAGCAGCATTTGGCGCCGAGATTTCTGGCGGGCA 87

Db 239 AATTGAGTGAATCATCGAATCTTTGAAGCAGCATTTGGCGCCGAGATTTCTGGCGGGCA 298

Qy 88 TGCCGTTCGAGCGGTCAATTTCAACCTTCAGGCC 121

Db 299 TGCCGTTCGAGCGGTCAATTTCAACCTTCAGGCC 332

# RESULT 10

AA08426 ID AA08426 standard; DNA; 504 BP.

AA08426; AC

26-SEP-2001 (first entry) DT

Internal transcribed spacer, ITS, region #16. DE

Internal transcribed spacer; ITS; fungal pathogen; ss; wheat disease; KW

Sharp eyespot; fungal pathotype identification; isolate 62215. XX

Fusarium culmorum. OS

WO200151653-A1. XX

19-JUL-2001. PD

09-JAN-2001; 2001WO-EP000172. PF

11-JAN-2000; 2000US-00481293. PR

(SYGN) SYNGENTA PARTICIPATIONS AG. PA

Beck JJ, Barnett CJ; PI

WPI; 2001-442154/47. DR

New internal transcribed spacer DNA sequences, useful for identifying PT fungal pathogen, particularly Rhizoctonia cerealis, and for monitoring PT disease development in plant population.

PS Disclosure; Page 31; 35pp; English.

CC The sequence is an internal transcribed spacer (ITS) region from Fusarium CC culmorum, isolate 62215. The ITS DNA sequences are useful for detecting CC Rhizoctonia cerealis, a fungal pathogen of wheat causing Sharp eyespot, CC for monitoring disease development in plant population, and for providing CC detailed information on the development and spread of specific pathogen CC races over extended geographical areas. The DNA sequences are CC specifically used as primers in PCR-based analysis for the identification CC of fungal pathotypes

CC Sequence 504 BP; 132 A; 133 C; 114 G; 123 T; 0 U; 2 Other;

Query Match 30.3%; Score 94; DB 4; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AATTGAGTGAATCATCGAATCTTTGAAGCAGCATTTGGCGCCGAGATTTCTGGCGGGCA 87  
 Db 242 AATTGAGTGAATCATCGAATCTTTGAAGCAGCATTTGGCGCCGAGATTTCTGGCGGGCA 301

Qy 88 TGCCGTTCGAGCGGTCAATTTCAACCTTCAGGCC 121  
 Db 302 TGCCGTTCGAGCGGTCAATTTCAACCTTCAGGCC 335

# RESULT 11

ACC50000 ID ACC50000 standard; DNA; 521 BP.

ACC50000; AC

14-JUL-2003 (first entry) DT

Internal transcribed spacer RNA encoding sequence #2. DE

Mitochondria; fungal pathogen; ds. KW

Gibberella zeae. OS

WO2003027635-A2. PN

03-APR-2003. PD

19-SEP-2002; 2002WO-US030311. PF

24-SEP-2001; 2001US-00961755. PR

(SYGN) SYNGENTA PARTICIPATIONS AG. PA

Beck JJ, Barnett CJ; PI

WPI; 2003-363229/34. DR

Detecting a fungal pathogen, useful for monitoring disease development, PT comprises subjecting the DNA to PCR amplification using at least one PT primer having sequence identity with at least 10 contiguous nucleotides PT of Fusarium spp.

PS Claim 5; Page 38; 44pp; English.

CC This invention relates to the detection of a fungal pathogen comprising CC isolating DNA from a plant leaf infected with a pathogen. The methods and CC primers are useful for identifying fungal isolates of fungal pathogens CC and monitoring of disease development in plant populations. The present CC sequence represents an internal transcribed spacer RNA encoding sequence CC

CC Sequence 521 BP; 138 A; 140 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 30.3%; Score 94; DB 7; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AATTGAGTGAATCATCGAATCTTTGAAGCAGCATTTGGCGCCGAGATTTCTGGCGGGCA 87

Db 256 AATTGAGTGAATCATCGAATCTTTGAAGCAGCATTTGGCGCCGAGATTTCTGGCGGGCA 315

Qy 88 TGCCGTTCGAGCGGTCAATTTCAACCTTCAGGCC 121

Db 316 TGCCGTTCGAGCGGTCAATTTCAACCTTCAGGCC 349

# RESULT 12

ACC49999 ID ACC49999 standard; DNA; 522 BP.

ACC49999; AC

14-JUL-2003 (first entry) DT

Internal transcribed spacer RNA encoding sequence. DE

Mitochondria; fungal pathogen; ds. KW

```

OS Fuserium subglutinans.
XX
XX WO2003027635-A2.
XX
XX PD 03-APR-2003.
XX
XX PF 19-SEP-2002; 2002WO-US030311.
XX
XX PR 24-SEP-2001; 2001US-00961755.
XX
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Beck JU, Barnett CJ;
XX
XX DR WPI; 2003-363229/34.
XX
XX PT Detecting a fungal pathogen, useful for monitoring disease development,
XX comprises subjecting the DNA to PCR amplification using at least one
XX primer having sequence identity with at least 10 contiguous nucleotides
XX of Fuserium spp.
XX
XX PS Claim 5; Page 38; 44pp; English.
XX
XX CC This invention relates to the detection of a fungal pathogen comprising
XX isolating DNA from a plant leaf infected with a pathogen. The methods and
XX primers are useful for identifying fungal isolates of fungal pathogens
XX and monitoring of disease development in plant populations. The present
XX sequence represents an internal transcribed spacer RNA encoding sequence
XX
XX SQ Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;

Query Match          30.3%; Score 94; DB 7; Length 522;
Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATTCGATCTTTGAAAGCAGCATTTGCCGCCGAGATTTCTGGCGGCA 87
DB 256 AATTCAGTGAATCATTCGATCTTTGAAAGCAGCATTTGCCGCCGAGATTTCTGGCGGCA 315
QY 88 TGCCGTTCGAGCGGTCATTTCAACCTCAAGCCC 121
DB 316 TGCCGTTCGAGCGGTCATTTCAACCTCAAGCCC 349

RESULT 13
ACCS0002
ID ACCS0002 standard; DNA; 522 BP.
XX
XX AC ACCS0002;
XX
XX DT 27-OCT-2003 (revised)
XX DT 14-JUL-2003 (first entry)
XX
XX DE Internal transcribed spacer RNA encoding sequence #4.
XX
XX KW Mitochondria; fungal pathogen; ds.
XX
XX OS Gibberella moniliformis.
XX
XX PN WO2003027635-A2.
XX
XX PD 03-APR-2003.
XX
XX PF 19-SEP-2002; 2002WO-US030311.
XX
XX PR 24-SEP-2001; 2001US-00961755.
XX
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Beck JU, Barnett CJ;
XX
XX DR WPI; 2003-363229/34.
XX

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PT Detecting a fungal pathogen, useful for monitoring disease development,
PT comprises subjecting the DNA to PCR amplification using at least one
PT primer having sequence identity with at least 10 contiguous nucleotides
PT of Fuserium spp.
XX
XX PS Claim 5; Page 39; 44pp; English.
XX
XX CC This invention relates to the detection of a fungal pathogen comprising
XX isolating DNA from a plant leaf infected with a pathogen. The methods and
XX primers are useful for identifying fungal isolates of fungal pathogens
XX and monitoring of disease development in plant populations. The present
XX sequence represents an internal transcribed spacer RNA encoding sequence.
XX (Updated on 27-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;

Query Match          30.3%; Score 94; DB 7; Length 522;
Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATTCGATCTTTGAAAGCAGCATTTGCCGCCGAGATTTCTGGCGGCA 87
DB 256 AATTCAGTGAATCATTCGATCTTTGAAAGCAGCATTTGCCGCCGAGATTTCTGGCGGCA 315
QY 88 TGCCGTTCGAGCGGTCATTTCAACCTCAAGCCC 121
DB 316 TGCCGTTCGAGCGGTCATTTCAACCTCAAGCCC 349

RESULT 14
AAV62593
ID AAV62593 standard; DNA; 545 BP.
XX
XX AC AAV62593;
XX
XX DT 17-OCT-2003 (revised)
XX DT 17-DEC-1998 (first entry)
XX
XX DE Fuserium moniliforme PCR amplified ITS region DNA sequence.
XX
XX KW Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
XX Fuserium culmorum; Fuserium graminearum; Fuserium moniliforme; plant;
XX Septoria avenae; Microdochium nivale; Fuserium poae; Fuserium avenaceum;
XX PCR; nucleic acid detection; ss.
XX
XX OS Gibberella fujikuroi.
XX
XX FH Key Location/Qualifiers
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XX FT /note= "3' end of small subunit rRNA gene"
XX FT 31..178
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XX FT /*tag= c
XX FT /note= "5.8S rRNA gene"
XX FT 336..488
XX FT /*tag= d
XX FT /note= "ITS 2"
XX FT 489..545
XX FT /*tag= e
XX FT /note= "5' end of large subunit rRNA gene"

US5814453-A.
XX
XX PD 29-SEP-1998.
XX
XX PF 02-JUL-1997; 97US-00887480.
XX
XX PR 19-APR-1995; 95WO-US004712.
XX PR 15-OCT-1996; 96US-00722187.
XX

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PA (NOVS ) NOVARTIS FINANCE CORP.  
 XX Beck JJ;  
 PI  
 XX WPI; 1998-541745/46.  
 DR  
 XX DNA isolated from fungal RNA, and its internal transcribed spacer  
 PT sequence - used for detecting fungal pathogens in plant tissue.  
 XX  
 PS Claim 2; Fig 3; 56pp; English.  
 XX  
 CC This represents the DNA sequence of the internal transcribed spacer (ITS)  
 CC region that was PCR amplified from *Fusarium moniliforme*. The invention  
 CC provides a DNA molecule isolated from the ribosomal RNA gene region of a  
 CC fungal pathogen, where the DNA molecule consists of an ITS sequence  
 CC selected from ITS1 and ITS2 of *Fusarium culmorum*, *Fusarium graminearum*,  
 CC *Fusarium moniliforme*, *Septoria avenae* or *Microdochium nivale*. A method  
 CC for detecting *F. graminearum*, *F. culmorum*, *F. moniliforme*, *F. poae*, *F.*  
 CC *avenaceum* and *M. nivale* isolates is also provided. The method comprises  
 CC isolating DNA from a plant leaf infected with at least one of the above  
 CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by  
 CC PCR using specific primers from within these sequences. The pathogen(s)  
 CC are detected by visualising the amplified part of the ITS sequence.  
 CC (Updated on 17-OCT-2003 to standardise OS field)  
 CC  
 SO Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;  
 Query Match 30.3%; Score 94; DB 2; Length 545;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 28 AATTCAGTATCATCGATCTTTGAACGACATTGGCGCCGCCAGTATTCGGCGGCA 87  
 DB 256 AATTCAGTATCATCGATCTTTGAACGACATTGGCGCCGCCAGTATTCGGCGGCA 315  
 QY 88 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 121  
 DB 316 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 349  
 Db  
 RESULT 15  
 AAV59030  
 ID AAV59030 standard; DNA; 545 BP.  
 XX  
 AC AAV59030;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 06-JAN-1999 (first entry)  
 XX  
 DE F. moniliforme internal transcribed spacer.  
 XX  
 KW Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;  
 KW fungal pathogen identification; infection identification; ss.  
 XX  
 OS *Gibberella fujikuroi*.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 31..178  
 FT /\*tag= a  
 FT /note= "ITS1"  
 FT misc\_feature 336..488  
 FT /\*tag= b  
 FT /note= "ITS2"  
 XX  
 XX US5827695-A.  
 XX  
 XX 27-OCT-1998.  
 XX  
 XX 04-AUG-1997; 97US-00905314.  
 XX  
 XX 04-AUG-1997; 97US-00905314.  
 XX

PA (NOVS ) NOVARTIS FINANCE CORP.  
 XX Beck JJ;  
 PI  
 XX WPI; 1998-593995/50.  
 DR  
 XX Wheat pathogen internal transcribed spacer sequences - used as a basis  
 PT for primers for the species-specific polymerase chain reaction detection  
 PT of the pathogens.  
 XX  
 PS Disclosure; Col 23-26; 20pp; English.  
 XX  
 CC This sequence represents an internal transcribed spacer (ITS) sequence of  
 CC the invention. The primer pairs, based on the ITS sequences, are used for  
 CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal  
 CC pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*, *F.*  
 CC *avenaceum*, *F. poae*, *F. moniliforme* or *F. roseum*. The two different  
 CC strains of fungi show different symptoms during infection, which may or  
 CC may not be due to infection. Early identification of the strain causing  
 CC the infection allows early, and more specific fungicidal treatment.  
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to  
 CC correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)  
 CC  
 SO Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 U; 0 Other;  
 Query Match 30.3%; Score 94; DB 2; Length 545;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 28 AATTCAGTATCATCGATCTTTGAACGACATTGGCGCCGCCAGTATTCGGCGGCA 87  
 DB 256 AATTCAGTATCATCGATCTTTGAACGACATTGGCGCCGCCAGTATTCGGCGGCA 315  
 QY 88 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 121  
 DB 316 TGCCTGTTGAGCGTCATTTCAACCTCAAGCCC 349  
 Db

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
3356.386 Million cell updates/sec

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Searched: 682709 seqs, 277475446 residues

Word size : 10

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	310	100.0	310	US-09-423-233-7	Sequence 7, Appl1
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4	99	31.9	581	US-08-652-127C-6	Sequence 6, Appl1
5	94	30.3	504	US-08-887-480-82	Sequence 82, Appl1
6	94	30.3	504	US-08-905-314A-19	Sequence 19, Appl1
7	94	30.3	504	US-08-722-187-82	Sequence 82, Appl1
8	94	30.3	504	US-08-481-293-32	Sequence 32, Appl1
9	94	30.3	504	PCT-US95-04712-82	Sequence 82, Appl1
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12	94	30.3	546	US-08-887-480-96	Sequence 96, Appl1
13	94	30.3	546	US-08-905-314A-22	Sequence 22, Appl1
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25	46	14.8	545	PCT-US95-04712-85	Sequence 85, Appl1
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27	42	13.5	344	US-09-423-233-26	Sequence 26, Appl1

28	41	13.2	415	4	US-09-635-747-39	Sequence 39, Appl1
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30	41	13.2	451	3	US-09-037-990B-5	Sequence 5, Appl1
31	41	13.2	515	4	US-09-517-790-1	Sequence 1, Appl1
32	41	13.2	516	4	US-09-517-790-2	Sequence 2, Appl1
33	41	13.2	523	4	US-09-517-790-4	Sequence 4, Appl1
34	41	13.2	526	4	US-08-481-293-13	Sequence 33, Appl1
35	41	13.2	534	1	US-08-233-608-5	Sequence 5, Appl1
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#### ALIGNMENTS

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RESULT 1
US-09-423-233-7
; Sequence 7, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341WP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-7

Query Match      100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2e+160;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAATGCGATTAAGTAATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACA 60
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QY      61 TTGGCGCCCGCAGTATTCGCGGCGCATGCTGTTGAGCGTCAATTTCGAACCTCGAAGCC 120
DB      61 TTGGCGCCCGCAGTATTCGCGGCGCATGCTGTTGAGCGTCAATTTCGAACCTCGAAGCC 120

QY      121 CCCGGTTGGTGTGGGAGATCGGCAAGCCCTTGCGGCAAGCGGCGCCGGAATCTAGTG 180
DB      121 CCCGGTTGGTGTGGGAGATCGGCAAGCCCTTGCGGCAAGCGGCGCCGGAATCTAGTG 180

QY      181 GCGGTCCTGCTGAGCTTCATTCGAGTAGTAGTAAGAAACCTCGCACTGTAACGCGCGC 240
DB      181 GCGGTCCTGCTGAGCTTCATTCGAGTAGTAGTAAGAAACCTCGCACTGTAACGCGCGC 240

QY      241 GCGCAACCGTTAAACCCCACTTCTGAATGTTGACCTCGAGTCAGTGAATTAACCG 300
DB      241 GCGCAACCGTTAAACCCCACTTCTGAATGTTGACCTCGAGTCAGTGAATTAACCG 300

QY      301 CTGAACCTTAA 310
DB      301 CTGAACCTTAA 310

RESULT 2
US-09-645-073-1
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; Sequence 1, Application US/09645073  
; Patent No. 6287800  
; GENERAL INFORMATION:  
; APPLICANT: Lee, May  
; APPLICANT: Galazzo, Jorge  
; TITLE OF INVENTION: Production of High Titer of Gibberellins GA4 and GA7  
; FILE REFERENCE: L02-01NP  
; CURRENT APPLICATION NUMBER: US/09/645,073  
; CURRENT FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,770  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 2293  
; TYPE: DNA  
; ORGANISM: Gibberella fujikuroi  
; US-09-645-073-1

Query Match 74.8%; Score 232; DB 3; Length 2293;  
Best Local Similarity 99.6%; Pred. No. 1.2e-117;  
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATTCGATCTTTGAACGACATTTGGCCCGCCAGATTTCTGGCGGCA 87  
DB 1999 AATTCAGTGAATCATTCGATCTTTGAACGACATTTGGCCCGCCAGATTTCTGGCGGCA 2058  
QY 88 TGCCTGTTCGAGCGTCATTTCAACCCCTCAAGCCCGGTTGGTGTGGGATCGGCA 147  
DB 2059 TGCCTGTTCGAGCGTCATTTCAACCCCTCAAGCCCGGTTGGTGTGGGATCGGCA 2118  
QY 148 GCCCTGCGGCAAGCGCGCCGCAAACTGTGCGGTCTCGTGCAGCTTCCATTGCGT 207  
DB 2119 GCCCTGCGGCAAGCGCGCCGCAAACTGTGCGGTCTCGTGCAGCTTCCATTGCGT 2178  
QY 208 AGTAGTAAACCCCTCGAAGCTGTGACGCGCGCGCCCAAGCCGTTAAACCCCACTTCT 267  
DB 2179 AGTAGTAAACCCCTCGAAGCTGTGACGCGCGCGCCCAAGCCGTTAAACCCCACTTCT 2238  
QY 268 GAATGTTGACCTCGATTCAGTAGGAATACCCGCTGAATTTAA 310  
DB 2239 GAATGTTGACCTCGATTCAGTAGGAATACCCGCTGAATTTAA 2281

RESULT 3  
US-08-652-127C-7  
; Sequence 7, Application US/08652127C  
; Patent No. 5792611  
; GENERAL INFORMATION:  
; APPLICANT: Richard C. Hamelin  
; TITLE OF INVENTION: DETECTION OF PLANT  
; TITLE OF INVENTION: PATHOGEN FUNGI  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: George A. Seaby  
; ADDRESSEE: Seaby & Maclean  
; STREET: 880 Wellington Street, Suite 708  
; CITY: Ottawa  
; COUNTRY: Canada  
; ZIP: K1R 6K7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,127C  
; FILING DATE: May 23, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: George A. Seaby  
; REGISTRATION NUMBER: 24,034  
; REFERENCE/DOCKET NUMBER: 1898

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (613) 232-5815  
; TELEFAX: (613) 232-5831  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 531  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-652-127C-7

Query Match 31.9%; Score 99; DB 1; Length 531;  
Best Local Similarity 100.0%; Pred. No. 1e-44;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATTCGATCTTTGAACGACATTTGGCCCGCCAGATTTCTGGCGGCA 87  
DB 230 AATTCAGTGAATCATTCGATCTTTGAACGACATTTGGCCCGCCAGATTTCTGGCGGCA 289  
QY 88 TGCCTGTTCGAGCGTCATTTCAACCCCTCAAGCCCGCGG 126  
DB 290 TGCCTGTTCGAGCGTCATTTCAACCCCTCAAGCCCGCGG 328

RESULT 4  
US-08-652-127C-6  
; Sequence 6, Application US/08652127C  
; Patent No. 5792611  
; GENERAL INFORMATION:  
; APPLICANT: Richard C. Hamelin  
; TITLE OF INVENTION: DETECTION OF PLANT  
; TITLE OF INVENTION: PATHOGEN FUNGI  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: George A. Seaby  
; ADDRESSEE: Seaby & Maclean  
; STREET: 880 Wellington Street, Suite 708  
; CITY: Ottawa  
; COUNTRY: Canada  
; ZIP: K1R 6K7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,127C  
; FILING DATE: May 23, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: George A. Seaby  
; REGISTRATION NUMBER: 24,034  
; REFERENCE/DOCKET NUMBER: 1898  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (613) 232-5815  
; TELEFAX: (613) 232-5831  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 581  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-652-127C-6

Query Match 31.9%; Score 99; DB 1; Length 581;  
Best Local Similarity 100.0%; Pred. No. 1e-44;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATTCGATCTTTGAACGACATTTGGCCCGCCAGATTTCTGGCGGCA 87  
DB 280 AATTCAGTGAATCATTCGATCTTTGAACGACATTTGGCCCGCCAGATTTCTGGCGGCA 339  
QY 88 TGCCTGTTCGAGCGTCATTTCAACCCCTCAAGCCCGCGG 126



DB 340 TGCCTGTCGAGCGTCATTTCAACCTCAAGCCCCCGGG 378

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RESULT 5
US-08-887-480-82
; Sequence 82, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium culmorum
; INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
; INDIVIDUAL ISOLATE: (consensus sequence)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..12
; OTHER INFORMATION: /note= "3' end of small subunit
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 13..161
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 162..318
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 319..472
; OTHER INFORMATION: /note= "ITS 2"
; NAME/KEY: misc_feature
; LOCATION: 473..504
; OTHER INFORMATION: /note= "5' end of large subunit
; OTHER INFORMATION: rRNA gene"
US-08-887-480-82

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```

Query Match 30.3%; Score 94; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.8e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATTCGATCTTTGAAGCAGCATTTGGCGCCGAGTATCTGGCGGGCA 87
DB 239 AATTCAGTGAATCATTCGATCTTTGAAGCAGCATTTGGCGCCGAGTATCTGGCGGGCA 298
QY 88 TGCCTGTCGAGCGTCATTTCAACCTCAAGCCCC 121
DB 299 TGCCTGTCGAGCGTCATTTCAACCTCAAGCCCC 332

RESULT 6
US-08-905-314A-19
; Sequence 19, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827695artis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium culmorum
; INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
; INDIVIDUAL ISOLATE: (consensus sequence)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..12
; OTHER INFORMATION: /note= "3' end of small subunit
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 13..161
; OTHER INFORMATION: /note= "ITS 1"
; NAME/KEY: misc_feature
; LOCATION: 162..318
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 319..472

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OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 473..504
OTHER INFORMATION: /note= "5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-905-314A-19

Query Match      30.3%; Score 94; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.8e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATGCAATCTTTGAACGACATTTGGCCCGCAGATTTCTGGCGGCA 87
DB 239 AATTCAGTGAATCATGCAATCTTTGAACGACATTTGGCCCGCAGATTTCTGGCGGCA 298
QY 88 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 121
DB 299 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 332

RESULT 7
US-08-722-187-82
Sequence 82, Application US/08722187
Patent No. 5955274
GENERAL INFORMATION:
APPLICANT: Ligon, James M
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..504
OTHER INFORMATION: /note= "DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum
OTHER INFORMATION: (fcu1m.con)"
US-08-722-187-82
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Query Match      30.3%; Score 94; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.8e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATGCAATCTTTGAACGACATTTGGCCCGCAGATTTCTGGCGGCA 87
DB 239 AATTCAGTGAATCATGCAATCTTTGAACGACATTTGGCCCGCAGATTTCTGGCGGCA 298
QY 88 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 121
DB 299 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 332

RESULT 8
US-09-481-293-32
Sequence 32, Application US/09481293
Patent No. 6485907
GENERAL INFORMATION:
APPLICANT: Barnett, Jason
TITLE OF INVENTION: PCR-Based Detection of Rhizoctonia cerealis
FILE REFERENCE: PB/5-3113PI
CURRENT APPLICATION NUMBER: US/09/481,293
CURRENT FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 504
TYPE: DNA
ORGANISM: Fusarium culmorum
US-09-481-293-32
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Query Match      30.3%; Score 94; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.8e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATGCAATCTTTGAACGACATTTGGCCCGCAGATTTCTGGCGGCA 87
DB 242 AATTCAGTGAATCATGCAATCTTTGAACGACATTTGGCCCGCAGATTTCTGGCGGCA 301
QY 88 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 121
DB 302 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 335

RESULT 9
PCT-US95-04712-82
Sequence 82, Application PC/TUS9504712
GENERAL INFORMATION:
APPLICANT: Ligon, James M
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
```

ATTORNEY/AGENT INFORMATION:  
NAME: Walsh, Andrea C.  
REGISTRATION NUMBER: 34,988  
REFERENCE/DOCKET NUMBER: CGC 1739  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8666  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..504  
OTHER INFORMATION: /note="DNA sequence for the  
internal transcribed spacer region of Fusarium culmorum  
OTHER INFORMATION: (culm.con)"  
PCT-US95-04712-82

Query Match 30.3%; Score 94; DB 5; Length 504;  
Best Local Similarity 100.0%; Pred.No. 5,8e-42;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCCGCCAGATTTCTGGCGGCA 87  
DB 239 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCCGCCAGATTTCTGGCGGCA 298  
QY 88 TGCCGTTGAGCGCTCATTTCAACCTCAAGCCC 121  
DB 299 TGCCGTTGAGCGCTCATTTCAACCTCAAGCCC 332

RESULT 10  
US-08-887-480-84  
Sequence 84, Application US/08887480  
Patent No. 5814453  
GENERAL INFORMATION:  
APPLICANT: Beck, James J.  
TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
TITLE OF INVENTION: Polymerase Chain Reaction  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5814453artis Corporation  
STREET: 520 White Plains Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,480  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/722,187  
FILING DATE: 15-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:

LENGTH: 545 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Fusarium moniliforme  
INDIVIDUAL ISOLATE: 4551  
IMMEDIATE SOURCE:  
CLONE: PCRPMO1  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..30  
OTHER INFORMATION: /note="3' end of small subunit  
OTHER INFORMATION: rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 31..178  
OTHER INFORMATION: /note="ITS 1"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 179..335  
OTHER INFORMATION: /note="5.8S rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 336..488  
OTHER INFORMATION: /note="ITS 2"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 489..545  
OTHER INFORMATION: /note="5' end of large subunit  
OTHER INFORMATION: rRNA gene"  
US-08-887-480-84

Query Match 30.3%; Score 94; DB 1; Length 545;  
Best Local Similarity 100.0%; Pred.No. 5,7e-42;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCCGCCAGATTTCTGGCGGCA 87  
DB 256 AATTCAGTGAATCATCGAATCTTTGAACGACATTCGCCCGCCAGATTTCTGGCGGCA 315  
QY 88 TGCCGTTGAGCGCTCATTTCAACCTCAAGCCC 121  
DB 316 TGCCGTTGAGCGCTCATTTCAACCTCAAGCCC 349

RESULT 11  
US-08-905-314A-21  
Sequence 21, Application US/08905314A  
Patent No. 5827695  
GENERAL INFORMATION:  
APPLICANT: Beck, James J.  
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5827695artis Corporation Patent Department  
STREET: 3054 Cornwalis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 20779-2257  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,314A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

```

; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 545 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Fusarium moniliforme
; INDIVIDUAL ISOLATE: 4551
; CLONE: pCRFMON1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..178
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 179..335
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 336..488
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 489..545
; OTHER INFORMATION: /note= "5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
; US-08-905-314A-21

Query Match          30.3%; Score 94; DB 1; Length 545;
Best Local Similarity 100.0%; Pred. No. 5.7e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGCCCGCCAGTATTCTGGCGGCA 87
DB 256 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGCCCGCCAGTATTCTGGCGGCA 315
QY 88 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 121
DB 316 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 349

RESULT 12
US-08-887-480-96
; Sequence 96, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium poae
; INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
; INDIVIDUAL ISOLATE: sequence)
; IMMEDIATE SOURCE:
; CLONE: pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and
; CLONE: pCRFpoaeT756(3-1)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 31..180
; OTHER INFORMATION: /note= "ITS 1"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 181..337
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 338..489
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 490..546
; OTHER INFORMATION: /note= "5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
; US-08-887-480-96

Query Match          30.3%; Score 94; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. 5.7e-42;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGCCCGCCAGTATTCTGGCGGCA 87
DB 258 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGCCCGCCAGTATTCTGGCGGCA 317
QY 88 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 121
DB 318 TGCCTGTTGAGCGTCATTTCAACCCCTCAAGCCC 351

RESULT 13
US-08-905-314A-22
; Sequence 22, Application US/08905314A
; Patent No. 5827695
; GENERAL INFORMATION:
```

APPLICANT: Beck, James J.  
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 582769sartis Corporation Patent Department  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 20779-2257  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905.314A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Weigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1944  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 546 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Fusarium poae  
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus  
INDIVIDUAL ISOLATE: sequence)  
IMMEDIATE SOURCE:  
CLONE: PCRpoae1427(1-2), PCRpoaeT534(2-2), and  
FEATURE:  
CLONE: PCRpoaeT756(3-1)  
NAME/KEY: misc feature  
LOCATION: 1..30  
OTHER INFORMATION: /note= "3' end of small subunit  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 31..180  
OTHER INFORMATION: /note= "ITS 1"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 181..337  
OTHER INFORMATION: /note= "5.8S rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 338..489  
OTHER INFORMATION: /note= "ITS 2"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 490..546  
OTHER INFORMATION: /note= "5' end of large subunit  
OTHER INFORMATION: rRNA gene"  
US-08-905-314A-22

Query Match 30.3%; Score 94; DB 1; Length 546;  
Best Local Similarity 100.0%; Pred. No. 5,7e-42;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATTCGATCTTTGAAAGCAGCATTTGCCCGCAGATTTCTGCGGGCA 87  
DB 258 AATTCAGTGAATCATTCGATCTTTGAAAGCAGCATTTGCCCGCAGATTTCTGCGGGCA 317

QY 88 TGCGTTGAGGAGTCATTTCAACCCCTCAAGCC 121  
DB 318 TGCGTTGAGGAGTCATTTCAACCCCTCAAGCC 351

RESULT 14  
US-08-652-127C-5  
Sequence 5, Application US/08652127C  
Patent No. 5792611  
GENERAL INFORMATION:  
APPLICANT: Richard C. Hamelin  
TITLE OF INVENTION: DETECTION OF PLANT  
TITLE OF INVENTION: PATHOGEN FUNGI  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: George A. Seaby  
ADDRESSEE: Seaby & Maclean  
STREET: 880 Wellington Street, Suite 708  
CITY: Ottawa  
COUNTRY: Canada  
ZIP: K1R 6K7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652.127C  
FILING DATE: May 23, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George A. Seaby  
REGISTRATION NUMBER: 24,034  
REFERENCE/DOCKET NUMBER: 1898  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (613) 232-5815  
TELEFAX: (613) 232-5831  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 594  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-652-127C-5

Query Match 29.7%; Score 92; DB 1; Length 594;  
Best Local Similarity 100.0%; Pred. No. 7.2e-41;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATTCGATCTTTGAAAGCAGCATTTGCCCGCAGATTTCTGCGGGCA 87  
DB 285 AATTCAGTGAATCATTCGATCTTTGAAAGCAGCATTTGCCCGCAGATTTCTGCGGGCA 344

QY 88 TGCGTTGAGGAGTCATTTCAACCCCTCAAGC 119  
DB 345 TGCGTTGAGGAGTCATTTCAACCCCTCAAGC 376

RESULT 15  
US-09-423-233-6  
Sequence 6, Application US/09423233  
Patent No. 6372430  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America as  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
FILE REFERENCE: 03063-0341WP  
CURRENT APPLICATION NUMBER: US/09/423.233  
CURRENT FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 6  
LENGTH: 319

TYPE: DNA  
 ORGANISM: Fusarium solani  
 US-09-423-233-6

Query Match 25.5%; Score 79; DB 4; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-34;  
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	28	AATTCAGTGAATCATCTTTGAACGACATTGCGCCGCCAGTATTCTGGCGGCA	87
Db	30	AATTCAGTGAATCATCTTTGAACGACATTGCGCCGCCAGTATTCTGGCGGCA	89
QY	88	TGCGTGTGAGCGTCATT	106
Db	90	TGCGTGTGAGCGTCATT	108

Search completed: October 1, 2004, 11:12:57  
 Job time : 52.256 secs



Db 1 AATGCCAGTAGTATGTAATTCGAAATTCAGTGAATCATCGAATCTTTGAACGACA 60  
 QY 61 TTGGCCCGCCGCAATTCCTGGCGGCGCATGCTGTTTCAGCGCTCATTTCAACCTCAAGCC 120  
 Db 61 TTGGCCCGCCGCAATTCCTGGCGGCGCATGCTGTTTCAGCGCTCATTTCAACCTCAAGCC 120  
 QY 121 CCGCGGTTGGTGTGGGGATCGCAAGCCCTTCGCGCAAGCCGCGCCGCAAACTCTGTG 180  
 Db 121 CCGCGGTTGGTGTGGGGATCGCAAGCCCTTCGCGCAAGCCGCGCCGCAAACTCTGTG 180  
 QY 181 GCGGCTCGCTGCACTTCATTCAGTAGTAAACCCCTCGCACTGTGTACGCGCGC 240  
 Db 181 GCGGCTCGCTGCACTTCATTCAGTAGTAAACCCCTCGCACTGTGTACGCGCGC 240  
 QY 241 GGGCAAGCCGTTAAACCCCACTTCGATGTTGACCTGGATCAGTGAATATCCG 300  
 Db 241 GGGCAAGCCGTTAAACCCCACTTCGATGTTGACCTGGATCAGTGAATATCCG 300  
 QY 301 CTGAACCTTAA 310  
 Db 301 CTGAACCTTAA 310

## RESULT 2

US-09-961-755A-7  
 ; Sequence 7, Application US/09961755A  
 ; Publication No. US20030113722A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beck, Jim  
 ; APPLICANT: Barnett, Jason  
 ; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the  
 ; FILE REFERENCE: 60055  
 ; CURRENT APPLICATION NUMBER: US/09/961,755A  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 534  
 ; TYPE: DNA  
 ; ORGANISM: Fusarium proliferatum  
 ; US-09-961-755A-7

Query Match 73.5%; Score 228; DB 10; Length 534;  
 Best Local Similarity 99.6%; Pred. No. 1,3e-119;  
 Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGCGCCGCGCAGTATTCGGCGGCA 87  
 Db 256 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGCGCCGCGCAGTATTCGGCGGCA 315  
 QY 88 TGCCGTGTTGAGCGCTCATTTCAACCTCAAGCCCGGGTTGTGGTGGGATCGGCA 147  
 Db 316 TGCCGTGTTGAGCGCTCATTTCAACCTCAAGCCCGGGTTGTGGTGGGATCGGCA 375  
 QY 148 GCCCTTGCGGCAAGCCGCGCCGCAATCTAGTGGCGGTCTGCGCAGCTTCATTGGCGT 207  
 Db 376 GCCCTTGCGGCAAGCCGCGCCGCAATCTAGTGGCGGTCTGCGCAGCTTCATTGGCGT 435  
 QY 208 AGTAGTAAACCCCTCGCACTGTGTACGCGGCGCGCCAGCCGTTAAACCCCACTTCT 267  
 Db 436 AGTAGTAAACCCCTCGCACTGTGTACGCGGCGCGCCAGCCGTTAAACCCCACTTCT 495  
 QY 268 GAATGTTGACCTCGATCAGTGAATATCCCTGTGAC 306  
 Db 496 GAATGTTGACCTCGATCAGTGAATATCCCTGTGAC 534

## RESULT 3

US-09-961-755A-6  
 ; Sequence 6, Application US/09961755A  
 ; Publication No. US20030113722A1  
 ; GENERAL INFORMATION:

; APPLICANT: Beck, Jim  
 ; APPLICANT: Barnett, Jason  
 ; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the  
 ; FILE REFERENCE: 60055  
 ; CURRENT APPLICATION NUMBER: US/09/961,755A  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 6  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Glberella zeae  
 ; US-09-961-755A-6

Query Match 30.3%; Score 94; DB 10; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 5e-43;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGCGCCGCGCAGTATTCGGCGGCA 87  
 Db 256 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGCGCCGCGCAGTATTCGGCGGCA 315  
 QY 88 TGCCGTGTTGAGCGCTCATTTCAACCTCAAGCC 121  
 Db 316 TGCCGTGTTGAGCGCTCATTTCAACCTCAAGCC 349

## RESULT 4

US-09-961-755A-5  
 ; Sequence 5, Application US/09961755A  
 ; Publication No. US20030113722A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beck, Jim  
 ; APPLICANT: Barnett, Jason  
 ; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the  
 ; FILE REFERENCE: 60055  
 ; CURRENT APPLICATION NUMBER: US/09/961,755A  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 522  
 ; TYPE: DNA  
 ; ORGANISM: Fusarium subglutinans  
 ; US-09-961-755A-5

Query Match 30.3%; Score 94; DB 10; Length 522;  
 Best Local Similarity 100.0%; Pred. No. 5e-43;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGCGCCGCGCAGTATTCGGCGGCA 87  
 Db 256 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGCGCCGCGCAGTATTCGGCGGCA 315  
 QY 88 TGCCGTGTTGAGCGCTCATTTCAACCTCAAGCC 121  
 Db 316 TGCCGTGTTGAGCGCTCATTTCAACCTCAAGCC 349

## RESULT 5

US-09-961-755A-8  
 ; Sequence 8, Application US/09961755A  
 ; Publication No. US20030113722A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Beck, Jim  
 ; APPLICANT: Barnett, Jason  
 ; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the  
 ; FILE REFERENCE: 60055  
 ; CURRENT APPLICATION NUMBER: US/09/961,755A  
 ; CURRENT FILING DATE: 2001-09-24



NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 8  
LENGTH: 522  
TYPE: DNA  
ORGANISM: Fusarium verticillioides (syn. F. moniliforme)  
US-09-961-755A-8

Query Match 30.3%; Score 94; DB 10; Length 522;  
Best Local Similarity 100.0%; Pred. No. 5e-43;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 AATTCAGTAATCATCGAATCTTTGAACGACATTCGCCGCCAGATTTCTGGCGGCA 87  
DB 256 AATTCAGTAATCATCGAATCTTTGAACGACATTCGCCGCCAGATTTCTGGCGGCA 315  
OY 88 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 121  
DB 316 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 349

RESULT 6  
US-10-046-955-6

Sequence 6, Application US/10046955  
Publication No. US20030129600A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the  
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis  
APPLICANT: Control and Prevention  
APPLICANT: Morrison, Christine J.  
APPLICANT: Reiss, Errol  
APPLICANT: Aidorevich, Lilliana

APPLICANT: Choi, Jong Seo  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
TITLE OF INVENTION: Other Filamentous Fungi  
FILE REFERENCE: 6395-62064  
CURRENT APPLICATION NUMBER: US/10/046,955  
CURRENT FILING DATE: 2002-06-04  
PRIOR APPLICATION NUMBER: US 09/423,233  
PRIOR FILING DATE: 2000-06-27  
PRIOR APPLICATION NUMBER: PCT/US98/08926  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: US 60/045,400  
PRIOR FILING DATE: 1997-05-02  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 6  
LENGTH: 319  
TYPE: DNA  
ORGANISM: Fusarium solani  
US-10-046-955-6

Query Match 25.5%; Score 79; DB 15; Length 319;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 AATTCAGTAATCATCGAATCTTTGAACGACATTCGCCGCCAGATTTCTGGCGGCA 87  
DB 30 AATTCAGTAATCATCGAATCTTTGAACGACATTCGCCGCCAGATTTCTGGCGGCA 89  
OY 88 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 106  
DB 90 TGCCTGTTGAGCGCTCATTTCAACCTCAAGCCC 108

RESULT 7  
US-10-046-955-27

Sequence 27, Application US/10046955  
Publication No. US20030129600A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the  
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis  
APPLICANT: Control and Prevention

APPLICANT: Morrison, Christine J.  
APPLICANT: Reiss, Errol  
APPLICANT: Aidorevich, Lilliana  
APPLICANT: Choi, Jong Seo  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
TITLE OF INVENTION: Other Filamentous Fungi  
FILE REFERENCE: 6395-62064  
CURRENT APPLICATION NUMBER: US/10/046,955  
CURRENT FILING DATE: 2002-06-04  
PRIOR APPLICATION NUMBER: US 09/423,233  
PRIOR FILING DATE: 2000-06-27  
PRIOR APPLICATION NUMBER: PCT/US98/08926  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: US 60/045,400  
PRIOR FILING DATE: 1997-05-02  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 27  
LENGTH: 343  
TYPE: DNA  
ORGANISM: Scedosporium apiospermum  
US-10-046-955-27

Query Match 13.5%; Score 42; DB 15; Length 343;  
Best Local Similarity 100.0%; Pred. No. 2.6e-13;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 AATTCAGTAATCATCGAATCTTTGAACGACATTCGCCGCCG 69  
DB 28 AATTCAGTAATCATCGAATCTTTGAACGACATTCGCCGCCG 69

RESULT 8  
US-10-046-955-26

Sequence 26, Application US/10046955  
Publication No. US20030129600A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the  
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis  
APPLICANT: Control and Prevention  
APPLICANT: Morrison, Christine J.  
APPLICANT: Reiss, Errol  
APPLICANT: Aidorevich, Lilliana

APPLICANT: Choi, Jong Seo  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
TITLE OF INVENTION: Other Filamentous Fungi  
FILE REFERENCE: 6395-62064  
CURRENT APPLICATION NUMBER: US/10/046,955  
CURRENT FILING DATE: 2002-06-04  
PRIOR APPLICATION NUMBER: US 09/423,233  
PRIOR FILING DATE: 2000-06-27  
PRIOR APPLICATION NUMBER: PCT/US98/08926  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: US 60/045,400  
PRIOR FILING DATE: 1997-05-02  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 26  
LENGTH: 344  
TYPE: DNA  
ORGANISM: Scedosporium apiospermum  
US-10-046-955-26

Query Match 13.5%; Score 42; DB 15; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2.6e-13;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 AATTCAGTAATCATCGAATCTTTGAACGACATTCGCCGCCG 69  
DB 29 AATTCAGTAATCATCGAATCTTTGAACGACATTCGCCGCCG 70

RESULT 9

US-09-961-663-14  
; Sequence 14, Application US/09961663  
; Patent No. US20020115084A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnett, Jason  
; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain  
; FILE REFERENCE: PB/5-31382A  
; CURRENT APPLICATION NUMBER: US/09/961,663  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/211902  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 377  
; TYPE: DNA  
; ORGANISM: Mycosphaerella sp.  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(377)  
; OTHER INFORMATION: Truncated DNA sequence for the Internal  
; OTHER INFORMATION: Transcribed Spacer of a fungus amplified from  
; OTHER INFORMATION: banana sample "Capesterre-babin 2".  
US-09-961-663-14

Query Match 13.2%; Score 41; DB 9; Length 377;  
Best Local Similarity 100.0%; Pred. No. 9.7e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 68  
DB 118 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 158

RESULT 10  
US-09-961-663-15  
; Sequence 15, Application US/09961663  
; Patent No. US20020115084A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnett, Jason  
; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain  
; FILE REFERENCE: PB/5-31382A  
; CURRENT APPLICATION NUMBER: US/09/961,663  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/211902  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 377  
; TYPE: DNA  
; ORGANISM: Mycosphaerella sp.  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(377)  
; OTHER INFORMATION: Truncated DNA sequence for the Internal  
; OTHER INFORMATION: Transcribed Spacer of fungus amplified from banana  
; OTHER INFORMATION: sample "Matouba bas 3"  
US-09-961-663-15

Query Match 13.2%; Score 41; DB 9; Length 377;  
Best Local Similarity 100.0%; Pred. No. 9.7e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 68  
DB 118 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 158

RESULT 11  
US-09-961-663-16  
; Sequence 16, Application US/09961663  
; Patent No. US20020115084A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnett, Jason  
; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain  
; FILE REFERENCE: PB/5-31382A  
; CURRENT APPLICATION NUMBER: US/09/961,663  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/211902  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 377  
; TYPE: DNA  
; ORGANISM: Mycosphaerella sp.  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(377)  
; OTHER INFORMATION: Truncated DNA sequence for the Internal  
; OTHER INFORMATION: Transcribed Spacer of a fungus amplified from  
; OTHER INFORMATION: banana sample "Remoin Insect Forte"  
US-09-961-663-16

Query Match 13.2%; Score 41; DB 9; Length 377;  
Best Local Similarity 100.0%; Pred. No. 9.7e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 68  
DB 118 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 158

RESULT 12  
US-09-961-663-19  
; Sequence 19, Application US/09961663  
; Patent No. US20020115084A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnett, Jason  
; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain  
; FILE REFERENCE: PB/5-31382A  
; CURRENT APPLICATION NUMBER: US/09/961,663  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/211902  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 377  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Consensus  
; OTHER INFORMATION: sequence of Mycosphaerella sp. ITS sequences shown  
US-09-961-663-19

Query Match 13.2%; Score 41; DB 9; Length 377;  
Best Local Similarity 100.0%; Pred. No. 9.7e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 68  
DB 118 AATTCAGTGAATCATCGAATCTTTGAACGACATTTGGCGCC 158

RESULT 13

US-10-356-320-1  
; Sequence 1, Application US/10356320  
; Publication No. US20040009573A1  
; GENERAL INFORMATION:  
; APPLICANT: Strobel, Gary  
; APPLICANT: Ford, Eugene  
; APPLICANT: James, Harper K.  
; TITLE OF INVENTION: Pestalotiopsis Microsporia Isolates and Compounds Derived  
; TITLE OF INVENTION: Therefrom  
; FILE REFERENCE: A-72093 (470425-4)  
; CURRENT APPLICATION NUMBER: US/10/356,320  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US 60/352,254  
; PRIOR FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 466  
; TYPE: DNA  
; ORGANISM: Pestalotiopsis sp. NG12-30  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank Acc. No. US20040009573A1 AF377301  
; DATABASE ENTRY DATE: 2002-06-02  
; RELEVANT RESIDUES: (1)..(466)  
US-10-356-320-1

Query Match 13.2%; Score 41; DB 16; Length 466;  
Best Local Similarity 100.0%; Pred. No. 9.7e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGACGACATTGGCGCC 68  
DB 221 AATTCAGTGAATCATCGAATCTTTGACGACATTGGCGCC 261

RESULT 14  
US-09-961-663-17  
; Sequence 17, Application US/09961663  
; Patent No. US20020115084A1  
; GENERAL INFORMATION:  
; APPLICANT: Beck, James  
; APPLICANT: Barnett, Jason  
; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain  
; TITLE OF INVENTION: Reaction  
; FILE REFERENCE: PB/5-31382A  
; CURRENT APPLICATION NUMBER: US/09/961,663  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/211902  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 534  
; TYPE: DNA  
; ORGANISM: Mycosphaerella fijiensis  
US-09-961-663-17

Query Match 13.2%; Score 41; DB 9; Length 534;  
Best Local Similarity 100.0%; Pred. No. 9.8e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AATTCAGTGAATCATCGAATCTTTGACGACATTGGCGCC 68  
DB 249 AATTCAGTGAATCATCGAATCTTTGACGACATTGGCGCC 289

RESULT 15  
US-09-961-663-18  
; Sequence 18, Application US/09961663  
; Patent No. US20020115084A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnett, Jason  
; APPLICANT: Beck, James

; TITLE OF INVENTION: Detection of Mycosphaerella Using the Polymerase Chain  
; TITLE OF INVENTION: Reaction  
; FILE REFERENCE: PB/5-31382A  
; CURRENT APPLICATION NUMBER: US/09/961,663  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/211902  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 540  
; TYPE: DNA  
; ORGANISM: Mycosphaerella musicola  
US-09-961-663-18

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Best Local Similarity 100.0%; Pred. No. 9.8e-13;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 258 AATTCAGTGAATCATCGAATCTTTGACGACATTGGCGCC 298

Search completed: October 1, 2004, 11:22:42  
Job time : 278.951 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 08:04:24 : Search time 2101.99 seconds  
(without alignments)  
4404.059 Million cell updates/sec

Title: US-10-046-955-7

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Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 10

Total number of hits satisfying chosen parameters: 5796139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	67	21.6	755	14	CF870665 tric024xj
4	67	21.6	796	14	CB900742 CB900742b

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6	67	21.6	840	14	CB907036	CB907036 tric081xc
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8	45	14.5	725	13	B0752001	B0752001 EST632564
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#### ALIGNMENTS

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LOCUS CF880267 735 bp mRNA linear EST 31-OCT-2003  
DEFINITION tric081xc18.b2 T.reesei mycelial culture, Version 6 October 2003  
ACCESSION CF880267  
VERSION CF880267.1 GI:38134949  
KEYWORDS EST.

SOURCE  
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)

REFERENCE  
AUTHORS Diener, S.E., Dankmeyer, L., Dunn-Coleman, N., Houfek, T.D.,  
1 (bases 1 to 735)  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

TITLE  
JOURNAL  
COMMENT Analysis of the protein processing and secretion pathways in a  
Trichoderma reesei EST dataset  
Unpublished (2003)  
Contact: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: UT-F1 primer.

FEATURES  
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/note="Vector: PREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

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Db 88 TGCCTGT 94  
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LOCUS trico24xb14.b1 T.reesei mycelial culture, Version 6 October 2003  
DEFINITION Hypocrea jecorina cDNA clone trico24xb14, mRNA sequence.  
ACCESSION CF870552  
VERSION CF870552.1 GI:38125234  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaeae; Hypocrea.  
Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D., Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and Dean,R.A.  
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset  
Unpublished (2003)  
Contact: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: Tr-F1 primer.  
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Db 88 TGCCTGT 94  
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CF870665 755 bp mRNA linear EST 31-OCT-2003  
LOCUS trico24xb104.b1 T.reesei mycelial culture, Version 6 October 2003  
DEFINITION Hypocrea jecorina cDNA clone trico24xb104, mRNA sequence.  
ACCESSION CF870665  
VERSION CF870665.1 GI:38125347  
KEYWORDS EST.  
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)  
ORGANISM Hypocrea jecorina  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaeae; Hypocrea.  
Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D., Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and Dean,R.A.  
Analysis of the protein processing and secretion pathways in a Trichoderma reesei EST dataset  
Unpublished (2003)  
Contact: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: Tr-F1 primer.  
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Db 88 TGCCTGT 94  
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RESULT 4  
CB900742 796 bp mRNA linear EST 02-JUL-2003  
LOCUS trico24xb14 T.reesei mycelial culture, Version 3 april Hypocrea  
DEFINITION jecorina cDNA clone trico24xb14, mRNA sequence.  
ACCESSION CB900742  
VERSION CB900742.1 GI:30115400  
KEYWORDS EST.

**SOURCE**  
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)  
Hypocrea jecorina  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

**REFERENCE**  
1 (bases 1 to 796)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

**TITLE**  
JOURNAL MEDLINE  
PUBMED  
22803314  
Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
Seq primer: LT-P1 primer.

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tric024x104 T. reesei mycelial culture, Version 3 april Hypocrea  
jecorina cDNA clone tric024x104, mRNA sequence.

**ACCESSION**  
CB900860

**VERSION**  
CB900860.1 GI:30115518

**KEYWORDS**  
EST.

**SOURCE**  
Hypocrea jecorina (anamorph: Trichoderma reesei)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 808)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

**TITLE**  
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PUBMED  
22803314  
Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
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**ACCESSION**  
CB907036

**VERSION**  
CB907036.1 GI:30121694

**KEYWORDS**  
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 840)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

**TITLE**  
JOURNAL MEDLINE  
PUBMED  
12788920  
Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
Seq primer: LT-P1 primer.

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**SOURCE**  
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)  
Hypocrea jecorina  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

**REFERENCE**  
1 (bases 1 to 796)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

**TITLE**  
JOURNAL MEDLINE  
PUBMED  
22803314  
Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
Seq primer: LT-P1 primer.

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Query Match 21.6%; Score 67; DB 14; Length 796;  
Best Local Similarity 100.0%; Pred. No. 1.8e-24;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**LOCUS**  
CB900860 808 bp mRNA linear EST 02-JUL-2003  
tric024x104 T. reesei mycelial culture, Version 3 april Hypocrea  
jecorina cDNA clone tric024x104, mRNA sequence.

**ACCESSION**  
CB900860

**VERSION**  
CB900860.1 GI:30115518

**KEYWORDS**  
EST.

**SOURCE**  
Hypocrea jecorina (anamorph: Trichoderma reesei)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 808)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

**TITLE**  
JOURNAL MEDLINE  
PUBMED  
22803314  
Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
Seq primer: LT-P1 primer.

**FEATURES**  
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culture grown from 24 hrs to 6 days with varying Carbon  
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**ORIGIN**  
Query Match 21.6%; Score 67; DB 14; Length 808;  
Best Local Similarity 100.0%; Pred. No. 1.8e-24;  
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**LOCUS**  
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tric081xc18 T. reesei mycelial culture, Version 3 april Hypocrea  
jecorina cDNA clone tric081xc18, mRNA sequence.

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**VERSION**  
CB907036.1 GI:30121694

**KEYWORDS**  
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
1 (bases 1 to 840)  
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,  
Dunn-Coleman, N.S., Goedegebuer, F., Houfek, T.D., England, G.J.,  
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,  
Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)

**TITLE**  
JOURNAL MEDLINE  
PUBMED  
12788920  
Contact: Pamela K. Foreman  
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Seq primer: LT-P1 primer.

**FEATURES**  
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 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
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 mitosporic Phyllostachyaceae; Colletotrichum.  
 1 (bases 1 to 704)  
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,  
 Cheung,F. and Fraser,C.M.  
 ESTs from mycelia of Colletotrichum trifolii race 1  
 Unpublished (2002)  
 Other ESTs: EST631847  
 Contact: Deborah A. Samac  
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 Tel: 612 625 1243  
 Fax: 651 649 5058  
 Email: debbys@puccini.crl.umn.edu  
 TIGR sequence name: MTSAD17TV More information is available at:  
 www.medicago.org  
 Seq primer: (gca Aca Cga Ctc Act Aca ggg C).  
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 Strategene and packaged using Gigapack packaging extracts.  
 An aliquot of the amplified library was used to transduce  
 E. coli Y1090 and phage DNA was purified from a liquid  
 lysate. The cDNA inserts were gel purified after EcoRI  
 digestion and ligated into Bluescript SK+. Aliquots of  
 the ligation were used to transform E. coli DHSalpa which  
 were plated onto medium with X-gal for selection of  
 recombinants."

ORIGIN  
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 mitosporic Phyllostachyaceae; Colletotrichum.  
 1 (bases 1 to 725)  
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,  
 Cheung,F. and Fraser,C.M.  
 ESTs from mycelia of Colletotrichum trifolii race 1  
 Unpublished (2002)  
 Other ESTs: EST632563  
 Contact: Deborah A. Samac  
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 University of Minnesota  
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
 Tel: 612 625 1243  
 Fax: 651 649 5058  
 Email: debbys@puccini.crl.umn.edu  
 TIGR sequence name: MTSAD122TV More information is available at:  
 www.medicago.org  
 Seq primer: (gca Aca Cga Ctc Act Aca ggg C).  
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 enriched RNA The cDNA was ligated into Lambda gtl1 from  
 Strategene and packaged using Gigapack packaging extracts.  
 An aliquot of the amplified library was used to transduce  
 E. coli Y1090 and phage DNA was purified from a liquid  
 lysate. The cDNA inserts were gel purified after EcoRI  
 digestion and ligated into Bluescript SK+. Aliquots of  
 the ligation were used to transform E. coli DHSalpa which  
 were plated onto medium with X-gal for selection of  
 recombinants."

ORIGIN  
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accession B0751027 GI:21906432  
 version B0751027  
 keywords EST  
 source Colletotrichum trifolii  
 organism Colletotrichum trifolii  
 comment Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllostachyales; Phyllostachyaceae; mitosporic Phyllostachyaceae; Colletotrichum.  
 reference 1 (bases 1 to 743)  
 authors Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T., Cheung,F. and Fraser,C.M.  
 title ESTs from mycelia of Colletotrichum trifolii race 1  
 journal Unpublished (2002)  
 comment Other ESTs: EST615589  
 contact: Deborah A. Samac  
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 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
 tel: 612 625 1243  
 fax: 651 649 5058  
 email: debby@puccini.crl.umn.edu  
 tigr sequence name: MTSAB20TV More information is available at: www.medicago.org  
 seq primer: (gta ata cga ctc act ata ggg c).  
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Query Match 14.5%; Score 45; DB 13; Length 743;  
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 accession B0751971  
 version B0751971  
 keywords EST  
 source Colletotrichum trifolii  
 organism Colletotrichum trifolii  
 comment Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllostachyales; Phyllostachyaceae; mitosporic Phyllostachyaceae; Colletotrichum.

reference 1 (bases 1 to 745)  
 authors Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T., Cheung,F. and Fraser,C.M.  
 title ESTs from mycelia of Colletotrichum trifolii race 1  
 journal Unpublished (2002)  
 comment Contact: Deborah A. Samac  
 department of Plant Pathology  
 University of Minnesota  
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
 tel: 612 625 1243  
 fax: 651 649 5058  
 email: debby@puccini.crl.umn.edu  
 tigr sequence name: MTSAB103TV More information is available at: www.medicago.org  
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Query Match 14.5%; Score 45; DB 13; Length 745;  
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RESULT 11  
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 sequence.  
 accession B0751399  
 version B0751399  
 keywords EST  
 source Colletotrichum trifolii  
 organism Colletotrichum trifolii  
 comment Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllostachyales; Phyllostachyaceae; mitosporic Phyllostachyaceae; Colletotrichum.

reference 1 (bases 1 to 758)  
 authors Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T., Cheung,F. and Fraser,C.M.  
 title ESTs from mycelia of Colletotrichum trifolii race 1  
 journal Unpublished (2002)  
 comment Other ESTs: EST631961  
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 Fax: 651 649 5058  
 Email: debbys@pucini.crl.umn.edu  
 TIGR sequence name: MTSAD95TV More information is available at:  
 www.medicago.org  
 Seq primer: (gta Aca Cga Ctc Act Aca 999 C).

## FEATURES

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## ORIGIN

Query Match 14.5%; Score 45; DB 13; Length 758;  
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 ORGANISM Colletotrichum trifolii  
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 Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae;  
 mitosporic Phyllochoraceae; Colletotrichum.  
 1 (bases 1 to 774)  
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,  
 Cheung,F. and Frazer,C.M.  
 ESTs from mycelia of Colletotrichum trifolii race 1  
 Unpublished (2002)  
 Other ESTs: EST632698  
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 Email: debbys@pucini.crl.umn.edu  
 TIGR sequence name: MTSAD95TV More information is available at:  
 www.medicago.org

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

## FEATURES

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## ORIGIN

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 Bacteria; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae;  
 mitosporic Phyllochoraceae; Colletotrichum.  
 1 (bases 1 to 806)  
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,  
 Cheung,F. and Frazer,C.M.  
 ESTs from mycelia of Colletotrichum trifolii race 1  
 Unpublished (2002)  
 Other ESTs: EST631577  
 Contact: Deborah A. Samac  
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 Tel: 612 625 1243  
 Fax: 651 649 5058  
 Email: debbys@pucini.crl.umn.edu  
 TIGR sequence name: MTSAB07TV More information is available at:  
 www.medicago.org

## FEATURES

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## ORIGIN

Query Match 14.5%; Score 45; DB 13; Length 806;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
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ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae;  
mitosporic Phyllochoraceae; Colletotrichum.  
1 (bases 1 to 806)

REFERENCE  
AUTHORS  
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T.,  
Cheung, F., and Fraser, C.M.  
ESTs from mycelia of Colletotrichum trifolii race 1  
Unpublished (2002)

JOURNAL  
COMMENT  
Other ESTs: EST632046  
Contact: Deborah A. Samac  
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495 Borlang Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debby@puccini.crl.umn.edu

TIGR sequence name: MTSAB48TV More information is available at:  
www.medicago.org  
Seq primer: (gtA ACA CGA CTC ACT ACA 999 C).  
Location/Qualifiers

FEATURES  
source

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the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

## ORIGIN

Query Match 14.5%; Score 45; DB 13; Length 806;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SEQUENCE.  
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BQ752289.1 GI:21907694

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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Colletotrichum trifolii  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae;  
mitosporic Phyllochoraceae; Colletotrichum.  
1 (bases 1 to 994)

REFERENCE  
AUTHORS  
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Uterback, T.,  
Cheung, F., and Fraser, C.M.  
ESTs from mycelia of Colletotrichum trifolii race 1  
Unpublished (2002)

JOURNAL  
COMMENT  
Other ESTs: EST632851  
Contact: Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlang Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debby@puccini.crl.umn.edu

TIGR sequence name: MTSAK50TV More information is available at:  
www.medicago.org  
Seq primer: (gtA ACA CGA CTC ACT ACA 999 C).  
Location/Qualifiers

FEATURES  
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/note="Vector: pBluescript SK+; Site\_1: EcoRI; Site\_2: EcoRI; isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

## ORIGIN

Query Match 14.5%; Score 45; DB 13; Length 994;  
Best Local Similarity 100.0%; Pred. No. 1e-12;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Oct 1 16:15:52 2004

us-10-046-955-7.olig10.rst

Page 8

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Search completed: October 1, 2004, 11:11:05  
Job time : 2104.99 secs

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## OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 146.608 Seconds

(without alignments)  
5321.503 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgtcaatcgcgtccctc 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
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11: gb\_sgs: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vt: \*  
15: em\_da: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sgs: \*  
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29: em\_vt: \*  
30: em\_hcg\_hum: \*  
31: em\_hcg\_inv: \*  
32: em\_hcg\_other: \*  
33: em\_hcg\_mus: \*  
34: em\_hcg\_pln: \*  
35: em\_hcg\_rtd: \*  
36: em\_hcg\_mam: \*  
37: em\_hcg\_vrt: \*  
38: em\_sy: \*  
39: em\_hcgo\_hum: \*  
40: em\_hcgo\_mus: \*  
41: em\_hcgo\_other: \*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	# Match	Length	DB ID	Description
1	18	100.0	18	6 AR206444	AR206444 Sequence
2	18	100.0	18	6 BD083635	BD083635 Nucleic a
3	18	100.0	335	8 AF162898	AF162898 Fusarium
4	18	100.0	335	8 AF162899	AF162899 Fusarium
5	18	100.0	336	8 AF162900	AF162900 Fusarium
6	18	100.0	338	8 AF339418	AF339418 Fusarium
7	18	100.0	426	8 AF383320	AF383320 Fusarium
8	18	100.0	430	8 AF502842	AF502842 Leat 11ct
9	18	100.0	441	8 AY387703	AY387703 Fusarium
10	18	100.0	445	8 AY380575	AY380575 Fusarium
11	18	100.0	445	8 AY387698	AY387698 Fusarium
12	18	100.0	445	8 AY387699	AY387699 Fusarium
13	18	100.0	445	8 AY387702	AY387702 Fusarium
14	18	100.0	445	8 AY387704	AY387704 Fusarium
15	18	100.0	445	8 AY387705	AY387705 Fusarium
16	18	100.0	447	8 AY387701	AY387701 Fusarium
17	18	100.0	455	8 FOU28159	U28159 Fusarium ox
18	18	100.0	455	8 FOU28161	U28161 Fusarium ox
19	18	100.0	456	8 AF440527	AF440527 Fusarium
20	18	100.0	456	8 AF440529	AF440529 Fusarium
21	18	100.0	456	8 AF440531	AF440531 Fusarium
22	18	100.0	456	8 AF440532	AF440532 Fusarium
23	18	100.0	456	8 AF440534	AF440534 Fusarium
24	18	100.0	456	8 AF440539	AF440539 Fusarium
25	18	100.0	456	8 AF440540	AF440540 Fusarium
26	18	100.0	456	8 AF440542	AF440542 Fusarium
27	18	100.0	456	8 AF440552	AF440552 Fusarium
28	18	100.0	456	8 AF440561	AF440561 Fusarium
29	18	100.0	456	8 AF440563	AF440563 Fusarium
30	18	100.0	457	8 AF440533	AF440533 Fusarium
31	18	100.0	457	8 AF440538	AF440538 Fusarium
32	18	100.0	457	8 AF440560	AF440560 Fusarium
33	18	100.0	457	8 AF440562	AF440562 Fusarium
34	18	100.0	458	8 AF055220	AF055220 Fusarium
35	18	100.0	460	8 AY258214	AY258214 Fusarium
36	18	100.0	497	8 AY243058	AY243058 Ascomycet
37	18	100.0	501	8 AY247553	AY247553 Fusarium
38	18	100.0	501	8 AY262831	AY262831 Fusarium
39	18	100.0	501	8 AY354386	AY354386 Fusarium
40	18	100.0	501	8 AY354388	AY354388 Fusarium
41	18	100.0	501	8 AY354389	AY354389 Fusarium
42	18	100.0	501	8 AY354390	AY354390 Fusarium
43	18	100.0	501	8 AY354393	AY354393 Fusarium
44	18	100.0	501	8 AY354396	AY354396 Fusarium
45	18	100.0	501	8 AY354397	AY354397 Fusarium

## ALIGNMENTS

RESULT 1  
AR206444  
LOCUS AR206444 18 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 50 from patent US 6372430.  
ACCESSION AR206444  
VERSION AR206444.1 GI:21505047  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Morrison,C.J., Reles,E., Aldorevich,L. and Choi,J.Soo.  
TITLE Nucleic acids for detecting Aspergillus species and other filamentous fungi  
JOURNAL Patent: US 6372430-A 50 16-APR-2002;

FEATURES  
source Location/Qualifiers  
1. .18  
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Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
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RESULT 2  
BD083635 18 bp DNA linear PAT 27-AUG-2002  
LOCUS Nucleic acids for detecting Aspergillus species and other  
DEFINITION filamentous fungi.  
ACCESSION BD083635  
VERSION BD083635.1 GI:22629245  
KEYWORDS JP 2001525665-A/50.  
SOURCE Fusarium oxysporum  
ORGANISM Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
1 (bases 1 to 18)  
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.  
Nucleic acids for detecting Aspergillus species and other  
filamentous fungi  
Patent: JP 2001525665-A 50 11-DEC-2001;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY  
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES  
SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES  
CENTERS FOR DISEASE PREVENTION AND CONTROL  
PREVENTION TECHNOLOGY TRANSFER OFFICE  
OS Fusarium oxysporum  
PN JP 2001525665-A/50  
PD 11-DEC-2001  
PF 01-MAY-1998 JP 1998548275  
PR 02-MAY-1997 US 60/045400  
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO  
PI CHOI  
PC C1201/68  
CC Strandedness: Single;  
CC Topology: Linear;  
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1. .18  
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1. .18  
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Query Match 100.0%; Score 18; DB 6; Length 18;  
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
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RESULT 3  
AF162898 335 bp DNA linear PLN 15-NOV-2001  
LOCUS Fusarium oxysporum f. sp. conglutinans 5.8S ribosomal RNA gene,  
DEFINITION partial sequence; internal transcribed spacer 2, complete sequence;  
and 28S ribosomal RNA gene, partial sequence.  
ACCESSION AF162898  
VERSION AF162898.1 GI:5690387

KEYWORDS  
SOURCE Fusarium oxysporum f. sp. conglutinans  
ORGANISM Fusarium oxysporum f. sp. conglutinans  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
1 (bases 1 to 335)  
Min,B.R.  
Direct Submission  
Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji  
Dong, Chong Ro-Gu, Seoul 110-743, Korea.  
Location/Qualifiers  
1. .335  
/organism="Fusarium oxysporum f. sp. conglutinans"  
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/product="5.8S ribosomal RNA"  
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/product="28S ribosomal RNA"

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Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
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162 CGTTAATTCGCGTTCCTC 179

RESULT 4  
AF162899 335 bp DNA linear PLN 04-AUG-1999  
LOCUS Fusarium oxysporum f. sp. fragariae 5.8S ribosomal RNA gene,  
DEFINITION partial sequence; internal transcribed spacer 2, complete sequence;  
and 28S ribosomal RNA gene, partial sequence.  
ACCESSION AF162899  
VERSION AF162899.1 GI:5690388  
KEYWORDS Fusarium oxysporum f. sp. fragariae  
Fusarium oxysporum f. sp. fragariae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
1 (bases 1 to 335)  
Min,B.R.  
Direct Submission  
Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji  
Dong, Chong Ro-Gu, Seoul 110-743, Korea  
Location/Qualifiers  
1. .335  
/organism="Fusarium oxysporum f. sp. fragariae"  
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/db\_xref="taxon:100903"  
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<1. .128  
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278. .>335  
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18  
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Db 162 CGTTAATTCGGCTTCCTC 179

RESULT 5  
AF162900

LOCUS AF162900 336 bp DNA linear PLN 04-AUG-1999

DEFINITION Fusarium oxysporum f. sp. raphani 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF162900

VERSION AF162900.1 GI:5690389

KEYWORDS

SOURCE

ORGANISM Fusarium oxysporum f. sp. raphani  
Fusarium oxysporum f. sp. raphani  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 336)  
Min, B. R.  
Direct Submission  
Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji  
Dong, Chong Ro-Gu, Seoul 110-743, Korea

TITLE JOURNAL

FEATURES  
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275..336  
/product="28S ribosomal RNA"

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misc\_RNA

RNA

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18  
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Db 163 CGTTAATTCGGCTTCCTC 180

RESULT 6  
AF339418

LOCUS AF339418 338 bp DNA linear PLN 25-OCT-2002

DEFINITION Fusarium oxysporum strain FS-1 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF339418

VERSION AF339418.1 GI:24369714

KEYWORDS

SOURCE

ORGANISM Fusarium oxysporum  
Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 338)  
Tooley, P. W., Hatziloukas, E., Scott, D. L. Jr. and Carras, M. M.  
Use of ligase chain reaction for detection of Phytophthora  
infestans in potatoes  
Unpublished  
2 (bases 1 to 338)  
Tooley, P. W., Hatziloukas, E., Scott, D. L. Jr. and Carras, M. M.  
Direct Submission  
Submitted (23-JAN-2001) Agricultural Research Service, U.S.

TITLE JOURNAL

Department of Agriculture, 1301 Ditto Ave., Ft. Detrick, MD  
21702-5023, USA

FEATURES  
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Location/Qualifiers  
1..338  
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spacer 2, and 28S ribosomal RNA"

misc\_RNA

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18  
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Db 162 CGTTAATTCGGCTTCCTC 179

RESULT 7  
AY383320

LOCUS AY383320 426 bp DNA linear PLN 05-OCT-2003

DEFINITION Fusarium oxysporum f. sp. vanillae isolate DL-1-1 internal  
transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,  
complete sequence; and internal transcribed spacer 2, partial  
sequence.

ACCESSION AY383320

VERSION AY383320.1 GI:37142968

KEYWORDS

SOURCE

ORGANISM Fusarium oxysporum f. sp. vanillae  
Fusarium oxysporum f. sp. vanillae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 426)  
Wang, Y. Y., Whitehead, M., Zhu, Y., Burns, A., Hocking, T. and Ruan, X. Y.  
ITS 2 sequence  
Unpublished  
2 (bases 1 to 426)  
Wang, Y. Y., Whitehead, M., Zhu, Y., Burns, A., Hocking, T. and Ruan, X. Y.  
Direct Submission  
Submitted (08-SEP-2003) Dept. Plant Pathology, Yunnan Agricultural  
University, Long Tou Street, Kunming, Yunnan 650201, P. R. China

TITLE JOURNAL

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RNA

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ORIGIN

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 309 CGTTAATTCGGCTTCCTC 326

RESULT 8  
AF502842/c

LOCUS AF502842 430 bp DNA linear PLN 13-MAY-2002  
 DEFINITION Leaf litter ascomycete strain its331 isolate 1000502849 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
 ACCESSION AF502842  
 VERSION AF502842  
 KEYWORDS  
 SOURCE leaf litter ascomycete strain its331  
 ORGANISM Eukaryota; Fungi; Ascomycota.  
 REFERENCE 1 (bases 1 to 430)  
 AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
 TITLE Biogeography of leaf litter fungi  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 430)  
 AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA  
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 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGTTAATTCGCGTTCCTC 18  
 Db 82 CGTTAATTCGCGTTCCTC 65  
 RESULT 9  
 LOCUS AY387703 441 bp DNA linear PLN 07-OCT-2003  
 DEFINITION Fusarium oxysporum isolate DU-2-7 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
 ACCESSION AY387703  
 VERSION AY387703  
 KEYWORDS  
 SOURCE Fusarium oxysporum  
 ORGANISM Fusarium oxysporum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
 REFERENCE 1 (bases 1 to 441)  
 AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Li,X.  
 TITLE Fusarium oxysporum isolate DU-2-7 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence Unpublished  
 REFERENCE 2 (bases 1 to 441)  
 AUTHORS Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Li,X.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China  
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 Location/Qualifiers

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 QY 1 CGTTAATTCGCGTTCCTC 18  
 Db 327 CGTTAATTCGCGTTCCTC 344  
 RESULT 10  
 LOCUS AY380575 445 bp DNA linear PLN 04-OCT-2003  
 DEFINITION Fusarium oxysporum f. sp. vanillae internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
 ACCESSION AY380575  
 VERSION AY380575  
 KEYWORDS  
 SOURCE Fusarium oxysporum f. sp. vanillae  
 ORGANISM Fusarium oxysporum f. sp. vanillae  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
 REFERENCE 1 (bases 1 to 445)  
 AUTHORS Wang,Y.Y., Whitehead,M., Burns,A., Zhu,Y.Y., Hocking,T. and Ruan,X.Y.  
 TITLE ITS1, 5.8S and ITS2 rDNA sequence from Fusarium oxysporum f. sp. vanillae Unpublished  
 REFERENCE 2 (bases 1 to 445)  
 AUTHORS Wang,Y.Y., Whitehead,M., Burns,A., Zhu,Y.Y., Hocking,T. and Ruan,X.Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-SEP-2003) Plant Pathology, Yunnan Agricultural University, Longtou Street, Kunming, Yunnan 650201, Peoples Republic of China  
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 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGTTAATTCGCGTTCCTC 18  
 Db 327 CGTTAATTCGCGTTCCTC 344



RESULT 11  
 AY387698 445 bp DNA linear PLN 07-OCT-2003  
 LOCUS  
 DEFINITION Fusarium oxysporum f. sp. vanillae isolate ML-8-1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
 ACCESSION AY387698  
 VERSION  
 KEYWORDS AY387698.1 GI:37362903  
 SOURCE  
 ORGANISM Fusarium oxysporum f. sp. vanillae  
 Fusarium oxysporum f. sp. vanillae  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
 REFERENCE 1 (bases 1 to 445)  
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Liao, B.  
 Molecular investigation of isolates of *Fusarium oxysporum* in relation to the control of root rot disease in vanilla plantfolia Andr  
 TITLE  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 445)  
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Liao, B.  
 Direct Submission  
 JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China  
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 294..>445  
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 rRNA  
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 Query Match 100.0%; Score 18; DB 8; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 CGTTAATTCGGCTTCCTC 18  
 ||||||||||||||||  
 Db 327 CGTTAATTCGGCTTCCTC 344  
 RESULT 12  
 AY387699 445 bp DNA linear PLN 07-OCT-2003  
 LOCUS  
 DEFINITION Fusarium oxysporum f. sp. vanillae isolate DL-4b internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
 ACCESSION AY387699  
 VERSION  
 KEYWORDS AY387699.1 GI:37362904  
 SOURCE  
 ORGANISM Fusarium oxysporum f. sp. vanillae  
 Fusarium oxysporum f. sp. vanillae  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
 REFERENCE 1 (bases 1 to 445)  
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Liao, B.  
 Fusarium oxysporum f. sp. vanillae isolate DL-4b internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal

transcribed spacer 2 sequence  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 445)  
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Liao, B.  
 Direct Submission  
 JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China  
 FEATURES  
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 /db\_xref="taxon:247126"  
 /note="forma\_specialis: vanillae"  
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 136..293  
 /product="5.8S ribosomal RNA"  
 294..>445  
 /product="internal transcribed spacer 2"  
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 rRNA  
 misc\_RNA  
 ORIGIN  
 Query Match 100.0%; Score 18; DB 8; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 CGTTAATTCGGCTTCCTC 18  
 ||||||||||||||||  
 Db 327 CGTTAATTCGGCTTCCTC 344  
 RESULT 13  
 AY387702 445 bp DNA linear PLN 07-OCT-2003  
 LOCUS  
 DEFINITION Fusarium oxysporum isolate ML-7-1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
 ACCESSION AY387702  
 VERSION  
 KEYWORDS AY387702.1 GI:37362907  
 SOURCE  
 ORGANISM Fusarium oxysporum  
 Fusarium oxysporum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
 REFERENCE 1 (bases 1 to 445)  
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Yang, J.  
 Fusarium oxysporum isolate ML-7-1 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence  
 TITLE  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 445)  
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Yang, J.  
 Direct Submission  
 JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China  
 FEATURES  
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 1..445  
 /organism="Fusarium oxysporum"  
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 /isolate="ML-7-1"  
 /db\_xref="taxon:5507"  
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 136..293  
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 /product="internal transcribed spacer 2"  
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 rRNA  
 misc\_RNA  
 ORIGIN

QY	1	CGTAAATTCGGGCTTC	18
Db	327	CGTAAATTCGGGCTTC	344

LOCUS	445 bp	DNA	linear	PLN 07-OCT-2003
DEFINITION	Fusarium oxysporum isolate M-8-4 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.			

REFERENCE  
AUTHORS  
1 (bases 1 to 445)  
Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y  
and Yang, J.

**JOURNAL** Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China

**FEATURES**

**source** 1. .445

**Location/Qualifiers**

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misc_RNA      294. .>445
               /product="internal transcribed spacer 2"
ORIGIN
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RESULT 15	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AY387705	AY387705	445 bp DNA linear Fusarium oxysporum isolate ML-5-2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.	AY387705	AY387705.1	GI:37362910	Fusarium oxysporum Fusarium oxysporum	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocretomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium

REFERENCE	<i>Fusarium oxysporum</i> complex.
AUTHORS	1 (bases 1 to 445) Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Chen,J.B.
TITLE	<i>Fusarium oxysporum</i> isolate M-5-2 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 445)
AUTHORS	Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Chen,J.B.
TITLE	Direct Submission
JOURNAL	Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China
FEATURES	Location/Qualifiers
SOURCE	1..445

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misc_RNA      294. .>445
              /product="internal transcribed spacer 2"
ORIGIN
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Best Local Similarity	100.0%	100.0%	Pred. No.	24
Matches	18	Conservative	0	Mismatches
			0	Indels
				Gaps
Qy	1	CGTAAATCGCGTCTC	18	
Db	327	CGTAAATCGCGTCTC	344	

Search completed: October 1, 2004, 05:17:02  
Job time : 148.108 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 23:11:57 ; Search time 31.9347 Seconds  
(without alignments)  
2394.501 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaacgcgcgtccctc 18

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: N Geneseq\_29Jan04:\*

2: Geneseqn1980s:\*

3: Geneseqn1990s:\*

4: Geneseqn2000s:\*

5: Geneseqn2001s:\*

6: Geneseqn2002s:\*

7: Geneseqn2003as:\*

8: Geneseqn2003bs:\*

9: Geneseqn2003cs:\*

10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	2	AAV83697 Species-B
2	18	100.0	382	3	AAV72783 5.8s rRNA
3	15.4	85.6	538	6	ABQ37055 Oligonuc
4	15.4	85.6	538	6	ABQ37054 Oligonuc
5	15	83.3	127	7	ACA13108 Prokaryot
6	15	83.3	128	4	AA548419 Enterococ
7	15	83.3	250	4	AA547978 Enterococ
8	15	83.3	250	7	ACA12661 Prokaryot
9	15	83.3	1467	7	ACA18462 Prokaryot
10	15	83.3	9212	7	AA113271 Enterococ
11	15	83.3	9212	6	AB899066 Enterococ
12	14.8	82.2	207	9	ADC92275 E. faeciu
13	14.8	82.2	554	6	ABQ14482 Oligonuc
14	14.8	82.2	554	6	ABQ14483 Oligonuc
15	14.8	82.2	650	5	AA505503 Mammalian
16	14.8	82.2	755	7	ACF65787 Photornab
17	14.8	82.2	1200	4	AB112625 Drosophi1
18	14.8	82.2	1231	6	ABQ28091 Oligonuc
19	14.8	82.2	1231	6	ABQ28090 Oligonuc
20	14.8	82.2	3135	7	ACA32983 Prokaryot
21	14.8	82.2	3138	4	AA552883 Enterococ
22	14.8	82.2	3257	4	AB112624 Drosophi1
23	14.8	82.2	4491	4	AB102050 Drosophi1

24	14.8	82.2	5864	4	AB103754 Drosophi1
25	14.8	82.2	10587	7	ACF72118 Photornab
26	14.8	82.2	15428	4	AB102692 Drosophi1
27	14.8	82.2	110000	7	ACF67367_53
28	14.8	82.2	110000	7	ACF65387_5
29	14.4	80.0	65	6	AB226380 Candida e
30	14.4	80.0	306	6	ABK79312 Bacillus
31	14.4	80.0	540	6	ABQ18322 Oligonuc
32	14.4	80.0	540	6	ABQ18323 Oligonuc
33	14.4	80.0	601	6	ABQ34055 Oligonuc
34	14.4	80.0	601	6	ABQ34054 Oligonuc
35	14.4	80.0	939	4	AAH53833 S. epider
36	14.4	80.0	963	6	ABN91904 Stephyloc
37	14.4	80.0	2815	4	AAH54455 S. epider
38	14.4	80.0	5278	4	AB128982 Drosophi1
39	14.4	80.0	6711	8	AA557212 Perunia R
40	14.4	80.0	8440	8	AA557200 8.5 Kb DN
41	14.4	80.0	110000	6	ABQ69245_02
42	14.4	80.0	110000	6	ABQ67197_01
43	14	77.8	549	6	ABQ29382 Oligonuc
44	14	77.8	549	6	ABQ29383 Oligonuc
45	14	77.8	704	6	ABQ36596 Oligonuc

## ALIGNMENTS

RESULT 1	AAV83697 standard; DNA, 18 BP.
ID	AAV83697
XX	AAV83697;
AC	26-FEB-1999 (first entry)
XX	Species-specific probe targeted to the internal transcribed spacer 2.
DE	Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger;
XX	A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;
KW	M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
KW	M. circinellioidei; F. circinellioidei; Rhizopus oryzae; R. microsporus;
KW	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW	Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX	Synthetic.
OS	Fusarium oxysporum.
XX	Key modified_base 1 location/Qualifiers
FT	modified_base 1 /*tag= A
FT	/note= "labelled with digoxigenin"
XX	W09850584-A2.
XX	12-NOV-1998.
XX	01-MAY-1998; 98WO-US008926.
XX	02-MAY-1997; 97US-0045400P.
XX	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX	Morrison CJ, Reiss E, Aidorevich L, Choi JS;
XX	WPI; 1999-034737/03.
XX	New nucleic acid probes for filamentous fungi - for detecting e.g.
XX	Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
XX	Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
XX	species.
XX	Example 1, Page 22; 45pp; English.

```
XX Probes AAV83677-708 are derived from the internal transcribed spacer 2
CC (ITS2) region of various filamentous fungi (see AAV70845-73). The probes
CC are species-specific, and can be used for identifying a species selected
CC from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
CC Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
CC M. indicus, M. circinellus, Rhizoglyphus, Rhizopus oryzae, R.
CC microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus, Abidia
CC corymbifera, Cunninghamella elegans, Pseudallesheria boydii (teleomorph
CC of Scedosporium apiospermum), Penicillium notatum, or Sporothrix
CC schenkl. The probes can be used for differentiating filamentous fungal
CC species from each other and from other medically important fungi
XX
SQ Sequence 18 BP; 2 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CGTTAATTCGGCTTCCTC 18
Db 1 CGTTAATTCGGCTTCCTC 18
RESULT 2
ID AAA72783 standard; DNA; 382 BP.
AC AAA72783;
XX AAA72783;
DT 13-DEC-2000 (first entry)
XX
DE 5.8s rRNA gene sequence.
XX
KM Black spot disease; brown spot disease; fungi; fruit vegetable;
KM field crop; Alternaria; 5.8s rRNA; detection; ds.
XX
OS Fusarium oxysporum.
XX
PN WO200046397-A1.
XX
PD 10-AUG-2000.
XX
PF 24-JAN-2000; 2000WO-US001466.
XX
PR 02-FEB-1999; 99US-00241427.
XX
PA (TECR ) TECHNION RES & DEV FOUND LTD.
PA (KASH/) KASHI Y.
XX
PI Kaeshi Y, Zur G, Sharf R, Hallerman E;
XX
DR WPI; 2000-499381/44.
XX
PT Nucleic acid based assay and kit for detection of Alternaria
PT contamination in food products involves analyzing the sample of food
PT product for nucleic acid sequences unique to Alternaria.
XX
XX
PS Example; Fig 1; 47pp; English.
XX
XX The invention relates to a nucleic acid based method for the detection of
CC Alternaria contamination in a food product. The method involves obtaining
CC and analysing a food product sample for a nucleic acid sequence unique to
CC Alternaria. Detectable levels of the nucleic acid sequence can be used as
CC an indication of Alternaria contamination. Fungi from the genus
CC Alternaria are ubiquitous saprophytes and are economically important
CC pathogens affecting a wide range of plants. Alternaria are the causative
CC agents of black or brown spot disease in many fruits, vegetables and
CC field crops. The method is used for the detection of Alternaria
CC contamination in food products. The present sequence represents the
CC Fusarium oxysporum 5.8s rRNA gene, used in examples illustrating the
CC invention
XX
```

```
SQ Sequence 382 BP; 101 A; 99 C; 87 G; 95 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CGTTAATTCGGCTTCCTC 18
Db 287 CGTTAATTCGGCTTCCTC 304
RESULT 3
ID ABQ37055 standard; DNA; 538 BP.
AC ABQ37055;
XX ABQ37055;
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 23646.
XX
KM Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KM drug; side effect; cancer; central nervous system; cardiovascular;
KM gastrointestinal; respiratory system; single nucleotide polymorphism;
KM SNP; cell differentiation; ds.
XX
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Gueitig D;
XX
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (1) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNPs); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ1410-
CC ABQ5121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 538 BP; 256 A; 160 C; 61 G; 61 T; 0 U; 0 Other;
Query Match 85.6%; Score 15.4; DB 6; Length 538;
```

Best Local Similarity 94.1%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTCCTC 18  
|||||  
Db 105 GTTAATTCGCGTTCCTC 89

## RESULT 4

ABQ37054  
ID ABQ37054 standard; DNA; 538 BP.

XX AC ABQ37054;

XX DT 12-JUN-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 23645.

XX Human; cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;  
XX drug; side effect; cancer; central nervous system; cardiovascular;  
XX gastrointestinal; respiratory system; single nucleotide polymorphism;  
XX SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX PN MO200218632-A2.

XX PD 07-MAR-2002.

XX PF 01-SEP-2001; 2001WO-EP010074.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PR 05-SEP-2000; 2000DE-01044543.

XX PA (EPIC-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX DR WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.

XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CPG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert in a  
CC cytosine (C) but not methylated C to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ3410-  
CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention

XX SQ Sequence 538 BP; 61 A; 61 C; 160 G; 256 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 538;  
Best Local Similarity 94.1%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTCCTC 18  
|||||  
Db 434 GTTAATTCGCGTTCCTC 450

## RESULT 5

ACAI3108/c  
ID ACAI3108 standard; DNA; 127 BP.

XX AC ACAI3108;

XX DT 27-OCT-2003 (revised)

XX DT 19-JUN-2003 (first entry)

DE Prokaryotic essential gene antisense oligonucleotide #978.

XX Antisense; ss; prokaryotic essential gene; cell proliferation;  
XX drug design.

XX OS Archaea.

XX PN MO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 1; SEQ ID NO 978; 176pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the 6213

CC antisense sequences of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences. (updated on 27-OCT-2003 to  
 CC standardise OS field)

XX SQ Sequence 127 BP; 42 A; 31 C; 22 G; 32 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 7; Length 127;

Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Gaps 0;

Matches 15; Conservative 0; Indels 0; Gaps 0;

XX DB 117 GTTAATTCGCGTTCC 103

XX 2 GTTAATTCGCGTTCC 16

RESULT 6

XX AAS48419/C

XX ID AAS48419 standard; DNA; 128 BP.

XX AC AAS48419;

XX DT 13-FEB-2002 (first entry)

XX DE Enterococcus faecalis cellular proliferation inhibitory sequence #899.

XX KM Antisense; ss; prokaryotic cellular proliferation; antibiotic;

XX OS Enterococcus faecalis.

XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009180.

XX PR 21-MAR-2000; 2000US-0191078P.

XX PR 23-MAY-2000; 2000US-0206848P.

XX PR 26-MAY-2000; 2000US-0207727P.

XX PR 23-OCT-2000; 2000US-0242578P.

XX PR 27-NOV-2000; 2000US-0253625P.

XX PR 22-DEC-2000; 2000US-0257931P.

XX PR 16-FEB-2001; 2001US-0269308P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX PI Yamamoto RT, Xu HH;

XX DR WPI; 2001-611495/70.

XX PT New polynucleotides for the identification and development of

XX PT antibiotics, comprise sequences of antisense nucleic acids.

XX PS Claim 1; SEQ ID NO 996; 511pp; English.

XX CC The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the genes,  
 CC their use in the discovery of novel antibiotics, the essential genes  
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
 CC useful for the identification of potential new targets for antibiotic  
 CC development. The antisense nucleic acids can also be used to identify  
 CC antibodies capable of binding to the expressed proteins, and to obtain  
 CC antisense nucleic acid sequence is also useful to screen for homologous  
 CC nucleic acids which are required for cell proliferation in a wide variety  
 CC of organisms. The present sequence is an antisense oligonucleotide of the  
 CC invention. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 128 BP; 42 A; 31 C; 22 G; 33 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 4; Length 128;

Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Gaps 0;

Matches 15; Conservative 0; Indels 0; Gaps 0;

XX DB 118 GTTAATTCGCGTTCC 104

XX 2 GTTAATTCGCGTTCC 16

RESULT 7

XX AAS47978/C

XX ID AAS47978 standard; DNA; 250 BP.

XX AC AAS47978;

XX DT 13-FEB-2002 (first entry)

XX DE Enterococcus faecalis cellular proliferation inhibitory sequence #548.

XX KM Antisense; ss; prokaryotic cellular proliferation; antibiotic;

XX OS Enterococcus faecalis.

XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009180.

XX PR 21-MAR-2000; 2000US-0191078P.

XX PR 23-MAY-2000; 2000US-0206848P.

XX PR 26-MAY-2000; 2000US-0207727P.

XX PR 23-OCT-2000; 2000US-0242578P.

XX PR 27-NOV-2000; 2000US-0253625P.

XX PR 22-DEC-2000; 2000US-0257931P.

XX PR 16-FEB-2001; 2001US-0269308P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX PI Yamamoto RT, Xu HH;

XX DR WPI; 2001-611495/70.

XX PT New polynucleotides for the identification and development of

XX PT antibiotics, comprise sequences of antisense nucleic acids.

XX PS Claim 1; SEQ ID NO 555; 511pp; English.

XX CC The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the genes,  
 CC their use in the discovery of novel antibiotics, the essential genes  
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
 CC useful for the identification of potential new targets for antibiotic  
 CC development. The antisense nucleic acids can also be used to identify  
 CC proteins used in proliferation, to express these proteins, and to obtain  
 CC antibodies capable of binding to the expressed proteins. The proteins can  
 CC be used to screen compounds in rational drug discovery programmes. The  
 CC antisense nucleic acid sequence is also useful to screen for homologous  
 CC nucleic acids which are required for cell proliferation in a wide variety  
 CC of organisms. The present sequence is an antisense oligonucleotide of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SQL Sequence 250 BP; 75 A; 53 C; 47 G; 75 T; 0 U; 0 Other;  
Query Match 83.3%; Score 15; DB 4; Length 250;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 GTTAATTCGCGTTCC 16  
|||||||  
54 GTTAATTCGCGTTCC 40  
DB

RESULT 8  
ACAL2661/c  
ID ACAL2661 standard; DNA; 250 BP.  
XX  
AC ACAL2661;  
XX  
DT 27-OCT-2003 (revised)  
DT 19-JUN-2003 (first entry)  
XX  
DE Prokaryotic essential gene antisense oligonucleotide #531.  
XX  
KW Antisense; ss; prokaryotic essential gene; cell proliferation;  
XX drug design.  
XX  
OS Archaea.  
XX  
FN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 1; SEQ ID NO 531; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the 6213  
CC antisense sequences of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 27-OCT-2003 to  
CC standardise OS field)  
XX

SQL Sequence 250 BP; 75 A; 53 C; 47 G; 75 T; 0 U; 0 Other;  
Query Match 83.3%; Score 15; DB 7; Length 250;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 GTTAATTCGCGTTCC 16  
|||||||  
54 GTTAATTCGCGTTCC 40  
DB

RESULT 9  
ACAL8462  
ID ACAL8462 standard; DNA; 1467 BP.  
XX  
AC ACAL8462;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Prokaryotic essential gene #119.  
XX  
KW Antisense; ds; prokaryotic essential gene; cell proliferation;  
XX drug design; gene.  
XX  
OS Enterococcus faecalis.  
XX  
FN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 14; SEQ ID NO 6332; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway;  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs; or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
 CC prokaryotic essential genes. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SO Sequence 1467 BP; 464 A; 268 C; 311 G; 424 T; 0 U; 0 Other;  
 Query Match 83.3%; Score 15; DB 7; Length 1467;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTAATTGCGCTTCC 16  
 Db 1027 GTTAATTGCGCTTCC 1041

RESULT 10  
 AAX13271  
 ID AAX13271 standard; DNA; 9212 BP.

XX AAX13271;

DT 19-MAR-1999 (first entry)

XX Enterococcus faecalis genome contig SEQ ID NO:334.

XX Enterococcus faecalis; contig; detection; Enterococcal infection;

KM vaccine; attenuation; computer readable medium; ds.

XX Enterococcus faecalis.

XX WO9850555-A2.

PD 12-NOV-1998.

XX 04-MAY-1998; 98WO-US008985.

XX 06-MAY-1997; 97US-0044031P.

XX 16-MAY-1997; 97US-004655P.

XX 14-NOV-1997; 97US-0066009P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunsch CA, Dillon PJ, Barash S;

XX WPI; 1999-045171/04.

PT New isolated Enterococcus faecalis polynucleotides and polypeptides -  
 PT used to develop products for the detection of Enterococcus and for use in  
 PT vaccines for prevention or attenuation of Enterococcus infection.

XX Claim 1; Page 1436-1441; 2084pp; English.

CC A computer readable medium has been developed which has recorded on it  
 CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.

CC AAX12938 to AAX13919 represent these nucleotide sequences which are  
 CC primary nucleotide sequences, also known as contigs. The computer-based  
 CC system can identify fragments of the Enterococcus faecalis genome with  
 CC commercial importance. The products can be used to detect the presence of  
 CC Enterococcus faecalis in samples. They can also be used for diagnosing  
 CC Enterococcal infection in an animal and monitoring progression of  
 CC disease, and for identifying agents which can be used to modulate the  
 CC growth or pathogenicity of Enterococcus faecalis, or another related  
 CC organism, in vivo or in vitro. In particular the polypeptides encoded by  
 CC the Enterococcus faecalis nucleotide sequences can be used in vaccines to  
 CC prevent or attenuate an Enterococcal infection

SO Sequence 9212 BP; 3045 A; 1564 C; 2061 G; 2529 T; 0 U; 13 Other;  
 Query Match 83.3%; Score 15; DB 2; Length 9212;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTAATTGCGCTTCC 16  
 Db 4989 GTTAATTGCGCTTCC 5003

RESULT 11  
 ABS99066  
 ID ABS99066 standard; DNA; 9212 BP.

XX ABS99066;

DT 18-DEC-2002 (first entry)

XX Enterococcus faecalis contig sequence #334.

KM Computer readable medium; Enterococcus faecalis; microbe; growth;  
 KM pathogenicity; vaccine; resistance; Enterococcal infection; commercial;  
 KM therapeutic; industrial; fermenting; sugar source; metabolite; vaccine;  
 KM biochip technology; antibacterial; modulator of nucleic acid expression;  
 KM contig; ds.

XX Enterococcus faecalis.

XX US2002120116-A1.

XX 29-AUG-2002.

XX 04-MAY-1998; 98US-00070927.

XX 04-MAY-1998; 98US-00070927.

XX (KUNS/) KUNSCH C A.

XX (DILL/) DILLON P J.

XX (BARA/) BARASH S.

XX Kunsch CA, Dillon PJ, Barash S;

XX WPI; 2002-750065/81.

PT Computer readable medium having recorded on it a Enterococcus faecalis  
 PT nucleotide sequence useful for detecting diseases related to Enterococcus  
 PT infections in animals.

XX Claim 1; Page; 119pp; English.

CC The present invention relates to a new computer readable medium with an  
 CC Enterococcus faecalis nucleotide sequence. The invention is useful to  
 CC diagnose the presence of *E. faecalis* in a sample or determining the  
 CC presence of a specific microbe in a sample. The invention is also useful  
 CC for modulating the growth or pathogenicity of *E. faecalis*, in a vaccine to  
 CC confer resistance to Enterococcal infection, for commercial, therapeutic  
 CC and industrial purposes, and for fermenting a particular sugar source or  
 CC to produce a particular metabolite. The invention is useful for detecting  
 CC diseases related to Enterococcus infections in animals, and for detecting  
 CC *E. faecalis* using biochip technology. The present nucleic acid sequence



CC represents an Enterococcus faecalis contig DNA sequence of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format directly from USPTO  
CC at http:seqdata.uspto.gov

XX Sequence 9212 BP; 3045 A; 1564 C; 2061 G; 2529 T; 0 U; 13 Other;

Query Match 83.3%; Score 15; DB 6; Length 9212;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 16  
DB 4989 GTTAATTCGCGTTC 5003

RESULT 12  
ADC92275/C  
ID ADC92275 standard; DNA; 207 BP.

XX ADC92275;

XX 01-JAN-2004 (first entry)

DE E. faecium DNA sequence SEQ ID 1902.

XX ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;  
KW abdominal-pelvic infection.

XX Enterococcus faecium.

XX US6583275-B1.

XX 24-JUN-2003.

XX 30-JUN-1998; 98US-00107532.

XX 02-JUL-1997; 97US-0051571P.

XX 14-MAY-1998; 98US-0085598P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Doucette-Stamm LA, Bush D;

XX WPI; 2003-799836/75.

XX P-PSDB; ADC95929.

PT New isolated nucleic acid derived from Enterococcus faecium encoding an  
PT Enterococcus faecium polypeptide useful for detection, prevention and  
PT treatment of a pathological condition resulting from a bacterial  
PT infection.

XX Example 1; SEQ ID NO 1902; 243bp; English.

CC The invention relates to an isolated nucleic acid derived from  
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having  
CC one of 10 fully defined sequences given in the (or comprising 40  
CC sequential nucleotides chosen from any of the nucleic acids, its  
CC complement or sequences hybridising to it). Also included are a  
CC recombinant vector comprising the nucleic acid operably linked to  
CC transcription regulatory element, a cell comprising the vector and a  
CC single-stranded probe comprising the nucleic acid. The nucleic acids are  
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.  
CC The nucleic acids are useful for diagnosing pathological conditions  
CC resulting from E. faecium bacterial infection (e.g. urinary tract  
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic  
CC infection) and for screening drugs such as agonists and antagonists. The  
CC nucleic acid is useful for recombinant production of Candida albicans -  
CC derived peptides or antisense polypeptides. Pharmaceutical compositions  
CC and vaccines containing the nucleic acid are useful for preventing or  
CC treating Enterococcus faecium infections. The present sequence represents  
XX one if the disclosed E. faecium nucleic acids.

SQ Sequence 207 BP; 68 A; 36 C; 47 G; 55 T; 0 U; 1 Other;

Query Match 82.2%; Score 14.8; DB 9; Length 207;  
Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
DB 84 CGTTAATTCCTTTCCTC 67

RESULT 13  
AB014482  
ID AB014482 standard; DNA; 554 BP.

XX AB014482;

XX 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1073.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;

KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.

XX Homo sapiens.

XX WO200218632-A2.

XX 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP010074.

XX 01-SEP-2000; 2000DE-01043826.

XX 05-SEP-2000; 2000DE-01044543.

XX (EPIC-) EPICENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. AB013410-  
CC AB054121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention

XX Sequence 554 BP; 76 A; 67 C; 169 G; 242 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 554;

Best Local Similarity 88.9%; Pred. No. 3.5e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCTC 18  
113 CGTTAATTCGGCTTCCTC 130  
Db

RESULT 14  
ABQ14483/C  
ID ABQ14483 standard; DNA; 554 BP.  
XX  
AC ABQ14483;  
XX

DT 12-JUN-2002 (first entry)  
XX

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1074.  
XX

KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KM drug; side effect; cancer; central nervous system; cardiovascular;  
KM gastrointestinal; respiratory system; single nucleotide polymorphism;  
KM SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX

PN W0200218632-A2.  
XX

PD 07-MAR-2002.  
XX

PF 01-SEP-2001; 2001WO-EP010074.  
XX

PR 01-SEP-2000; 2000DE-01043825.  
XX

PR 05-SEP-2000; 2000DE-01044543.  
XX

PA (EPIC-) EPIGENOMICS AG.  
XX

PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX

DR WPI; 2002-371829/40.  
XX

PT Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX

PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX

CC This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNPs); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ13410-  
CC ABQ34121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX

XX Sequence 554 BP; 242 A; 169 C; 67 G; 76 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 554;  
Best Local Similarity 88.9%; Pred. No. 3.5e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCTC 18  
442 CGTTAATTCGGCTTCCTC 425  
Db

RESULT 15  
AAS05503  
ID AAS05503 standard; DNA; 650 BP.  
XX  
AC AAS05503;  
XX

DT 07-SEP-2001 (first entry)  
XX

DE Mammalian vestibular system geotactic behaviour modulator gene #103.  
XX

KW Mammalian vestibular system; invertebrate; geotactic behaviour; vertigo;  
KM graviperceptive disorder; motion sickness; labyrinthitis; syphilis; ds;  
KM Meniere's disease; acoustic neuroma; multiple sclerosis; epilepsy;  
KM trauma; infection of the middle ear; ototoxic agent exposure.  
XX

OS Drosophila melanogaster.  
XX

PN W0200140519-A2.  
XX

PD 07-JUN-2001.  
XX

PF 01-DEC-2000; 2000WO-US032639.  
XX

PR 02-DEC-1999; 99US-0168579P.  
XX

PR 26-SEP-2000; 2000US-00669751.  
XX

PA (NEUR-) NEUROSCIENCES RES FOUND INC.  
XX

PI Greenspan RJ;  
XX

DR WPI; 2001-356159/37.  
XX

PT New isolated nucleic acid having mammalian vestibular system-modulating  
PT activity useful in the treatment of disorders such as motion sickness and  
PT vertigo.  
XX

PS Claim 59; Page 126; 179pp; English.  
XX

CC The sequences shown in AAS05401-AAS05661 represent DNA with mammalian  
CC vestibular system-modulating activity. The DNA sequences can be used in a  
CC method whereby a first and second strain of an invertebrate is obtained,  
CC and both are subjected to conditions in which the strains exhibit  
CC different geotactic behaviour. Genes that are differentially expressed in  
CC the first strain relative to the second strain are then identified.  
CC Mammalian genes having substantially the same nucleic acid sequence as  
CC these modulate the mammalian vestibular system. Compounds containing  
CC these genes are used to decrease the symptoms of graviperceptive  
CC disorders such as motion sickness, vertigo, labyrinthitis, Meniere's  
CC disease, acoustic neuroma, multiple sclerosis, syphilis, trauma,  
CC infection of the middle ear, exposure to ototoxic agents and epilepsy  
XX

XX Sequence 650 BP; 182 A; 181 C; 167 G; 120 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 5; Length 650;  
Best Local Similarity 88.9%; Pred. No. 3.5e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCTC 18  
69 CGTTAATTCGGCTTCCTC 86  
Db

Search completed: October 1, 2004, 03:41:16  
Job time : 37.9347 secs

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:09:43 ; Search time 5.93182 Seconds

(without alignments)  
1683.989 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18  
Sequence: 1 cgttaattcgcgttcctc 18Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: Issued Patents NA: \*  
2: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/PCUTS\_COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	US-09-423-233-50	Sequence 50, Appl
2	15	83.3	615	US-09-134-000C-314	Sequence 314, Ap
3	14.8	82.2	207	US-09-107-532A-1902	Sequence 1902, Ap
4	14.8	82.2	650	US-09-669-751-103	Sequence 103, Ap
5	14.8	82.2	2457	US-09-134-000C-2950	Sequence 2950, Ap
6	14.4	80.0	963	US-09-134-001C-1367	Sequence 1367, Ap
7	14	77.8	3208	US-07-972-791-3	Sequence 3, Appl
8	14	77.8	3346	US-07-972-791-7	Sequence 7, Appl
9	14	77.8	3347	US-07-972-791-5	Sequence 5, Appl
10	14	77.8	3347	US-07-972-791-2	Sequence 2, Appl
11	14	77.8	3347	US-07-972-791-8	Sequence 8, Appl
12	14	77.8	3361	US-07-972-791-6	Sequence 6, Appl
13	14	77.8	3361	US-07-972-791-6	Sequence 7, Appl
14	14	77.8	702	US-09-543-681A-4125	Sequence 4125, Ap
15	13.8	76.7	1356	US-09-328-352-1886	Sequence 1886, Ap
16	13.8	76.7	1386	US-09-134-001C-984	Sequence 984, Ap
17	13.8	76.7	5679	US-08-844-274-10	Sequence 10, Appl
18	13.8	76.7	5679	US-09-598-421-10	Sequence 10, Appl
19	13.8	76.7	6723	US-08-844-274-13	Sequence 13, Appl
20	13.8	76.7	6723	US-08-844-274-14	Sequence 14, Appl
21	13.8	76.7	6723	US-09-598-421-13	Sequence 13, Appl
22	13.8	76.7	6723	US-09-598-421-14	Sequence 14, Appl
23	13.8	76.7	7560	US-08-844-274-20	Sequence 20, Appl
24	13.8	76.7	7560	US-09-598-421-20	Sequence 20, Appl
25	13.8	76.7	9704	US-09-814-951A-3	Sequence 3, Appl
26	13.8	76.7	9717	US-09-251-645-1	Sequence 1, Appl
27	13.8	76.7	12666	US-08-961-527-137	Sequence 137, Ap

c	28	13.8	76.7	49795	4	US-09-453-7028-60	Sequence 60, Appl
c	29	13.6	75.6	3378	1	US-07-972-791-1	Sequence 1, Appl
c	30	13.4	74.4	549	4	US-09-328-352-1243	Sequence 3283, Ap
c	31	13.4	74.4	720	4	US-09-134-000C-1003	Sequence 1003, Ap
c	32	13.4	74.4	1293	4	US-09-489-039A-409	Sequence 409, Ap
c	33	13.4	74.4	2122	4	US-09-833-381-1392	Sequence 1392, Ap
c	34	13.4	74.4	2430	4	US-09-620-312D-176	Sequence 176, Ap
c	35	13.4	74.4	2967	4	US-09-185-501B-12	Sequence 12, Appl
c	36	13.4	74.4	10144	4	US-10-204-708-94	Sequence 94, Appl
c	37	13.2	73.3	23	3	US-09-561-741A-10	Sequence 10, Appl
c	38	13.2	73.3	23	4	US-09-558-795-10	Sequence 10, Appl
c	39	13.2	73.3	305	4	US-09-489-039A-11	Sequence 11, Appl
c	40	13.2	73.3	305	4	US-09-489-039A-1305	Sequence 1305, Ap
c	41	13.2	73.3	465	4	US-09-181-183-1	Sequence 1, Appl
c	42	13.2	73.3	471	3	US-09-280-040-1	Sequence 1, Appl
c	43	13.2	73.3	471	4	US-09-277-700-1	Sequence 1, Appl
c	44	13.2	73.3	471	4	US-09-874-585D-1	Sequence 1, Appl
c	45	13.2	73.3	471	4	US-09-874-585D-1	Sequence 1, Appl

## ALIGNMENTS

```
RESULT 1
US-09-423-233-50
; Sequence 50, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 03063-0331mp
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-09-423-233-50

Query Match      100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CGTTAATTCGCTTCCTC 18
Db      1 CGTTAATTCGCTTCCTC 18

RESULT 2
US-09-134-000C-314
; Sequence 314, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 314
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-314

Query Match      83.3%; Score 15; DB 4; Length 615;
```

Best Local Similarity 100.0%; Pred. No. 37;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 16  
Db 172 GTTAATTCGCGTTC 186

## RESULT 3

US-09-107-532A-1902/c  
; Sequence 1902, Application US/09107532A  
; Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 1902:

SEQUENCE CHARACTERISTICS:

LENGTH: 207 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...207

SEQUENCE DESCRIPTION: SEQ ID NO: 1902:

US-09-107-532A-1902

Query Match 82.2%; Score 14.8; DB 4; Length 207;

Best Local Similarity 88.9%; Pred. No. 44;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTC 18  
Db 84 CGTTAATTCGCGTTC 67

## RESULT 4

US-09-669-751-103

; Sequence 103, Application US/09669751

Patent No. 6551575

GENERAL INFORMATION:

APPLICANT: Greenspan, Ralph J.

TITLE OF INVENTION: Methods for Identifying Compounds for

TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to

TITLE OF INVENTION: Balance and the Perception of Gravity

FILE REFERENCE: P-NI 3864

CURRENT APPLICATION NUMBER: US/09/669,751

CURRENT FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US 60/168,579

PRIOR FILING DATE: 1999-12-02

NUMBER OF SEQ ID NOS: 261

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 103

LENGTH: 650

TYPE: DNA

ORGANISM: Drosophila

US-09-669-751-103

Query Match 82.2%; Score 14.8; DB 4; Length 650;

Best Local Similarity 88.9%; Pred. No. 48;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTC 18  
Db 69 CGTTAATTCGCGTTC 86

## RESULT 5

US-09-134-000C-2950/c

; Sequence 2950, Application US/09134000C

Patent No. 6617155

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2950

LENGTH: 2457

TYPE: DNA

ORGANISM: Enterococcus faecalis

US-09-134-000C-2950

Query Match 82.2%; Score 14.8; DB 4; Length 2457;

Best Local Similarity 88.9%; Pred. No. 54;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTC 18  
Db 963 CGTTAATTCGCGTTC 946

## RESULT 6

US-09-134-001C-1367/c

; Sequence 1367, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 1367  
LENGTH: 963  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-1367

Query Match 80.0%; Score 14.4; DB 4; Length 963;  
Best Local Similarity 93.8%; Pred. No. 82;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TTAATTGCGCTTC 18  
|||||  
Db 640 TTAATTGCGCTTC 625

RESULT 7  
US-07-972-791-3/c  
Sequence 3, Application US/07972791  
Patent No. 5348857  
GENERAL INFORMATION:  
APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAVEL, GAMBERELL, HEWITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3208 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella abortus  
STRAIN: biovar 1 (S2308)  
US-07-972-791-3

Query Match 77.8%; Score 14; DB 1; Length 3208;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCTTC 15  
|||||  
Db 1488 GTTAATTCGCTTC 1475

RESULT 8  
US-07-972-791-7/c  
Sequence 7, Application US/07972791

Patent No. 5348857  
GENERAL INFORMATION:  
APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAVEL, GAMBERELL, HEWITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3345 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella melitensis  
STRAIN: biovar 1  
US-07-972-791-7

Query Match 77.8%; Score 14; DB 1; Length 3345;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCTTC 15  
|||||  
Db 1487 GTTAATTCGCTTC 1474

RESULT 9  
US-07-972-791-5/c  
Sequence 5, Application US/07972791  
Patent No. 5348857  
GENERAL INFORMATION:  
APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAVEL, GAMBERELL, HEWITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3346 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella neotomae  
US-07-972-791-5

Query Match 77.8%; Score 14; DB 1; Length 3346;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGGCTTC 15  
DB 1488 GTTAATTCGGCTTC 1475

RESULT 10  
US-07-972-791-2/c  
Sequence 2, Application US/07972791  
Patent No. 5348857  
GENERAL INFORMATION:  
APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAVEL, GAMARELL, HEWITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3347 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella abortus

STRAIN: biovar 5  
US-07-972-791-2

Query Match 77.8%; Score 14; DB 1; Length 3347;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGGCTTC 15  
DB 1488 GTTAATTCGGCTTC 1475

RESULT 11  
US-07-972-791-8/c  
Sequence 8, Application US/07972791  
Patent No. 5348857  
GENERAL INFORMATION:  
APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAVEL, GAMARELL, HEWITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3347 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella suis  
STRAIN: biovar 1  
US-07-972-791-8

Query Match 77.8%; Score 14; DB 1; Length 3347;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGGCTTC 15  
DB 1488 GTTAATTCGGCTTC 1475

RESULT 12  
US-07-972-791-6/c  
Sequence 6, Application US/07972791  
Patent No. 5348857  
GENERAL INFORMATION:  
APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.

APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAVEL, GAMBRELL, HEMITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3361 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella ovis  
US-07-972-791-6

Query Match 77.8%; Score 14; DB 1; Length 3361;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 15  
|||  
Db 1503 GTTAATTCGCGTTC 1450

RESULT 13  
5310649-1/c  
Patent No. 5310649  
APPLICANT: Ficht, Thomas A.; Sowa, Blair A.; Adams, Gary L.  
TITLE OF INVENTION: METHOD OF DETECTING SPECIES AND BIOVARS  
OF BRUCELLA  
NUMBER OF SEQUENCES: 11  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/527,017  
FILING DATE: 22-MAY-1990  
SEQ ID NO: 1;  
LENGTH: 3434  
5310649-1

Query Match 77.8%; Score 14; DB 6; Length 3434;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 15  
|||  
Db 1692 GTTAATTCGCGTTC 1679

RESULT 14  
US-09-543-681A-4125/c  
Sequence 4125, Application US/09543681A  
Patent No. 6605709

GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 4125  
LENGTH: 702  
TYPE: DNA  
ORGANISM: Proteus mirabilis  
US-09-543-681A-4125

Query Match 76.7%; Score 13.8; DB 4; Length 702;  
Best Local Similarity 88.2%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCCTC 18  
|||  
Db 44 GTTAATTCGCGATCCTC 28

RESULT 15  
US-09-328-352-1886  
Sequence 1886, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 1886  
LENGTH: 1356  
TYPE: DNA  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-1886

Query Match 76.7%; Score 13.8; DB 4; Length 1356;  
Best Local Similarity 88.2%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCCTC 18  
|||  
Db 600 GTTAATTCGCGTTCCTC 616

Search completed: October 1, 2004, 08:05:44  
Job time : 7.33182 secs

*This Page Blank (uspto)*



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:20:11 ; Search time 73.104 Seconds

(without alignments)  
1244.847 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaattcgcgttcctc 18

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
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6: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
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8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
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11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
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15: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	US-10-046-955-50	Sequence 50, Appl
2	15.4	85.6	4461	US-10-437-963-93618	Sequence 9613, A
3	15	83.3	127	US-10-282-122A-978	Sequence 978, App
4	15	83.3	128	US-09-815-242-996	Sequence 996, App
5	15	83.3	250	US-09-815-242-555	Sequence 555, App
6	15	83.3	250	US-10-282-122A-531	Sequence 531, App
7	15	83.3	1467	US-10-282-122A-6332	Sequence 6332, App
8	15	83.3	9212	US-09-070-927A-334	Sequence 334, App
9	14.8	82.2	262	US-09-535-459-1371	Sequence 1371, App
10	14.8	82.2	438	US-10-424-599-43896	Sequence 43896, A
11	14.8	82.2	585	US-10-437-963-81762	Sequence 81762, A
12	14.8	82.2	650	US-10-255-536-103	Sequence 103, App
13	14.8	82.2	3135	US-10-282-122A-20853	Sequence 20853, A
14	14.8	82.2	3138	US-09-815-242-6520	Sequence 6520, App

15	14.8	82.2	2731748	17	US-10-297-465A-1	Sequence 1, Appl
16	14.4	80.0	65	15	US-10-032-585-259	Sequence 259, App
17	14.4	80.0	230	13	US-10-085-783A-247	Sequence 247, App
18	14.4	80.0	230	16	US-10-242-535A-247	Sequence 247, App
19	14.4	80.0	306	9	US-09-974-300-6603	Sequence 6603, App
20	14.4	80.0	559	15	US-10-029-386-7594	Sequence 7594, App
21	14.4	80.0	651	13	US-10-027-632-266929	Sequence 266929, App
22	14.4	80.0	651	16	US-10-027-632-266929	Sequence 266929, App
23	14.4	80.0	914	16	US-10-369-493-35000	Sequence 35000, A
24	14.4	80.0	948	13	US-10-424-599-78398	Sequence 78398, A
25	14.4	80.0	1520	13	US-10-424-599-116221	Sequence 116221, App
26	14.4	80.0	6711	15	US-10-341-200-42	Sequence 42, Appl
27	14.4	80.0	8440	15	US-10-341-200-19	Sequence 19, Appl
28	14.4	80.0	1163020	16	US-10-398-221-10	Sequence 10, Appl
29	14.4	80.0	3011208	16	US-10-398-221-2058	Sequence 2058, App
30	14	77.8	926	13	US-10-424-599-59512	Sequence 59512, A
31	14	77.8	1496	13	US-10-424-599-59514	Sequence 59514, A
32	14	77.8	1585	17	US-10-437-963-93652	Sequence 93652, A
33	14	77.8	1773	17	US-10-437-963-93609	Sequence 93609, A
34	14	77.8	1806	17	US-10-437-963-93471	Sequence 93471, A
35	14	77.8	2102	17	US-10-437-963-93615	Sequence 93615, A
36	14	77.8	2455	17	US-10-437-963-93584	Sequence 93584, A
37	14	77.8	2569	16	US-10-369-493-36500	Sequence 36500, A
38	14	77.8	5917	17	US-10-437-963-93655	Sequence 93655, A
39	14	77.8	13627	17	US-10-433-793-6	Sequence 6, Appl
40	13.8	76.7	285	12	US-09-987-899-201	Sequence 201, App
41	13.8	76.7	346	12	US-10-424-599-93085	Sequence 93085, A
42	13.8	76.7	407	12	US-09-987-899-182	Sequence 182, App
43	13.8	76.7	418	12	US-09-987-899-160	Sequence 160, App
44	13.8	76.7	432	12	US-09-987-899-168	Sequence 168, App
45	13.8	76.7	432	12	US-09-987-899-169	Sequence 169, App

#### ALIGNMENTS

RESULT 1  
US-10-046-955-50  
Sequence 50, Application US/10046955  
Publication No. US20030129600A1  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America, as Represented by the  
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease  
APPLICANT: Control and Prevention  
APPLICANT: Morrison, Christine J.  
APPLICANT: Reiss, Errol  
APPLICANT: Aidorevich, Lilianna  
APPLICANT: Choi, Jong Soo  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
FILE REFERENCE: 6395-62064  
CURRENT APPLICATION NUMBER: US/10/046, 955  
CURRENT FILING DATE: 2002-06-04  
PRIOR APPLICATION NUMBER: US 09/423, 233  
PRIOR FILING DATE: 2000-06-27  
PRIOR APPLICATION NUMBER: PCT/US98/08926  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: US 60/045, 400  
PRIOR FILING DATE: 1997-05-02  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 50  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Fusarium oxysporum  
US-10-046-955-50  
Query Match 100.0%; Score 18; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.3; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0

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Db      1  CGTTAATTCGGCTTCCTC 18

RESULT 2
US-10-437-963-93618/c
; Sequence 93618, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 93618
; LENGTH: 4461
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91986C.1
US-10-437-963-93618

Query Match      85.6%; Score 15.4; DB 17; Length 4461;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  GTTAATTCGGCTTCCTC 18
Db      1209 GTTAATTCACGTTCTC 1193

RESULT 3
US-10-282-122A-978/c
; Sequence 978, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
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; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 978
; LENGTH: 127
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-978

Query Match      83.3%; Score 15; DB 13; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  GTTAATTCGGCTTC 16
Db      117  GTTAATTCGGCTTC 103

RESULT 4
US-09-815-242-996/c
; Sequence 996, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 996
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-996

Query Match      83.3%; Score 15; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  GTTAATTCGGCTTC 16
Db      118  GTTAATTCGGCTTC 104
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RESULT 5
US-09-815-242-555/c
; Sequence 555, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815.242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 555
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-555

Query Match      83.3%; Score 15; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTAATTCGCGTTCC 16
      |||||
Db      54 GTTAATTCGCGTTCC 40

RESULT 6
US-10-282-122A-531/c
; Sequence 531, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
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; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 531
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-531

Query Match      83.3%; Score 15; DB 13; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTAATTCGCGTTCC 16
      |||||
Db      54 GTTAATTCGCGTTCC 40

RESULT 7
US-10-282-122A-6332
; Sequence 6332, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6332  
LENGTH: 1467  
TYPE: DNA  
ORGANISM: Enterococcus faecalis  
US-10-282-122A-6332

Query Match 83.3%; Score 15; DB 13; Length 1467;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 16  
Db 1027 GTTAATTCGCGTTC 1041

RESULT 8  
US-09-070-927A-334  
Sequence 334, Application US/09070927A  
Patent No. US20020120116A1  
GENERAL INFORMATION:

APPLICANT: Charles A. Kunsch  
Patrick J. Dillon  
Steven Barash

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
NUMBER OF SEQUENCES: 982  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,927A  
FILING DATE: 04-May-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,655  
FILING DATE: 1997-05-16  
APPLICATION NUMBER: 60/044,031  
FILING DATE: 1997-05-06

APPLICATION NUMBER: 60/066,009  
FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PB369  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 334:

SEQUENCE CHARACTERISTICS:  
LENGTH: 9212 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 334:

US-09-070-927A-334

Query Match 83.3%; Score 15; DB 9; Length 9212;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 16  
Db 4989 GTTAATTCGCGTTC 5003

RESULT 9

US-09-535-459-1371/C  
Sequence 1371, Application US/09535459  
Publication No. US20030040615A1  
GENERAL INFORMATION:

APPLICANT: Sellhammer, Jeffrey J.  
APPLICANT: Delegeane, Angelo M.

APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.

APPLICANT: Mullahy, Sara J.  
APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULES  
FILE REFERENCE: PD-1014 CIP

CURRENT APPLICATION NUMBER: US/09/535,459  
CURRENT FILING DATE: 2000-03-24

Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 2170

SOFTWARE: PERL Program  
SEQ ID NO 1371

LENGTH: 262  
TYPE: DNA

ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: msc feature  
OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01153717

US-09-535-459-1371

Query Match 82.2%; Score 14.8; DB 10; Length 262;  
Best Local Similarity 88.9%; Pred. No. 4.6e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTC 18  
Db 102 CTTAATTCGCGTTC 85

RESULT 10

US-10-424-599-43896  
Sequence 43896, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J  
APPLICANT: Kovalic, David K

APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 43896

LENGTH: 438  
TYPE: DNA

ORGANISM: Glycine max  
FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT3847\_139637C.1  
US-10-424-599-43896

Query Match 82.2%; Score 14.8; DB 13; Length 438;  
Best Local Similarity 88.9%; Pred. No. 4.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTC 18  
Db 297 CGTTAATTCGCGTTC 314

```
RESULT 11
US-10-437-963-81762
; Sequence 81762, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 81762
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81256C.1
US-10-437-963-81762

Query Match      82.2%  Score 14.8;  DB 17;  Length 585;
Best Local Similarity 88.9%;  Pred. No. 5e+02;
Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      1  CGTTAATTCGGCTTCCTC 18
      |||||
DB      230  CGTTCATTCGGCTTCAC 247

RESULT 12
US-10-255-536-103
; Sequence 103, Application US/10255536
; Publication No. US20030087807A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/10/255,536
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/669,751
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Drosophila
US-10-255-536-103

Query Match      82.2%  Score 14.8;  DB 15;  Length 650;
Best Local Similarity 88.9%;  Pred. No. 5e+02;
Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      1  CGTTAATTCGGCTTCCTC 18
      |||||
DB      69  CGTTCATTCGGCTTCCTC 86

RESULT 13
US-10-282-122A-20853/c
```

```
; Sequence 20853, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20853
; LENGTH: 3135
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-20853

Query Match      82.2%  Score 14.8;  DB 13;  Length 3135;
Best Local Similarity 88.9%;  Pred. No. 5.9e+02;
Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      1  CGTTAATTCGGCTTCCTC 18
      |||||
DB      1644  CGTTAATTCGGCTTCCTC 1627

RESULT 14
US-09-815-242-6520/c
; Sequence 6520, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
```

```

; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6520
; LENGTH: 3138
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3138)
US-09-815-242-6520

```

```

Query Match      82.2%; Score 14.8; DB 9; Length 3138;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 CGTTAATTCGGCTTCCTC 18
        |||||
Db      1644 CGTTAATTCGGCTTCCTC 1627

```

```

RESULT 15
US-10-297-465A-1
; Sequence 1, Application US/10297465A
; Publication No. US20040142413A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Andrew
; APPLICANT: Reinach, Fernando
; APPLICANT: Setubal, Joao
; APPLICANT: Medians, Joao
; APPLICANT: Arruda, Paulo
; TITLE OF INVENTION: Isolated Genome of Xylella fastidiosa and Uses Thereof
; FILE REFERENCE: PAPER 202 US (10213376)
; CURRENT APPLICATION NUMBER: US/10/297,465A
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01618
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,906
; PRIOR FILING DATE: 2001-06-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2731748
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-297-465A-1

```

```

Query Match      82.2%; Score 14.8; DB 17; Length 2731748;
Best Local Similarity 88.9%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 CGTTAATTCGGCTTCCTC 18
        |||||
Db      2184289 CGTTAATTCGGCTTCCTC 2184306

```

Search completed: October 1, 2004, 08:53:55  
Job time : 83.304 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 ; Search time 252 Seconds  
(without alignments)  
2133.013 Million cell updates/sec

Title: US-10-046-955-50  
Perfect score: 18  
Sequence: 1 cgttaatcgcttcctc 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estc1:\*  
10: gb\_estc2:\*  
11: gb\_hic:\*  
12: gb\_estc3:\*  
13: gb\_estc4:\*  
14: gb\_estc5:\*  
15: em\_estlum:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrc:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vr1:\*  
28: gb\_gss2:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.4	91.1	667	13	BQ483402
C 2	15.4	85.6	262	28	A2359925
C 3	15.4	85.6	277	28	BH452985
C 4	15.4	85.6	402	29	CG858920

Result No.	Score	Query Match	Length	ID	Description
C 5	15.4	85.6	493	28	A2498171
C 6	15.4	85.6	499	28	BH144783
C 7	15.4	85.6	588	28	BZ508556
C 8	15.4	85.6	740	29	AG042918
C 9	15.4	85.6	819	29	CG810640
C 10	15.4	85.6	902	14	CA278228
C 11	15.4	85.6	908	13	BX434865
C 12	15.4	85.6	921	14	CK288913
C 13	15.4	85.6	968	14	CK286745
C 14	15.4	85.6	1000	12	BP512280
C 15	15.4	85.6	1278	12	BM543811
C 16	15.4	83.3	311	10	AM833312
C 17	15.4	83.3	543	12	BI881942
C 18	15.4	83.3	547	14	CB406133
C 19	15.4	83.3	563	14	CB406132
C 20	15.4	83.3	636	10	BE557132
C 21	15.4	83.3	728	12	BG723264
C 22	15.4	83.3	870	14	CK200815
C 23	15.4	83.3	1057	29	AG081712
C 24	14.8	82.2	140	14	CB066245
C 25	14.8	82.2	187	12	BM616169
C 26	14.8	82.2	206	28	AZ991070
C 27	14.8	82.2	206	28	AZ991080
C 28	14.8	82.2	282	14	CB066239
C 29	14.8	82.2	303	9	AA785231
C 30	14.8	82.2	338	9	AJ502973
C 31	14.8	82.2	359	9	AL714174
C 32	14.8	82.2	388	10	BF490378
C 33	14.8	82.2	398	10	BE995152
C 34	14.8	82.2	400	28	BH701453
C 35	14.8	82.2	411	9	A1869164
C 36	14.8	82.2	417	14	CB767429
C 37	14.8	82.2	426	9	A1212546
C 38	14.8	82.2	430	9	A1946050
C 39	14.8	82.2	443	14	CB339034
C 40	14.8	82.2	448	28	AQ945783
C 41	14.8	82.2	457	12	BM130898
C 42	14.8	82.2	463	12	BM130858
C 43	14.8	82.2	464	9	AA941852
C 44	14.8	82.2	475	14	CA408218
C 45	14.8	82.2	481	12	BM130610

## ALIGNMENTS

RESULT 1  
BQ483402/c  
LOCUS  
DEFINITION  
BQ483402  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 667)  
REFERENCE  
Anderson, O.D., Chao, S., Close, T.J., Crossman, C., Fenton, R.D.,  
Lazo, G.R., Nguyen, H.T., Rauech, C.J., Wilson, C., Woo, J., and Zhang, D.  
The structure and function of the expressed portion of the wheat  
genomes - Unstressed root cDNA library  
Unpublished (2002)  
CONTACT  
Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: oanderson@pw.usda.gov  
Sequences have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20  
Seq primer: SK primer.

## FEATURES

## SOURCE

Location/Qualifiers

1. .667  
/organism="Triticum aestivum"  
/mol\_type="rRNA"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="WB3508\_B09\_D18"  
/tissue\_type="Roots"  
/dev\_stage="Full tillering"  
/lab\_host="E. coli SOLR"  
/clone\_lib="Wheat unstrressed root cDNA library"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI; Plants were grown until full tillering stage and root tissue was collected at Texas Tech University (Zhang, HT Nguyen Lab). Total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript SK(-) phagemids in the TU Close lab (Close, Penon) at the University of California, Riverside. Colony plating, plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

## ORIGIN

Query Match 91.1%; Score 16.4; DB 13; Length 667;  
Best Local Similarity 94.4%; Pred. No. 3.4e+02;  
Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTCTC 18  
|||||

Db 243 GGTAAATTCGCTTCTC 226

## RESULT 2

## AZ359925/c

LOCUS 262 bp DNA linear GSS 02-OCT-2000  
DEFINITION clone UUCGCM0103B02 F, genomic survey sequence.

## ACCESSION

AZ359925  
VERSION 1  
KEYWORDS GI:10473625  
GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 262)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weis, R.

## REFERENCE

## AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts

## JOURNAL

Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0103 row: B column: 02

Seq primer: CGTTGTAAACGACGCGCAGT

Class: Plasmid ends

High quality sequence stop: 262.

## FEATURES

## SOURCE

1. .262  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"

## ORIGIN

Query Match 85.6%; Score 15.4; DB 28; Length 262;  
Best Local Similarity 94.1%; Pred. No. 9.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTCTC 18  
|||||

Db 214 GTTAATTCGCTTCTC 198

## RESULT 3

## BH452985/c

LOCUS 277 bp DNA linear GSS 12-DEC-2001  
DEFINITION BOHGA60TF BOHG Brassica oleracea genomic clone BOHGA60, genomic survey sequence.

## ACCESSION

BH452985  
VERSION 1  
KEYWORDS GI:1763696  
GSS.

## SOURCE

Brassica oleracea

## ORGANISM

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 277)  
Town, C.D., Van Aken, S., Uterback, T., Koo, H. and Frazer, C.M.

## REFERENCE

## AUTHORS

Whole genome shotgun sequencing of Brassica oleracea  
Unpublished (2001)

Other GSSs: BOHGA60TR

## JOURNAL

Contact: Chris Town

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

## FEATURES

## SOURCE

1. .277  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="TO1000DH3"  
/db\_xref="taxon:3712"  
/clone="BOHGA60"  
/clone\_lib="BOHG"  
/note="Vector: pHS01, Site\_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHS01 using BstXI linkers"

## ORIGIN



Query Match 85.6%; Score 15.4; DB 28; Length 277;  
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCT 17  
 |||||  
 Db 94 CGTTAATTCGCGTTCT 78

RESULT 4  
 CG858920 402 bp DNA linear GSS 19-NOV-2003  
 LOCUS ZMMBc0267L01f ZMMBc (EcoRI) Zea mays subsp. mays genomic clone

DEFINITION ZMMBc0267L01 5', genomic survey sequence.  
 CG858920

ACCESSION CG858920.1 GI:38431633  
 VERSION GSS.  
 KEYWORDS Zea mays subsp. mays (maize)  
 SOURCE Zea mays subsp. mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 402)  
 Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,  
 Zohovetz,V., Fuke,G., Yu,Y., Wing,R. and Messing,J.  
 Sequencing of the maize genome at PCR (2003c)  
 Unpublished (2003)

REFERENCE  
 AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,  
 Zohovetz,V., Fuke,G., Yu,Y., Wing,R. and Messing,J.  
 TITLE Sequencing of the maize genome at PCR (2003c)  
 JOURNAL Unpublished (2003)  
 COMMENT

Dr. Joachim Messing's lab  
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
 University  
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
 Tel: 732 445 3801  
 Fax: 732 445 5735  
 Email: bharti@waksman.rutgers.edu  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence start: 110.  
 Location/Qualifiers

FEATURES  
 source  
 1..402  
 /organism="Zea mays subsp. mays"  
 /mol\_type="genomic DNA"  
 /cultivar="B73"  
 /sub\_species="mays"  
 /db\_xref="taxon:4578"  
 /clone="ZMMBc0267L01"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="ZMMBc (EcoRI)"  
 /note="Vector: pTABBAC2.1; Site\_1: EcoRI; Site\_2: EcoRI"

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 29; Length 402;  
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCT 17  
 |||||  
 Db 69 CGTTAATTCGCGTTCT 85

RESULT 5  
 AZ498171 493 bp DNA linear GSS 05-OCT-2000  
 LOCUS AZ498171/c  
 DEFINITION IM0335P13F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0335P13 F, genomic survey sequence.  
 AZ498171

ACCESSION AZ498171.1 GI:10675786  
 VERSION GSS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von  
 Niederhausen,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0335 row: P column: 13  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 493.  
 Location/Qualifiers

FEATURES  
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 1..493  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0335P13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: pMD42ny: Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi14732114|gb|AF129072.1) a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 28; Length 493;  
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTTAATTCGCGTTCTC 18  
 |||||  
 Db 383 GTTAATTCGCGTTCTC 367

RESULT 6  
 BH144783 499 bp DNA linear GSS 16-AUG-2001  
 LOCUS BH144783  
 DEFINITION TDGB091TH CTGG Lycopersicon esculentum genomic clone CTG030P13,  
 genomic survey sequence.  
 BH144783

ACCESSION BH144783.1 GI:15200046  
 VERSION GSS.  
 KEYWORDS Lycopersicon esculentum (tomato)  
 SOURCE Lycopersicon esculentum  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE 1  
 AUTHORS van der Hoeven, R., Sun, R., Cho, J., Uterback, T., Romning, C. and Tanksley, S.  
 TITLE Tomato Demethylated Genomic DNA Sequences  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 tomato demethylated genomic DNA  
 Insert Length: 1270 Std Error: 0.00  
 Seq primer: M13F-R  
 Class: shotgun.

FEATURES  
 source  
 1. 499  
 /organism="Lycopersicon esculentum"  
 /mol\_type="genomic DNA"  
 /cultivar="B6203"  
 /db\_xref="taxon:4081"  
 /clone="CTG30P13"  
 /issue\_type="young leaves"  
 /dev\_stage="12-14 weeks post harvest"  
 /lab\_host="E.coli JM109"  
 /clone\_lib="CTG"  
 /note="Vector: Bluescript SK(-); Site 1: EcoRI; Site 2: XhoI; This library was made from short EcoRI digested fragments of the genome of Lycopersicon esculentum ligated into PBS (SK-). The fragments were cloned into the methylation restrictive E.coli strain JM109 with the purpose of enriching the library for non-methylated DNA fragments. This procedure may enrich the pool of cloned fragments in JM109 cells for sequences representing expressed genes. Average insert size 1.27 kb."

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 28; Length 499;  
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 GTTATTCGCGTTCTC 18  
 |||||  
 Db 116 GTTATTCGCGTTCTC 132

RESULT 7  
 BZ508556/c 588 bp DNA linear GSS 16-DEC-2002  
 LOCUS BONSH38TF\_BO\_1.6\_2\_KB.tot Brassica oleracea genomic clone BONSH38,  
 DEFINITION genomic survey sequence.  
 ACCESSION E2508556  
 VERSION E2508556  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 588)  
 Town, C.D., Van Aken, S., Uterback, T., Koo, H. and Fraser, C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other\_GSSs: BONSH38TR  
 COMMENT Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: [cdtown@tigr.org](mailto:cdtown@tigr.org)  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TF  
 Class: sheared ends.

FEATURES  
 source  
 1. 588  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO100DH3"  
 /db\_xref="taxon:3712"  
 /clone="BONSH38"  
 /clone\_lib="BO\_1.6\_2\_KB.tot"  
 /note="Vector: pBOS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pBOS1 using BstXI linkers"

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 28; Length 588;  
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 CGTTATTCGCGTTCT 17  
 |||||  
 Db 445 CGTTATTCGCGTTCT 429

RESULT 8  
 AG042918 740 bp DNA linear GSS 01-NOV-2001  
 LOCUS Pan troglodytes DNA, clone: PTB-021B05.R, genomic survey sequence.  
 DEFINITION  
 ACCESSION AG042918  
 VERSION AG042918.1 GI:16571643  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.

REFERENCE 1  
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
 TITLE BAC end sequences of library PTB  
 JOURNAL Unpublished  
 2 (bases 1 to 740)  
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
 Direct Submision  
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenho-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: [chimps@gsc.riken.go.jp](mailto:chimps@gsc.riken.go.jp), [URL:http://hgp.gsc.riken.go.jp/](mailto:URL:http://hgp.gsc.riken.go.jp/), Tel:81-45-503-9111, Fax:81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.  
 PRIMERS  
 Sequencing: M13Rev  
 LIBRARY  
 Vector : pKS145  
 R.site 1 : SacI  
 R.site 2 : SacI.  
 Location/Qualifiers  
 1. 740  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /clone="PTB-021B05.R"  
 /sex="male"  
 /cell\_type="lymphoblast"  
 /clone\_lib="PTB Chimpanzee Male BAC Library"

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 29; Length 740;  
 Best Local Similarity 94.1%; Pred. No. 1.2e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 GTTATTCGCGTTCTC 18  
 |||||  
 Db 614 GTTATTCGCGTTCTC 630

RESULT 9  
LOCUS CG810640  
DEFINITION FSA0827F largeinsertGenomicLibrary Fusarium virguliforme genomic clone KMFv4N19, genomic survey sequence.  
ACCESSION CG810640  
VERSION CG810640.1 GI:38264114  
KEYWORDS GSS.  
SOURCE Fusarium virguliforme  
ORGANISM Fusarium virguliforme  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; Nectriaceae; Nectria.  
REFERENCE 1 (bases 1 to 819)  
AUTHORS Meksem,K., Ishihara,H., Koo,H., Shultz,J., Ali,S., Iqbal,J., Lightfoot,D.A. and Town,C.D.  
TITLE End sequencing of BACs from a fingerprint physical map of the causative agent of soybean sudden death syndrome, *Fusarium virguliforme*  
JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: FSA0827R  
Contact: Chris Town and K. Meksem  
The Center of Excellence in Soybean Research, Teaching and Plant Outreach, Southern Illinois University at Carbondale and Plant Genomics, The Institute for Genomic Research  
Room 176, Ag. Building, Mail Code 4415, Carbondale, IL 62901-4415, USA and 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 618 453 3103 and 301-838-3523  
Fax: 618 453-7457 and 301-838-0208  
Email: meksem@siu.edu; cdtown@icgr.org (URL: <http://Fusariumvirguliforme.siu.edu>)  
Seq primer: TGTAAAACGACGGCCAGT  
Class: BAC ends.  
FEATURES  
Location/Qualifiers  
source  
1..819  
/organism="Fusarium virguliforme"  
/mol\_type="genomic DNA"  
/cul\_tivar="Monticello"  
/db\_xref="taxon:232082"  
/clone="KMFv4N19"  
/clone\_1id="LargeinsertGenomicLibrary"  
/note="Organ: Hyphae; Vector: pINDIGOBACK; A single spore derived culture was used. Hyphae were grown in an incubator for four days. Nuclei were isolated and embedded in agarose, restriction digested with Hind III. Large size DNA fragments were ligated in vector pINDIGOBACK and electro-transformed into DH10B cells."

AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
TITLE The libraries that made SUCCEST  
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
COMMENT Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parvada@unicamp.br  
Clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcap.unesp.br>  
Plate: 037 row: A column: 01  
Seq primer: T7 Promoter Primer.  
FEATURES  
source  
1..902  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCBFS02037A01"  
/lab\_host="DH10B"  
/clone\_1id="SD2"  
/note="Organ: Developing seeds (small insert library); Vector: pSport1; Site 1: SalI; Site 2: NotI. An unidirectional cDNA library generated from [developing seeds (small insert library)]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://succest.lad.ic.unicamp.br/public>  
ORIGIN  
Location/Qualifiers  
Query Match 85.6%; Score 15.4; DB 14; Length 902;  
Best Local Similarity 94.1%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 GTTAATTCGCGTTCCTC 18  
Db 542 GTTAATTCGCGTTCCTC 526  
RESULT 11  
LOCUS BX434865  
DEFINITION BX434865 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
ACCESSION CS0DP012YH19 3-PRIME, mRNA sequence.  
VERSION BX434865  
KEYWORDS BX434865.1 GI:30781342  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 908)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayres,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7207.r For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAK033AB03NM1&cluster=7207.r>. Contact : Feng Liang Email : [liang@lifetech.com](mailto:liang@lifetech.com) URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0BAK033AB03NM1.

FEATURES  
SOURCE

Location/Qualifiers  
1. .908  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DF012YH19"  
/tissue\_type="FETAL BRAIN"  
/dev\_stage="fetal"  
/clone\_lib="Homo sapiens FETAL BRAIN"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 85.6%; Score 15.4; DB 13; Length 908;  
Best Local Similarity 94.1%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTAAATTCGGTTCCT 17  
|||||  
759 CCTAATTCGGTTCCT 775

RESULT 12  
LOCUS CK288913 921 bp mRNA linear EST 15-DEC-2003  
DEFINITION EST751635 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NMBX06 5' end, mRNA sequence.

ACCESSION CK288913  
VERSION CK288913.1 GI:39866895  
KEYWORDS EST.  
SOURCE Nicotiana benthamiana  
ORGANISM Nicotiana benthamiana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 921)  
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.  
Skaskawicz, B., Jin, H. and Baker, B.  
Generation of EST sequences from Nicotiana benthamiana  
Unpublished (2003)  
Other ESTs: EST751636  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from TIGR via potato@tigr.org  
Seq primer: ATT TAG GTG ACA CTA TAG.  
Location/Qualifiers

FEATURES  
SOURCE

1. .921  
/organism="Nicotiana benthamiana"  
/mol\_type="mRNA"  
/db\_xref="taxon:4100"  
/clone="NMBX06"  
/tissue\_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"  
/lab\_host="DH10B-Tona"  
/clone\_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"  
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 921;  
Best Local Similarity 94.1%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTAAATTCGGTTCCTC 18  
|||||  
208 GTTCATTCGGTTCCTC 224

RESULT 13  
LOCUS CK286745 968 bp mRNA linear EST 15-DEC-2003  
DEFINITION EST749467 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NMBX430 5' end, mRNA sequence.

ACCESSION CK286745  
VERSION CK286745.1 GI:39862605  
KEYWORDS EST.  
SOURCE Nicotiana benthamiana  
ORGANISM Nicotiana benthamiana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 968)  
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.  
Generation of EST sequences from Nicotiana benthamiana  
Unpublished (2003)  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from TIGR via potato@tigr.org  
Seq primer: ATT TAG GTG ACA CTA TAG.  
Location/Qualifiers

FEATURES  
SOURCE

1. .968  
/organism="Nicotiana benthamiana"  
/mol\_type="mRNA"  
/db\_xref="taxon:4100"  
/clone="NMBX430"  
/tissue\_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"  
/lab\_host="DH10B-Tona"  
/clone\_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"  
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 968;  
Best Local Similarity 94.1%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTAAATTCGGTTCCTC 18  
|||||  
200 GTTCATTCGGTTCCTC 216

RESULT 14  
LOCUS BP512280/c 1000 bp mRNA linear EST 16-SEP-2003  
DEFINITION BP512280 Hydra magnipapillata cDNA library Hydra magnipapillata

```

ACCESSION      BPS12280
VERSION        BPS12280.1  GI:34778413
KEYWORDS
SOURCE
ORGANISM       Hydra magnipapillata
                Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                Hydroidea; Hydra.
REFERENCE      1 (bases 1 to 1000)
                Hayakawa,S., Hwang,J.S., Nishimiya-Fujisawa,C., Ogura,A., Ikeo,K.,
                Fujisawa,T. and Gojobori,T.
                Hydra EST project
                Unpublished (2003)
COMMENT        Contact: Jung Shan Hwang
                Center for Information Biology and DNA Data Bank of Japan
                National Institute of Genetics
                111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-55-981-6847(ex.6898)
                Fax: 81-55-981-6848
                Email: jhwang@lab.nig.ac.jp, URL:http://www.cdb.nig.ac.jp.
                Location/Qualifiers
FEATURES
  source
    1..1000
     /organism="Hydra magnipapillata"
     /mol_type="mRNA"
     /strain="105"
     /db_xref="taxon:6085"
     /clone="hmp_05882"
     /tissue_type="whole body"
     /dev_stage="adult budding stage"
     /clone_idb="Hydra magnipapillata cDNA library"

ORIGIN
Query Match      85.6%; Score 15.4; DB 12; Length 1000;
Best Local Similarity 94.1%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTAATTCGGCTTCCT 17
        |||||
        419 CGTTAATTCGGCTTCCT 403

RESULT 15
BMS43811      1278 bp      mRNA      linear      EST 20-FEB-2002
LOCUS         AGENCOURT_6492104 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5589146
DEFINITION    5' mRNA sequence.
ACCESSION     BMS43811
VERSION       BMS43811.1  GI:18774526
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 1278)
                NIH-MGC http://mgs.nci.nih.gov/.
                National Institutes of Health, Mammalian Gene Collection (MGC)
                unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-remail.nih.gov
                Tissue Procurement: Invitrogen
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
                DNA Sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LNLN at:
                http://image.llnl.gov
                Plate: LHAM12361 row: 9 column: 03
                High quality sequence start: 8
                High quality sequence stop: 548.
                Location/Qualifiers
FEATURES
  source
    1..1278
     /organism="Homo sapiens"
     /mol_type="mRNA"

```

```

/db_xref="taxon:9606"
/clone="IMAGE:5589146"
/lab_host="DH10B"
/clone_idb="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 Kb, insert size range 1-3.5 Kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

ORIGIN
Query Match      85.6%; Score 15.4; DB 12; Length 1278;
Best Local Similarity 94.1%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTAATTCGGCTTCCT 17
        |||||
        794 CGTTAATTCGGCTTCCT 810

Search completed: October 1, 2004, 08:01:51
Job time : 260.333 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 13:33:17 ; Search time 1409 Seconds  
(without alignments)  
604.127 Million cell updates/sec

Title: US-10-046-955-50  
Perfect score: 18  
Sequence: 1 cgttaatcgcgttcctc 18

Scoring table: IDENTITY NUC  
Gapop 10'-0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits: 4526729  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Maximum Match 100%

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 5000 summaries

Database :

GenBank: 1: gb\_ba: 2: gb\_hcg: 3: gb\_in: 4: gb\_om: 5: gb\_ov: 6: gb\_pat: 7: gb\_pl: 8: gb\_pr: 9: gb\_ro: 10: gb\_ests: 11: gb\_ests: 12: gb\_by: 13: gb\_un: 14: gb\_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	AR206444	AR206444 Sequence
2	18	100.0	18	BD083635	BD083635 Nucleic a
3	18	100.0	335	AF162898	AF162898 Fusarium
4	18	100.0	335	AF162899	AF162899 Fusarium
5	18	100.0	336	AF162900	AF162900 Fusarium
6	18	100.0	338	AF339418	AF339418 Fusarium
7	18	100.0	426	AF502842	AF502842 Leaf 11ct
8	18	100.0	430	AF502842	AF502842 Leaf 11ct
9	18	100.0	441	AY387703	AY387703 Fusarium
10	18	100.0	441	AY387703	AY387703 Fusarium
11	18	100.0	445	AY387698	AY387698 Fusarium
12	18	100.0	445	AY387699	AY387699 Fusarium
13	18	100.0	445	AY387702	AY387702 Fusarium
14	18	100.0	445	AY387704	AY387704 Fusarium
15	18	100.0	445	AY387705	AY387705 Fusarium
16	18	100.0	447	AY667482	AY667482 Fusarium
17	18	100.0	447	AY667484	AY667484 Fusarium
18	18	100.0	447	AY667490	AY667490 Fusarium
19	18	100.0	447	AY387701	AY387701 Fusarium

20	18	100.0	455	8	FOU28159	U28159 Fusarium ox
21	18	100.0	455	8	FOU28161	U28161 Fusarium ox
22	18	100.0	456	8	AF440527	AF440527 Fusarium
23	18	100.0	456	8	AF440529	AF440529 Fusarium
24	18	100.0	456	8	AF440531	AF440531 Fusarium
25	18	100.0	456	8	AF440532	AF440532 Fusarium
26	18	100.0	456	8	AF440534	AF440534 Fusarium
27	18	100.0	456	8	AF440539	AF440539 Fusarium
28	18	100.0	456	8	AF440540	AF440540 Fusarium
29	18	100.0	456	8	AF440542	AF440542 Fusarium
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32	18	100.0	456	8	AF440563	AF440563 Fusarium
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35	18	100.0	457	8	AF440560	AF440560 Fusarium
36	18	100.0	457	8	AF440562	AF440562 Fusarium
37	18	100.0	458	8	AF055220	AF055220 Fusarium
38	18	100.0	460	8	AY259214	AY259214 Fusarium
39	18	100.0	496	8	AY208788	AY208788 Fusarium
40	18	100.0	497	8	AY243058	AY243058 Ascomycet
41	18	100.0	501	8	AY247553	AY247553 Fusarium
42	18	100.0	501	8	AY262831	AY262831 Fusarium
43	18	100.0	501	8	AY354386	AY354386 Fusarium
44	18	100.0	501	8	AY354388	AY354388 Fusarium
45	18	100.0	501	8	AY354389	AY354389 Fusarium
46	18	100.0	501	8	AY354390	AY354390 Fusarium
47	18	100.0	501	8	AY354393	AY354393 Fusarium
48	18	100.0	501	8	AY354396	AY354396 Fusarium
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52	18	100.0	506	8	AF069310	AF069310 Fusarium
53	18	100.0	506	8	AY127697	AY127697 Fusarium
54	18	100.0	506	8	AY127698	AY127698 Fusarium
55	18	100.0	506	8	AY127699	AY127699 Fusarium
56	18	100.0	515	8	AY555719	AY555719 Fusarium
57	18	100.0	520	8	FOU34566	U34566 Fusarium ox
58	18	100.0	521	8	AF176656	AF176656 Fusarium
59	18	100.0	523	8	AF502841	AF502841 Leaf 11ct
60	18	100.0	531	8	AF242876	AF242876 Fusarium
61	18	100.0	544	8	FOXYRNA	X94173 Fusarium ox
62	18	100.0	545	8	FOVBI58	X78260 F. oxysporum
63	18	100.0	546	8	FOVCS58	X78259 F. oxysporum
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65	18	100.0	552	8	AY147369	AY147369 Fusarium
66	18	100.0	552	8	AY462580	AY462580 Fusarium
67	18	100.0	555	8	AY462579	AY462579 Fusarium
68	18	100.0	616	8	AF322074	AF322074 Fusarium
69	18	100.0	616	8	AF322075	AF322075 Fusarium
70	18	100.0	616	8	AF322076	AF322076 Fusarium
71	18	100.0	636	8	AF443071	AF443071 Fusarium
72	18	100.0	655	8	AF469120	AF469120 Fusarium
73	18	100.0	666	8	AY667489	AY667489 Fusarium
74	18	100.0	671	8	AY669122	AY669122 Fusarium
75	18	100.0	678	8	AY188919	AY188919 Fusarium
76	18	100.0	1134	8	AY188919	AY188919 Fusarium
77	18	100.0	1471	8	FO588RNA	Y07991 F. oxysporum

#### ALIGNMENTS

RESULT 1  
AR206444  
DEFINITION Sequence 50 from patent US 6372430.  
ACCESSION AR206444  
VERSION AR206444.1  
KEYWORDS GI:21505047  
SOURCE Unknown.  
ORGANISM Unclassified.

DNA  
linear PAT 20-JUN-2002

REFERENCE	1 (bases 1 to 18)
AUTHORS	Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.Soo.,
TITLE	Nucleic acids for detecting Aspergillus species and other filamentous fungi
JOURNAL	Patent: US 6372430-A 50 16-APR-2002;
FEATURES	Location/Qualifiers
SOURCE	1..18 /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Query Match	100.0%; Score 18; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 24;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CGTTAATTGCGCTTC 18                     Db        1 CGTTAATTGCGCTTC 18
RESULT 2	
BD083635	
LOCUS	18 bp DNA linear PAT 27-AUG-2002
DEFINITION	Nucleic acids for detecting Aspergillus species and other filamentous fungi.
ACCESSION	BD083635
VERSION	BD083635.1 GI:22629245
KEYWORDS	JP 2001525665-A/50.
SOURCE	Fusarium oxysporum
ORGANISM	Fusarium oxysporum Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex. 1 (bases 1 to 18) Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S. Nucleic acids for detecting Aspergillus species and other filamentous fungi Patent: JP 2001525665-A 50 11-DEC-2001; THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR DISEASE PREVENTION AND CONTROL PREVENTION TECHNOLOGY TRANSFER OFFICE
COMMENT	OS Fusarium oxysporum PN JP 2001525665-A/50 PD 11-DEC-2001 PF 01-MAY-1998 JP 1998548275 PR 02-MAY-1997 US 60/045400 PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO PC CHOI CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers
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SOURCE	Location/Qualifiers
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Query Match	100.0%; Score 18; DB 6; Length 18;
Best Local Similarity	100.0%; Pred. No. 24;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CGTTAATTCGGCTTC 18                     Db        1 CGTTAATTCGGCTTC 18
RESULT 3	
AFI62898	
LOCUS	335 bp DNA linear PLN 15-NOV-2001

DEFINITION	Fusarium oxysporum f. sp. conglutinans 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence.
ACCESSION	AF162898
VERSION	AF162898.1 GI:5690387
KEYWORDS	
SOURCE	
ORGANISM	Fusarium oxysporum f. sp. conglutinans Fusarium oxysporum f. sp. conglutinans Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
REFERENCE	Fusarium oxysporum complex. 1 (bases 1 to 335) Min,B.R.
AUTHORS	Direct Submission
TITLE	Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea
JOURNAL	Location/Qualifiers
FEATURES	source 1..335 /organism="Fusarium oxysporum f. sp. conglutinans" /mol_type="genomic DNA" /strain="MAFF 74401" /db_xref="taxon:100902" /note="forma specialis: conglutinans forma specialis: conglutinans" <1..128 /product="5.8S ribosomal RNA" 129..277 /product="internal transcribed spacer 2" 278..>335 /product="26S ribosomal RNA"
ORIGIN	
Query Match	100.0%; Score 18; DB 8; Length 335; Best Local Similarity 100.0%; Pred. No. 26; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY	1 CGTTAATTCGGCTCCTC 18       162 CGTTAATTCGGCTCCTC 179
Db	
RESULT 4	
LOCUS	AF162899 335 bp DNA linear PLN 04-AUG-1999
AF162899	
DEFINITION	Fusarium oxysporum f. sp. fragariae 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence.
ACCESSION	AF162899
VERSION	AF162899.1 GI:5690388
KEYWORDS	
SOURCE	
ORGANISM	Fusarium oxysporum f. sp. fragariae Fusarium oxysporum f. sp. fragariae Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
REFERENCE	Fusarium oxysporum complex. 1 (bases 1 to 335) Min,B.R.
AUTHORS	Direct Submission
TITLE	Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea
JOURNAL	Location/Qualifiers
FEATURES	source 1..335 /organism="Fusarium oxysporum f. sp. fragariae" /mol_type="genomic DNA" /strain="MAFF 744009" /db_xref="taxon:100903" /note="forma specialis: fragariae forma specialis: fragariae" <1..128 /product="5.8S ribosomal RNA" 129..277 /product="internal transcribed spacer 2" 278..>335
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misc_RNA	
tRNA	
misc_RNA	
tRNA	



ORIGIN /product="28S ribosomal RNA"

Query Match 100.0%; Score 18; DB 8; Length 335;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18  
|||||  
Db 162 CGTTAATTCGCGTTCCTC 179

RESULT 5  
AF162900 336 bp DNA linear PLN 04-AUG-1999  
LOCUS Fusarium oxysporum f. sp. raphani 5.8S ribosomal RNA gene, partial  
DEFINITION sequence; internal transcribed spacer 2, complete sequence; and 28S  
ribosomal RNA gene, partial sequence.  
ACCESSION AF162900.1 GI:5690389  
VERSION  
KEYWORDS  
SOURCE Fusarium oxysporum f. sp. raphani  
ORGANISM Fusarium oxysporum f. sp. raphani  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
REFERENCE 1 (bases 1 to 336)  
AUTHORS Min, B.R.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji  
Dong, Chong Ro-Cu, Seoul 110-743, Korea  
LOCATION/Qualifiers  
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/product="internal transcribed spacer 2"  
275..>336  
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 336;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18  
|||||  
Db 163 CGTTAATTCGCGTTCCTC 180

RESULT 6  
AF339418 338 bp DNA linear PLN 25-OCT-2002  
LOCUS Fusarium oxysporum strain PS-1 5.8S ribosomal RNA gene, partial  
DEFINITION sequence; internal transcribed spacer 2, complete sequence; and 28S  
ribosomal RNA gene, partial sequence.  
ACCESSION AF339418  
VERSION AF339418.1 GI:24369714  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
REFERENCE 1 (bases 1 to 338)  
AUTHORS Toolley, P.W., Hatziloakas, E., Scott, D.L., Jr. and Carras, M.M.  
TITLE Use of ligase chain reaction for detection of Phytophthora  
infestans in potatoes

JOURNAL Unpublished  
2 (bases 1 to 338)  
AUTHORS Toolley, P.W., Hatziloakas, E., Scott, D.L., Jr. and Carras, M.M.  
TITLE Direct Submission  
JOURNAL Submitted (22-JAN-2001) Agricultural Research Service, U.S.  
Department of Agriculture, 1301 Dilton Ave., Ft. Detrick, MD  
21702-5023, USA  
LOCATION/Qualifiers  
source 1..338  
/organism="Fusarium oxysporum"  
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/strain="PS-1"  
/db\_xref="taxon:5507"  
<1..>338  
/note="contains 5.8S ribosomal RNA, internal transcribed  
spacer 2, and 28S ribosomal RNA"

misc\_RNA

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 338;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18  
|||||  
Db 162 CGTTAATTCGCGTTCCTC 179

RESULT 7  
AY383320 426 bp DNA linear PLN 05-OCT-2003  
LOCUS Fusarium oxysporum f. sp. vanillae isolate DL-1-1 internal  
DEFINITION transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,  
complete sequence; and internal transcribed spacer 2, partial  
sequence.  
ACCESSION AY383320  
VERSION AY383320.1 GI:37142968  
KEYWORDS  
SOURCE Fusarium oxysporum f. sp. vanillae  
ORGANISM Fusarium oxysporum f. sp. vanillae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
REFERENCE 1 (bases 1 to 426)  
AUTHORS Wang, Y.Y., Whitehead, M., Zhu, Y., Burns, A., Hocking, T. and Ruan, X.Y.  
TITLE Fusarium oxysporum f. sp. vanillae isolate DL-1-1 ITS1, 5.8S rDNA,  
ITS 2 sequence  
JOURNAL Unpublished  
2 (bases 1 to 426)  
AUTHORS Wang, Y.Y., Whitehead, M., Zhu, Y., Burns, A., Hocking, T. and Ruan, X.Y.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-2003) Dept. Plant Pathology, Yunnan Agricultural  
University, Long Tou Street, Kunming, Yunnan 650201, P.R. China  
LOCATION/Qualifiers  
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/organism="Fusarium oxysporum f. sp. vanillae"  
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118..274  
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275..>426  
/product="internal transcribed spacer 2"

misc\_RNA

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 426;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18  
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Db 309 CGTTAATTCGCGTTCCTC 326

RESULT 8  
AF502842/c 430 bp DNA linear PLN 13-MAY-2002  
LOCUS

DEFINITION  
Leaf litter ascomycete strain its31 isolate 1000502849 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION  
AF502842 GI:20531649

VERSION  
AF502842.1

KEYWORDS  
leaf litter ascomycete strain its31

SOURCE  
Eukaryota; Fungi; Ascomycota.

ORGANISM

REFERENCE  
1 (bases 1 to 430)  
Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
Biogeography of leaf litter fungi

TITLE  
Unpublished

JOURNAL  
2 (bases 1 to 430)  
Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
Direct Submission

AUTHORS  
Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA

FEATURES  
Location/Qualifiers

source  
1..430  
/organism="leaf litter ascomycete strain its31"  
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ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 430;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
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82 CGTTAATTCGCGTTCCTC 65

RESULT 9  
AY387703 441 bp DNA linear PLN 07-OCT-2003  
LOCUS

DEFINITION  
Fusarium oxysporum isolate DL-2-7 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION  
AY387703 GI:37362908

VERSION  
AY387703.1

KEYWORDS  
Fusarium oxysporum

SOURCE  
Fusarium oxysporum

ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

REFERENCE  
1 (bases 1 to 441)  
Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Li,X.  
Fusarium oxysporum isolate DL-2-7 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence

TITLE  
Unpublished

JOURNAL  
2 (bases 1 to 441)  
Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y. and Li,X.

AUTHORS

TITLE  
Direct Submission

JOURNAL  
Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China

FEATURES  
Location/Qualifiers

source  
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/db\_xref="taxon:5507"

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136..293  
/product="5.8S ribosomal RNA"

misc\_RNA  
294..>441  
/product="internal transcribed spacer 2"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
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327 CGTTAATTCGCGTTCCTC 344

RESULT 10  
AY380575 445 bp DNA linear PLN 04-OCT-2003  
LOCUS

DEFINITION  
Fusarium oxysporum f. sp. vanillae internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION  
AY380575 GI:37039595

VERSION  
AY380575.1

KEYWORDS  
Fusarium oxysporum f. sp. vanillae

SOURCE  
Fusarium oxysporum f. sp. vanillae

ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

REFERENCE  
1 (bases 1 to 445)  
Wang,Y.Y., Whitehead,M., Burns,A., Zhu,Y.Y., Hocking,T. and Ruan,X.Y.  
ITS1, 5.8S and ITS2 rDNA sequence from Fusarium oxysporum f. sp. vanillae

TITLE  
Unpublished

JOURNAL  
2 (bases 1 to 445)  
Wang,Y.Y., Whitehead,M., Burns,A., Zhu,Y.Y., Hocking,T. and Ruan,X.Y.  
Direct Submission

AUTHORS  
Submitted (03-SEP-2003) Plant Pathology, Yunnan Agricultural University, Longtou Street, Kunming, Yunnan 650201, Peoples Republic of China

FEATURES  
Location/Qualifiers

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misc\_RNA  
294..>445  
/product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 445;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18  
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 Db 327 CGTTAATTCGGCTTCCTC 344

RESULT 11  
 AY387698 445 bp DNA linear PLN 07-OCT-2003  
 LOCUS AY387698  
 DEFINITION Fusarium oxysporum f. sp. vanillae isolate ML-8-1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
 AY387698  
 AY387698.1 GI:37362903

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Fusarium oxysporum f. sp. vanillae  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Li, X.  
 Direct Submission  
 Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China  
 Location/Qualifiers

FEATURES  
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 136..293  
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 294..>445  
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ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18  
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 Db 327 CGTTAATTCGGCTTCCTC 344

RESULT 12  
 AY387699 445 bp DNA linear PLN 07-OCT-2003  
 LOCUS AY387699  
 DEFINITION Fusarium oxysporum f. sp. vanillae isolate DL-4b internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Fusarium oxysporum f. sp. vanillae  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Li, X.  
 Direct Submission  
 Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China  
 Location/Qualifiers

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Qy 1 CGTTAATTCGGCTTCCTC 18  
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 Db 327 CGTTAATTCGGCTTCCTC 344

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 LOCUS AY387702  
 DEFINITION Fusarium oxysporum isolate ML-7-1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Fusarium oxysporum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y. and Yang, J.  
 Direct Submission  
 Submitted (10-SEP-2003) Department of Plant Pathology, College of Plant Protection, Yunnan Agricultural University, Long Tou Street, Kunming, Yunnan 650201, P. R. China  
 Location/Qualifiers

FEATURES  
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QY 1 CGTTAATTCGCGTTCCTC 18  
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Db 327 CGTTAATTCGCGTTCCTC 344

RESULT 14  
AY387704 445 bp DNA linear PLN 07-OCT-2003  
LOCUS Fusarium oxysporum isolate ML-8-4 internal transcribed spacer 1,  
DEFINITION partial sequence; 5.8S ribosomal RNA gene, complete sequence; and  
internal transcribed spacer 2, partial sequence.  
ACCESSION AY387704  
VERSION  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
1 (bases 1 to 445)  
Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y.  
and Yang, J.  
Fusarium oxysporum isolate ML-8-4 internal transcribed spacer 1,  
5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence  
Unpublished  
2 (bases 1 to 445)  
Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y.  
and Yang, J.  
Direct Submission  
Submitted (10-SEP-2003) Department of Plant Pathology, College of  
Plant Protection, Yunnan Agricultural University, Long Tou Street,  
Kunming, Yunnan 650201, P. R. China  
Location/Qualifiers  
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QY 1 CGTTAATTCGCGTTCCTC 18  
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Db 327 CGTTAATTCGCGTTCCTC 344

RESULT 15  
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LOCUS Fusarium oxysporum isolate ML-5-2 internal transcribed spacer 1,  
DEFINITION partial sequence; 5.8S ribosomal RNA gene, complete sequence; and  
internal transcribed spacer 2, partial sequence.  
ACCESSION AY387705  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
1 (bases 1 to 445)  
Liu, B., Zhu, Y.J., Ling, Y.Z. and Cao, Y.  
Direct Submission  
Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of  
Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003,  
P. R. China  
Location/Qualifiers  
1. .447  
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KEYWORDS  
SOURCE  
ORGANISM  
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
1 (bases 1 to 445)  
Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y.  
and Chen, J.B.  
Fusarium oxysporum isolate ML-5-2 internal transcribed spacer 1,  
5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence  
Unpublished  
2 (bases 1 to 445)  
Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y.  
and Chen, J.B.  
Direct Submission  
Submitted (10-SEP-2003) Department of Plant Pathology, College of  
Plant Protection, Yunnan Agricultural University, Long Tou Street,  
Kunming, Yunnan 650201, P. R. China  
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QY 1 CGTTAATTCGCGTTCCTC 18  
|||||  
Db 327 CGTTAATTCGCGTTCCTC 344

RESULT 16  
AY667482 447 bp DNA linear PLN 20-JUL-2004  
LOCUS Fusarium oxysporum isolate 12-117 internal transcribed spacer 1,  
DEFINITION partial sequence; 5.8S ribosomal RNA gene, complete sequence; and  
internal transcribed spacer 2, partial sequence.  
ACCESSION AY667482  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Fusarium oxysporum  
Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
1 (bases 1 to 447)  
Liu, B., Zhu, Y.J., Ling, Y.Z. and Cao, Y.  
Direct Submission  
Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of  
Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003,  
P. R. China  
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Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCTC 18  
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330 CGTTAATTCGCGTTCTC 347

RESULT 17  
AY667484 447 bp DNA linear PLN 20-JUL-2004  
LOCUS Fusarium oxysporum isolate 12-132 internal transcribed spacer 1,  
DEFINITION partial sequence; 5.8S ribosomal RNA gene, complete sequence; and  
internal transcribed spacer 2, partial sequence.  
ACCESSION AY667484 GI:50313399  
VERSION  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
1 (bases 1 to 447)  
AUTHORS Liu, B., Zhu, Y.J., Ling, Y.Z. and Cao, Y.  
REFERENCE Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of  
JOURNAL Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003,  
P. R. China

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297..>447  
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCTC 18  
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330 CGTTAATTCGCGTTCTC 347

RESULT 18  
AY667490 447 bp DNA linear PLN 20-JUL-2004  
LOCUS Fusarium oxysporum isolate 12-136 internal transcribed spacer 1,  
DEFINITION partial sequence; 5.8S ribosomal RNA gene, complete sequence; and  
internal transcribed spacer 2, partial sequence.  
ACCESSION AY667490 GI:50313405  
VERSION  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
1 (bases 1 to 447)  
AUTHORS Liu, B., Zhu, Y.J., Ling, Y.Z. and Cao, Y.

TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of  
Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003,  
P. R. China

FEATURES  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCTC 18  
|||||  
330 CGTTAATTCGCGTTCTC 347

RESULT 19  
AY387701 447 bp DNA linear PLN 07-OCT-2003  
LOCUS Fusarium oxysporum isolate WJD-2-2 internal transcribed spacer 1,  
DEFINITION partial sequence; 5.8S ribosomal RNA gene, complete sequence; and  
internal transcribed spacer 2, partial sequence.  
ACCESSION AY387701 GI:37362906  
VERSION  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
1 (bases 1 to 447)  
AUTHORS Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y.  
and Kong, Q.  
REFERENCE Fusarium oxysporum isolate WJD-2-2 internal transcribed spacer 1,  
JOURNAL 5.8S ribosomal RNA gene and internal transcribed spacer 2 sequence  
2 (bases 1 to 447)  
REFERENCE Unpublished  
AUTHORS Wang, Y.Y., Whitehead, M., Zhu, Y.Y., Burns, A., Hocking, T., Ruan, X.Y.  
and Kong, Q.  
TITLE Direct Submission  
JOURNAL Submitted (10-SEP-2003) Department of Plant Pathology, College of  
Plant Protection, Yunnan Agricultural University, Long You Street,  
Kunming, Yunnan 650201, P. R. China

FEATURES  
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278..>447  
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ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 447;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



complete sequence.

AF440529  
AF440529.1 GI:18034397

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Fusarium oxysporum  
Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.

REFERENCE  
AUTHORS

1 (bases 1 to 456)  
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van  
Berkum,P.

TITLE

Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum  
from tomato plants

JOURNAL  
REFERENCE  
AUTHORS

2 (bases 1 to 456)  
Bao,J.R., Fravel,D.R. and Lazarovits,G.

TITLE

Direct Submission

JOURNAL

Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300  
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

LOCATION/Qualifiers

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306. .456  
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Qy 1 CGTTAATTCGGCTTCCTC 18  
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Db 339 CGTTAATTCGGCTTCCTC 356

RESULT 24  
AF440531 456 bp DNA linear PLN 24-SEP-2003  
LOCUS  
DEFINITION

Fusarium oxysporum isolate 44RK-35 internal transcribed spacer 1,  
5.8S ribosomal RNA gene, and internal transcribed spacer 2,  
complete sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF440531  
AF440531.1 GI:18034399

Fusarium oxysporum  
Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.

REFERENCE  
AUTHORS

1 (bases 1 to 456)  
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van  
Berkum,P.

TITLE

Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum  
from tomato plants

JOURNAL  
REFERENCE  
AUTHORS

2 (bases 1 to 456)  
Bao,J.R., Fravel,D.R. and Lazarovits,G.

TITLE

Direct Submission

JOURNAL

Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300  
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

LOCATION/Qualifiers

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148. .305  
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306. .456  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18  
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Db 339 CGTTAATTCGGCTTCCTC 356

RESULT 25  
AF440532 456 bp DNA linear PLN 24-SEP-2003  
LOCUS  
DEFINITION

Fusarium oxysporum isolate 73RK-1 internal transcribed spacer 1,  
5.8S ribosomal RNA gene, and internal transcribed spacer 2,  
complete sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF440532  
AF440532.1 GI:18034400

Fusarium oxysporum  
Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.

REFERENCE  
AUTHORS

1 (bases 1 to 456)  
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van  
Berkum,P.

TITLE

Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum  
from tomato plants

JOURNAL  
REFERENCE  
AUTHORS

2 (bases 1 to 456)  
Bao,J.R., Fravel,D.R. and Lazarovits,G.

TITLE

Direct Submission

JOURNAL

Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300  
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

LOCATION/Qualifiers

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misc\_RNA

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Query Match 100.0%; Score 18; DB 8; Length 456;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18  
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Db 339 CGTTAATTCGGCTTCCTC 356

RESULT 26  
AF440534 456 bp DNA linear PLN 24-SEP-2003  
LOCUS  
DEFINITION

Fusarium oxysporum isolate AL22 internal transcribed spacer 1, 5.8S  
ribosomal RNA gene, and internal transcribed spacer 2, complete  
sequence.

ACCESSION  
AF440534

VERSION AF440534.1 GI:180344402  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM  
REFERENCE  
AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.  
TITLE Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants  
JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)  
REFERENCE 2 (bases 1 to 456)  
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA  
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Qy 1 CGTTAATTCGCGTCTC 18  
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Db 339 CGTTAATTCGCGTCTC 356  
RESULT 27  
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LOCUS Fusarium oxysporum isolate DEH1 internal transcribed spacer 1, 5.8S  
DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete  
sequence.  
ACCESSION AF440539  
VERSION AF440539.1 GI:180344407  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM  
REFERENCE  
AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.  
TITLE Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants  
JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)  
REFERENCE 2 (bases 1 to 456)  
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA  
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGTTAATTCGCGTCTC 18  
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Db 339 CGTTAATTCGCGTCTC 356  
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LOCUS Fusarium oxysporum isolate DEH2 internal transcribed spacer 1, 5.8S  
DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete  
sequence.  
ACCESSION AF440540  
VERSION AF440540.1 GI:180344408  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM  
REFERENCE  
AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.  
TITLE Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants  
JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)  
REFERENCE 2 (bases 1 to 456)  
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA  
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Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGTTAATTCGCGTCTC 18  
|||||  
Db 339 CGTTAATTCGCGTCTC 356  
RESULT 29  
AF440542 456 bp DNA linear PLN 24-SEP-2003  
LOCUS Fusarium oxysporum isolate Fo47 internal transcribed spacer 1, 5.8S  
DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete  
sequence.  
ACCESSION AF440542  
VERSION AF440542.1 GI:180344410  
KEYWORDS



SOURCE  
ORGANISM Fusarium oxysporum  
Eusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
REFERENCE  
AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van  
Berkum,P.  
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum  
from tomato plants  
JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)  
REFERENCE  
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300  
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA  
FEATURES  
SOURCE  
misc\_RNA  
1. .147  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/isolate="P047"  
/db\_xref="taxon:5507"  
/product="internal transcribed spacer 1"  
rRNA  
148. .305  
/product="5.8S ribosomal RNA"  
306. .456  
/product="internal transcribed spacer 2"  
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Query Match 100.0%; Score 18; DB 8; Length 456;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CGTTAATTCGGCTTCCTC 18  
|||||  
339 CGTTAATTCGGCTTCCTC 356  
Db

RESULT 30  
AF440552 456 bp DNA linear PLN 24-SEP-2003  
LOCUS AF440552  
DEFINITION Fusarium oxysporum isolate IAT internal transcribed spacer 1, 5.8S  
ribosomal RNA gene, and internal transcribed spacer 2, complete  
sequence.  
ACCESSION AF440552  
VERSION AF440552.1 GI:18034420  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
REFERENCE  
AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van  
Berkum,P.  
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum  
from tomato plants  
JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)  
REFERENCE  
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300  
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA  
FEATURES  
SOURCE  
misc\_RNA  
1. .147  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/isolate="IA7"  
/db\_xref="taxon:5507"  
/product="internal transcribed spacer 1"  
rRNA  
148. .305  
/product="5.8S ribosomal RNA"  
306. .456  
/product="internal transcribed spacer 2"  
ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 456;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CGTTAATTCGGCTTCCTC 18  
|||||  
339 CGTTAATTCGGCTTCCTC 356  
Db

RESULT 32  
AF440563 456 bp DNA linear PLN 24-SEP-2003  
LOCUS AF440563  
DEFINITION Fusarium oxysporum isolate SA70 internal transcribed spacer 1, 5.8S  
ribosomal RNA gene, and internal transcribed spacer 2, complete  
sequence.  
ACCESSION AF440563  
VERSION AF440563.1 GI:18034431  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM Fusarium oxysporum

SOURCE  
ORGANISM Fusarium oxysporum  
Eusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
REFERENCE  
AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van  
Berkum,P.  
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum  
from tomato plants  
JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)  
REFERENCE  
AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300  
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA  
FEATURES  
SOURCE  
misc\_RNA  
1. .147  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/isolate="PE11"  
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/product="internal transcribed spacer 1"  
rRNA  
148. .305  
/product="5.8S ribosomal RNA"  
306. .456  
/product="internal transcribed spacer 2"  
ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 456;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CGTTAATTCGGCTTCCTC 18  
|||||  
339 CGTTAATTCGGCTTCCTC 356  
Db

RESULT 32  
AF440563 456 bp DNA linear PLN 24-SEP-2003  
LOCUS AF440563  
DEFINITION Fusarium oxysporum isolate PE11 internal transcribed spacer 1, 5.8S  
ribosomal RNA gene, and internal transcribed spacer 2, complete  
sequence.  
ACCESSION AF440563  
VERSION AF440563.1 GI:18034431  
KEYWORDS  
SOURCE Fusarium oxysporum  
ORGANISM Fusarium oxysporum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
1 (bases 1 to 456)  
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.

**TITLE**  
Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants

**JOURNAL**  
Can. J. Bot. 80 (3), 271-279 (2002)

**REFERENCE**  
2 (bases 1 to 456)

**AUTHORS**  
Bao,J.R., Fravel,D.R. and Lazarovits,G.

**JOURNAL**  
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

**FEATURES**  
Location/Qualifiers  
1..456  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/isolate="SA70"  
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1..147  
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148..305  
/product="5.8S ribosomal RNA"  
306..456  
/product="internal transcribed spacer 2"

**ORIGIN**  
Query Match 100.0%; Score 18; DB 8; Length 456;  
Best Local Similarity 100.0%; Pred. NO. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**  
1 CGTTAATTCGCGTTCCTC 18  
|||||  
339 CGTTAATTCGCGTTCCTC 356

**Db**  
339 CGTTAATTCGCGTTCCTC 356

**RESULT 33**  
AF440533 457 bp DNA linear PLN 24-SEP-2003

**LOCUS**  
Fusarium oxysporum isolate AU01 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.

**ACCESSION**  
AF440533

**VERSION**  
AF440533.1 GI:18034401

**KEYWORDS**  
Fusarium oxysporum  
Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

**ORGANISM**  
1 (bases 1 to 457)  
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.

**REFERENCE**  
1 (bases 1 to 457)  
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.

**AUTHORS**  
Bao,J.R., Fravel,D.R. and Lazarovits,G.

**JOURNAL**  
Can. J. Bot. 80 (3), 271-279 (2002)

**REFERENCE**  
2 (bases 1 to 457)

**AUTHORS**  
Bao,J.R., Fravel,D.R. and Lazarovits,G.

**JOURNAL**  
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

**FEATURES**  
Location/Qualifiers  
1..457  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/isolate="AU01"  
/db\_xref="taxon:5507"  
1..148  
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149..306  
/product="5.8S ribosomal RNA"  
307..457

/product="internal transcribed spacer 2"

**ORIGIN**  
Query Match 100.0%; Score 18; DB 8; Length 457;  
Best Local Similarity 100.0%; Pred. NO. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**  
1 CGTTAATTCGCGTTCCTC 18  
|||||  
340 CGTTAATTCGCGTTCCTC 357

**Db**  
340 CGTTAATTCGCGTTCCTC 357

**RESULT 34**  
AF440538 457 bp DNA linear PLN 24-SEP-2003

**LOCUS**  
Fusarium oxysporum isolate CS-20 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.

**ACCESSION**  
AF440538

**VERSION**  
AF440538.1 GI:18034406

**KEYWORDS**  
Fusarium oxysporum  
Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

**ORGANISM**  
1 (bases 1 to 457)  
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.

**REFERENCE**  
1 (bases 1 to 457)  
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.

**AUTHORS**  
Bao,J.R., Fravel,D.R. and Lazarovits,G.

**JOURNAL**  
Can. J. Bot. 80 (3), 271-279 (2002)

**REFERENCE**  
2 (bases 1 to 457)

**AUTHORS**  
Bao,J.R., Fravel,D.R. and Lazarovits,G.

**JOURNAL**  
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

**FEATURES**  
Location/Qualifiers  
1..457  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/isolate="CS-20"  
/db\_xref="taxon:5507"  
1..147  
/product="internal transcribed spacer 1"  
148..305  
/product="5.8S ribosomal RNA"  
306..457  
/product="internal transcribed spacer 2"

**ORIGIN**  
Query Match 100.0%; Score 18; DB 8; Length 457;  
Best Local Similarity 100.0%; Pred. NO. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**  
1 CGTTAATTCGCGTTCCTC 18  
|||||  
339 CGTTAATTCGCGTTCCTC 356

**Db**  
339 CGTTAATTCGCGTTCCTC 356

**RESULT 35**  
AF440560 457 bp DNA linear PLN 24-SEP-2003

**LOCUS**  
Fusarium oxysporum isolate Litom internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.

**ACCESSION**  
AF440560

**VERSION**  
AF440560.1 GI:18034428

**KEYWORDS**  
Fusarium oxysporum  
Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

**ORGANISM**  
1 (bases 1 to 457)  
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.

**REFERENCE**  
1 (bases 1 to 457)  
Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkum,P.

**AUTHORS**  
Bao,J.R., Fravel,D.R. and Lazarovits,G.

**JOURNAL**  
Can. J. Bot. 80 (3), 271-279 (2002)

**REFERENCE**  
2 (bases 1 to 457)

**AUTHORS**  
Bao,J.R., Fravel,D.R. and Lazarovits,G.

**JOURNAL**  
Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

**FEATURES**  
Location/Qualifiers  
1..457  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/isolate="Litom"  
/db\_xref="taxon:5507"  
1..148  
/product="internal transcribed spacer 1"  
149..306  
/product="5.8S ribosomal RNA"  
307..457

REFERENCE 1 (bases 1 to 457)  
 AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkmun,P.  
 TITLE Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants  
 JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)  
 REFERENCE 2 (bases 1 to 457)  
 AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.  
 JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES  
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 1..457  
 /organism="Fusarium oxysporum"  
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 /db\_xref="taxon:5507"  
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 307..457  
 /product="internal transcribed spacer 2"

ORIGIN  
 Query Match 100.0%; Score 18; DB 8; Length 457;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18  
 |||  
 Db 340 CGTTAATTCGCGTTCCTC 357

RESULT 36  
 AF440562 457 bp DNA linear PLN 24-SEP-2003  
 DEFINITION *Fusarium oxysporum* isolate PE13 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.  
 ACCESSION AF440562  
 VERSION AF440562.1 GI:18034430  
 KEYWORDS *Fusarium oxysporum*  
 SOURCE *Fusarium oxysporum*  
 ORGANISM *Fusarium oxysporum*  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; *Fusarium*; *Fusarium oxysporum* complex.  
 REFERENCE 1 (bases 1 to 457)  
 AUTHORS Bao,J.R., Fravel,D.R., O'Neill,N.R., Lazarovits,G. and van Berkmun,P.  
 TITLE Genetic analysis of pathogenic and nonpathogenic *Fusarium oxysporum* from tomato plants  
 JOURNAL Can. J. Bot. 80 (3), 271-279 (2002)  
 REFERENCE 2 (bases 1 to 457)  
 AUTHORS Bao,J.R., Fravel,D.R. and Lazarovits,G.  
 JOURNAL Direct Submission  
 TITLE Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES  
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 1..457  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /isolate="PE13"  
 /db\_xref="taxon:5507"  
 1..148  
 /product="internal transcribed spacer 1"  
 149..306  
 /product="5.8S ribosomal RNA"  
 307..457  
 /product="internal transcribed spacer 2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 457;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18  
 |||  
 Db 340 CGTTAATTCGCGTTCCTC 357

RESULT 37  
 AF055220 458 bp DNA linear PLN 29-JUN-2000  
 DEFINITION *Fusarium oxysporum* strain FO 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
 ACCESSION AF055220  
 VERSION AF055220  
 KEYWORDS *Fusarium oxysporum*  
 SOURCE *Fusarium oxysporum*  
 ORGANISM *Fusarium oxysporum*  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; *Fusarium*; *Fusarium oxysporum* complex.  
 REFERENCE 1 (bases 1 to 458)  
 AUTHORS Dodd,S.L., Crowhurst,R.N., Rodrigo,A.G., Samuels,G.J., Hill,R.A. and Stewart,A.  
 TITLE Examination of *Trichoderma* phylogenies derived from ribosomal DNA sequence data  
 JOURNAL Mycol. Res. 104, 23-34 (2000)  
 REFERENCE 2 (bases 1 to 458)  
 AUTHORS Dodd,Wilson,S.L., Crowhurst,R.N., Rodrigo,A.G. and Stewart,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-MAR-1998) Soil, Plant and Ecological Science Division, Lincoln University, P.O. Box 84, Canterbury, New Zealand  
 COMMENT On Apr 16, 1998 this sequence version replaced gi:3025822.  
 FEATURES  
 source  
 1..458  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /strain="FO"  
 /db\_xref="taxon:5507"  
 /note="pathogen of squash vegetable"  
 <1..6  
 /product="18S ribosomal RNA"  
 7..153  
 /product="internal transcribed spacer 1"  
 /note="ITS-1"  
 154..311  
 /product="5.8S ribosomal RNA"  
 312..>458  
 /product="internal transcribed spacer 2"  
 /note="ITS-2"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCCTC 18  
 |||  
 Db 345 CGTTAATTCGCGTTCCTC 362

RESULT 38  
 AY259214 460 bp DNA linear PLN 28-APR-2003  
 DEFINITION *Fusarium oxysporum* f. sp. *vasinfectum* 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
 ACCESSION AY259214

VERSION	AY2959214.1	GI:30171326
KEYWORDS	Fusarium oxysporum f. sp. vasinfectum Fusarium oxysporum f. sp. vasinfectum Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; mitosporic Hypocerales; Fusarium;	
SOURCE ORGANISM	Fusarium oxysporum complex. 1 (bases 1 to 460) Abd-Elisalam, K.A.	
REFERENCE AUTHORS	ITS sequence regions in Fov	
TITLE	Unpublished	
JOURNAL	2 (bases 1 to 460)	
REFERENCE AUTHORS	Add-Elisalam, K.A.	
TITLE	Direct Submission	
JOURNAL	Submitted (20-MAR-2003) Molecular Markers Lab., Plant Pathology Research Institute, 9-Gmaa St., Giza, 002 12619, Egypt	
FEATURES	location/Qualifiers	
SOURCE	1..460 /organism="Fusarium oxysporum f. sp. vasinfectum" /mol_type="genomic DNA" /db_xref="taxon:61374" /note="forma_specialis: vasinfectum"	
rRNA	<1..120 /product="18S ribosomal RNA"	
misc_RNA	121..240 /product="internal transcribed spacer 1"	
rRNA	241..320 /product="5.8S ribosomal RNA"	
misc_RNA	321..400 /product="internal transcribed spacer 2"	
rRNA	401..>460 /product="28S ribosomal RNA"	
ORIGIN		
Query Match	100.0%; Score 18; DB 8; Length 460;	
Best Local Similarity	100.0%; Pred. No. 26;	
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 CGTTAATTCGGCTTCTC 18       Db 343 CGTTAATTCGGCTTCTC 360	
RESULT 39		
LOCUS	AY208788 496 bp DNA linear PLN 30-JUN-2004	
DEFINITION	Fusarium oxysporum isolate Po23 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.	
ACCESSION	AY208788	
VERSION	AY208788.2 GI:40385898	
KEYWORDS	Fusarium oxysporum	
SOURCE ORGANISM	Fusarium oxysporum Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; mitosporic Hypocerales; Fusarium;	
REFERENCE AUTHORS	Fusarium oxysporum complex. 1 (bases 1 to 496) Gure,A., Wahlstrom,K. and Stenlid,J.	
TITLE	Diversity of Fungi Associated with Seeds of Tropical Forest Trees: Podocarpus falcatus and Prunus africana	
JOURNAL	Unpublished	
REFERENCE AUTHORS	2 (bases 1 to 496)	
TITLE	Gure,A. and Stenlid,J.	
JOURNAL	Direct Submission	
REFERENCE AUTHORS	Submitted (30-DEC-2002) Forest Mycology & Pathology, Swedish University of Agricultural Sciences, Ulls vag 26A, Uppsala, Uppland	
TITLE	750 07, Sweden	
JOURNAL	3 (bases 1 to 496)	
REFERENCE AUTHORS	Gure,A. and Stenlid,J.	
TITLE	Direct Submission	
JOURNAL	Submitted (30-DEC-2003) Forest Mycology & Pathology, Swedish University of Agricultural Sciences, Ulls vag 26A, Uppsala, Uppland	

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REMARK      750 07, Sweden
COMMENT     Sequence update by submitter
            On Dec 30, 2003 this sequence version replaced gi:26932934.
FEATURES
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            1..496
                /organism="Fusarium oxysporum"
                /mol_type="genomic DNA"
                /isolate="IPO23"
                /db_xref="taxon:5507"
            1..496
                /note="contains internal transcribed spacer 1, 5.8S
                ribosomal RNA, and internal transcribed spacer 2"

ORIGIN
Query Match          100.0%; Score 18; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTATTCCGGTTCCTC 18
         |||||
Db       357 CGTTATTCCGGTTCCTC 374

RESULT 40
LOCUS   AY243058                      497 bp    DNA             linear   PLN 14-APR-2003
DEFINITION Ascomycete sp. Dune17 internal transcribed spacer 1, partial
           sequence; 5.8S ribosomal RNA gene, complete sequence, and internal
           transcribed spacer 2, partial sequence.
ACCESSION AY243058
VERSION   AY243058.1 GI:29826153
KEYWORDS
SOURCE    ascomycete sp. Dune17
ORGANISM  ascomycete sp. Dune17
REFERENCE Eukaryota; Fungi; Ascomycota.
TITLE     1 (bases 1 to 497)
AUTHORS   Beckstead,J. and Parker,I.M.
JOURNAL   Invasiveness of Ammophila arenaria: Release from soil-borne
REFERENCE Unpublished
TITLE     2 (bases 1 to 497)
AUTHORS   Gambetta,G., Gilbert,G.S. and Parker,I.M.
JOURNAL   Direct Submission
TITLE     Submitted (24-FEB-2003) Ecology and Evolutionary Biology,
AUTHORS   University of California, Santa Cruz, 1156 High St., EMS, Santa
JOURNAL   Cruz, CA 95064, USA
FEATURES
    source
        Location/Qualifiers
            1..497
                /organism="ascomycete sp. Dune17"
                /mol_type="genomic DNA"
                /strain="Dune17"
                /isolation_source="plants grown in greenhouse in
                unsterilized soil collected from Dune Beach, Half Moon
                Bay, California"
                /specific_host="Ammophila arenaria"
                /db_xref="taxon:227272"
            <1..128
                /product="internal transcribed spacer 1"
            129..278
                /product="5.8S ribosomal RNA"
            279..>497
                /product="internal transcribed spacer 2"

ORIGIN
Query Match          100.0%; Score 18; DB 8; Length 497;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTATTCGGGTTCCTC 18
         |||||
Db       320 CGTTATTCGGGTTCCTC 337

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RESULT 41  
AY247553/c 501 bp DNA linear PLN 27-APR-2003  
LOCUS  
DEFINITION Fusarium oxysporum f. sp. vasinfectum isolate BANGD12/B2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
ACCESSION AY247553.1 GI:30143797  
VERSION  
KEYWORDS Fusarium oxysporum f. sp. vasinfectum  
SOURCE Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
ORGANISM  
REFERENCE 1 (bases 1 to 501)  
AUTHORS Thornton,C.R., Groenhof,A.C., Forrest,R., Lamotte,R. and Talbot,N.J.  
TITLE A one-step, immuno-chromatographic lateral flow device for the detection and quantification of Rhizoctonia solani in soil  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 501)  
AUTHORS Thornton,C.R., Groenhof,A.C., Forrest,R., Lamotte,R. and Talbot,N.J.  
TITLE Direct Submission  
REFERENCE Submitted (03-MAR-2003) Biological Sciences, University of Exeter, Perry Road, Exeter, Devon EX4 4QG, England  
JOURNAL Location/Qualifiers  
FEATURES  
source  
1. 501  
/organism="Fusarium oxysporum f. sp. vasinfectum"  
/mol\_type="genomic DNA"  
/isolate="BANGD12/B2"  
/db\_xref="taxon:61374"  
/note="forma\_specialis: vasinfectum"  
complement(<1..>501)  
/note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, and internal transcribed spacer 2"

ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 501;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTTAATTCGCGTTCCTC 18  
Db 119 CGTTAATTCGCGTTCCTC 102

RESULT 42  
AY262831 501 bp DNA linear PLN 04-MAY-2003  
LOCUS  
DEFINITION Fusarium oxysporum f. sp. vasinfectum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
ACCESSION AY262831  
VERSION AY262831.1 GI:30350871  
KEYWORDS Fusarium oxysporum f. sp. vasinfectum  
SOURCE Fusarium oxysporum f. sp. vasinfectum  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
REFERENCE 1 (bases 1 to 501)  
AUTHORS Abd-Elasalam,K.A.  
TITLE Molecular diagnostic of Fusarium oxysporum f. sp. vasinfectum  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 501)  
AUTHORS Abd-Elasalam,K.A.  
TITLE Direct Submission  
JOURNAL Submitted (27-MAR-2003) Molecular Markers Lab., Plant Pathology Research Institute, 9-Gmaa St., 002 12619, Egypt  
FEATURES Location/Qualifiers

source  
1. 501  
/organism="Fusarium oxysporum f. sp. vasinfectum"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:61374"  
/note="forma\_specialis: vasinfectum"  
rRNA  
1. 115  
/product="18S ribosomal RNA"  
misc\_RNA  
116..205  
/product="internal transcribed spacer 1"  
rRNA  
206..310  
/product="5.8S ribosomal RNA"  
misc\_RNA  
311..420  
/product="internal transcribed spacer 2"  
rRNA  
421..>501  
/product="28S ribosomal RNA"

ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 501;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTTAATTCGCGTTCCTC 18  
Db 349 CGTTAATTCGCGTTCCTC 366

RESULT 43  
AY354386 501 bp DNA linear PLN 15-SEP-2003  
LOCUS  
DEFINITION Fusarium oxysporum f. sp. radialis-lycopersici 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
ACCESSION AY354386  
VERSION AY354386.1 GI:34559391  
KEYWORDS Fusarium oxysporum f. sp. radialis-lycopersici  
SOURCE Fusarium oxysporum f. sp. radialis-lycopersici  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
REFERENCE 1 (bases 1 to 501)  
AUTHORS Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and Cifuentes,D.  
TITLE Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs  
JOURNAL Span. J. Agric. Res. 1 (3) (2003) in press  
REFERENCE 2 (bases 1 to 501)  
AUTHORS Arroyo-Garcia,R., Cenis,J.L., Tello,J., Martinez-Zapater,J.M. and Cifuentes,D.  
TITLE Direct Submission  
JOURNAL Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia) 30150, Spain  
FEATURES Location/Qualifiers  
1. 501  
/organism="Fusarium oxysporum f. sp. radialis-lycopersici"  
/mol\_type="genomic DNA"  
/strain="For1-12"  
/specific\_host="tomato"  
/db\_xref="taxon:61372"  
/country="Spain"  
/note="forma\_specialis: radialis-lycopersici"  
rRNA  
1. 28  
/product="18S ribosomal RNA"  
misc\_RNA  
29..175  
/product="internal transcribed spacer 1"  
rRNA  
176..333  
/product="5.8S ribosomal RNA"  
misc\_RNA  
334..484  
/product="internal transcribed spacer 2"  
rRNA  
485..>501  
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
 |||||  
 Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 44  
 AV354388 501 bp DNA linear PLN 15-SEP-2003  
 LOCUS AV354388  
 DEFINITION Fusarium oxysporum f. sp. dianthi 18S ribosomal RNA gene, partial  
 sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene  
 and internal transcribed spacer 2, complete sequence; and 28S  
 ribosomal RNA gene, partial sequence.

ACCESSION AV354388  
 VERSION AV354388.1 GI:34559393  
 KEYWORDS  
 ORGANISM Fusarium oxysporum f. sp. dianthi  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 501)  
 Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and  
 Cluettues, D.  
 Genetic relationships among seven specialized forms of Fusarium  
 oxysporum determined by DNA sequencing of the ITS region and AFLPs  
 Span. J. Agric. Res. 1 (3) (2003) In press

JOURNAL 2 (bases 1 to 501)  
 Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and  
 Cluettues, D.  
 Direct Submission  
 Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca  
 (Murcia) 30150, Spain

TITLE Location/Qualifiers

FEATURES  
 source  
 1..501  
 /organism="Fusarium oxysporum f. sp. dianthi"  
 /mol\_type="genomic DNA"  
 /strain="Sur-10"  
 /specific\_host="carnation"  
 /db\_xref="taxon:42551"  
 /country="Spain"  
 /note="forma\_specialis: dianthi"  
 <1..28  
 /product="18S ribosomal RNA"  
 29..175  
 /product="internal transcribed spacer 1"  
 176..333  
 /product="5.8S ribosomal RNA"  
 334..484  
 /product="internal transcribed spacer 2"  
 485..>501  
 /product="28S ribosomal RNA"

ORIGIN  
 Query Match 100.0%; Score 18; DB 8; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
 |||||  
 Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 45  
 AV354389 501 bp DNA linear PLN 15-SEP-2003  
 LOCUS AV354389  
 DEFINITION Fusarium oxysporum f. sp. dianthi 18S ribosomal RNA gene, partial  
 sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene  
 and internal transcribed spacer 2, complete sequence; and 28S

ribosomal RNA gene, partial sequence.

ACCESSION AV354389  
 VERSION AV354389.1 GI:34559394  
 KEYWORDS  
 SOURCE  
 ORGANISM Fusarium oxysporum f. sp. dianthi  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 501)  
 Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and  
 Cluettues, D.  
 Genetic relationships among seven specialized forms of Fusarium  
 oxysporum determined by DNA sequencing of the ITS region and AFLPs  
 Span. J. Agric. Res. 1 (3) (2003) In press

JOURNAL 2 (bases 1 to 501)  
 Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and  
 Cluettues, D.  
 Direct Submission  
 Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca  
 (Murcia) 30150, Spain

TITLE Location/Qualifiers

FEATURES  
 source  
 1..501  
 /organism="Fusarium oxysporum f. sp. dianthi"  
 /mol\_type="genomic DNA"  
 /strain="Gsa-2"  
 /specific\_host="carnation"  
 /db\_xref="taxon:42551"  
 /country="Spain"  
 /note="forma\_specialis: dianthi"  
 <1..28  
 /product="18S ribosomal RNA"  
 29..175  
 /product="internal transcribed spacer 1"  
 176..333  
 /product="5.8S ribosomal RNA"  
 334..484  
 /product="internal transcribed spacer 2"  
 485..>501  
 /product="28S ribosomal RNA"

ORIGIN  
 Query Match 100.0%; Score 18; DB 8; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
 |||||  
 Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 46  
 AV354390 501 bp DNA linear PLN 15-SEP-2003  
 LOCUS AV354390  
 DEFINITION Fusarium oxysporum f. sp. melonis 18S ribosomal RNA gene, partial  
 sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene  
 and internal transcribed spacer 2, complete sequence; and 28S  
 ribosomal RNA gene, partial sequence.

ACCESSION AV354390  
 VERSION AV354390.1 GI:34559395  
 KEYWORDS  
 SOURCE  
 ORGANISM Fusarium oxysporum f. sp. melonis  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 501)  
 Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and  
 Cluettues, D.  
 Genetic relationships among seven specialized forms of Fusarium  
 oxysporum determined by DNA sequencing of the ITS region and AFLPs  
 Span. J. Agric. Res. 1 (3) (2003) In press

JOURNAL 2 (bases 1 to 501)

**AUTHORS** Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia) 30150, Spain  
**FEATURES** location/Qualifiers  
 1..501  
 /organism="Fusarium oxysporum f. sp. melonis"  
 /mol\_type="genomic DNA"  
 /strain="ATCC 28858"  
 /specific\_host="muskmelon"  
 /db\_xref="ATCC:28858"  
 /db\_xref="taxon:61369"  
 /country="France"  
 /note="forma\_specialis: melonis"  
 <1..28  
 /product="18S ribosomal RNA"  
 29..175  
 /product="internal transcribed spacer 1"  
 176..333  
 /product="5.8S ribosomal RNA"  
 334..484  
 /product="internal transcribed spacer 2"  
 485..>501  
 /product="28S ribosomal RNA"

**ORIGIN**  
 Query Match 100.0%; Score 18; DB 8; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CGTTAATTCGGCTTCCTC 18  
 |||||  
 Db 367 CGTTAATTCGGCTTCCTC 384

**RESULT 47**  
**LOCUS** AY354393 501 bp DNA linear PLN 15-SEP-2003  
**DEFINITION** Fusarium oxysporum f. sp. melonis 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
**ACCESSION** AY354393  
**VERSION** AY354393.1 GI:34559398  
**KEYWORDS** Fusarium oxysporum f. sp. melonis  
**SOURCE** Fusarium oxysporum f. sp. melonis  
**ORGANISM** Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
 1 (bases 1 to 501)  
 Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.  
**REFERENCE** Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs Span. J. Agric. Res. 1 (3) (2003) In press  
 2 (bases 1 to 501)  
 Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia) 30150, Spain  
**FEATURES** location/Qualifiers  
 1..501  
 /organism="Fusarium oxysporum f. sp. melonis"  
 /mol\_type="genomic DNA"  
 /strain="Fon 1"  
 /specific\_host="muskmelon"  
 /db\_xref="taxon:61369"  
 /country="Spain"  
 /note="forma\_specialis: melonis"  
 <1..28

**ORIGIN**  
 Query Match 100.0%; Score 18; DB 8; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CGTTAATTCGGCTTCCTC 18  
 |||||  
 Db 367 CGTTAATTCGGCTTCCTC 384

**misc\_RNA** /product="18S ribosomal RNA"  
 29..175  
 /product="internal transcribed spacer 1"  
 176..333  
 /product="5.8S ribosomal RNA"  
 334..484  
 /product="internal transcribed spacer 2"  
 485..>501  
 /product="28S ribosomal RNA"

**ORIGIN**  
 Query Match 100.0%; Score 18; DB 8; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CGTTAATTCGGCTTCCTC 18  
 |||||  
 Db 367 CGTTAATTCGGCTTCCTC 384

**RESULT 48**  
**LOCUS** AY354396 501 bp DNA linear PLN 15-SEP-2003  
**DEFINITION** Fusarium oxysporum f. nivaeum strain Fon 1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
**ACCESSION** AY354396  
**VERSION** AY354396.1 GI:34559401  
**KEYWORDS** Fusarium oxysporum f. nivaeum  
**SOURCE** Fusarium oxysporum f. nivaeum  
**ORGANISM** Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
 1 (bases 1 to 501)  
 Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.  
**REFERENCE** Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs Span. J. Agric. Res. 1 (3) (2003) In press  
 2 (bases 1 to 501)  
 Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia) 30150, Spain  
**FEATURES** location/Qualifiers  
 1..501  
 /organism="Fusarium oxysporum f. nivaeum"  
 /mol\_type="genomic DNA"  
 /strain="Fon 1"  
 /specific\_host="watermelon"  
 /db\_xref="taxon:120297"  
 /country="Spain"  
 /note="forma: nivaeum"  
 <1..28  
 /product="18S ribosomal RNA"  
 29..175  
 /product="internal transcribed spacer 1"  
 176..333  
 /product="5.8S ribosomal RNA"  
 334..484  
 /product="internal transcribed spacer 2"  
 485..>501  
 /product="28S ribosomal RNA"

**ORIGIN**  
 Query Match 100.0%; Score 18; DB 8; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CGTTAATTCGGCTTCCTC 18  
 |||||  
 Db 367 CGTTAATTCGGCTTCCTC 384

Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 49  
AY354397  
LOCUS  
DEFINITION  
501 bp DNA linear PLN 15-SEP-2003  
Fusarium oxysporum f. niveum strain Fon 7 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AY354397.1 GI:34559402  
Fusarium oxysporum f. niveum  
Fusarium oxysporum f. niveum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
1 (bases 1 to 501)  
Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.  
Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs Span. J. Agric. Res. 1 (3) (2003) In press  
2 (bases 1 to 501)  
Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.  
Direct Submission  
Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia)  
Location/Qualifiers  
1. 501  
/organism="Fusarium oxysporum f. niveum"  
/mol\_type="genomic DNA"  
/strain="Fon 7"  
/specific\_host="watermelon"  
/db\_xref="taxon:120297"  
/country="Spain"  
/note="forma: 'niveum'  
<1. .28  
/product="18S ribosomal RNA"  
29. .175  
/product="internal transcribed spacer 1"  
176. .333  
/product="5.8S ribosomal RNA"  
334. .484  
/product="internal transcribed spacer 2"  
485. .>501  
/product="28S ribosomal RNA"

ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 501;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
|||||  
Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 50  
AY354398  
LOCUS  
DEFINITION  
501 bp DNA linear PLN 15-SEP-2003  
Fusarium oxysporum f. sp. lagenariae 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AY354398.1 GI:34559403  
Fusarium oxysporum f. sp. lagenariae  
Fusarium oxysporum f. sp. lagenariae

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1. 501  
/organism="Fusarium oxysporum f. sp. lagenariae"  
/mol\_type="genomic DNA"  
/strain="ATCC 18143"  
/db\_xref="ATCC:18143"  
/db\_xref="taxon:120295"  
/country="Japan"  
/note="forma: 'lagenariae'  
<1. .28  
/product="18S ribosomal RNA"  
29. .175  
/product="internal transcribed spacer 1"  
176. .333  
/product="5.8S ribosomal RNA"  
334. .484  
/product="internal transcribed spacer 2"  
485. .>501  
/product="28S ribosomal RNA"

ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 501;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
|||||  
Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 51  
AY354399  
LOCUS  
DEFINITION  
501 bp DNA linear PLN 15-SEP-2003  
Fusarium oxysporum f. sp. juiffae 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AY354399.1 GI:34559404  
Fusarium oxysporum f. sp. juiffae  
Fusarium oxysporum f. sp. juiffae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.  
1 (bases 1 to 501)  
Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.  
Genetic relationships among seven specialized forms of Fusarium oxysporum determined by DNA sequencing of the ITS region and AFLPs Span. J. Agric. Res. 1 (3) (2003) In press  
2 (bases 1 to 501)  
Arroyo-Garcia, R., Cenis, J.L., Tello, J., Martinez-Zapater, J.M. and Cifuentes, D.  
Direct Submission  
Submitted (29-JUL-2003) Biotechnology, IMIDA, Mayor s/n, La Alberca (Murcia)  
Location/Qualifiers



source 1. .501  
 /organism="Fusarium oxysporum f. sp. Jaffae"  
 /mol\_type="genomic DNA"  
 /strain="ATCC 28860"  
 /db\_xref="ATCC:28860"  
 /db\_xref="taxon:243110"  
 /country="Japan"  
 /note="forma\_specialis: Jaffae"  
 <1. .28  
 /product="18S ribosomal RNA"  
 29. .175  
 /product="internal transcribed spacer 1"  
 176. .333  
 /product="5.8S ribosomal RNA"  
 334. .484  
 /product="internal transcribed spacer 2"  
 485. .>501  
 /product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
 ||||||||||||||||  
 Db 367 CGTTAATTCGCGTTCCTC 384

RESULT 52  
 AF069310 506 bp rRNA linear PLN 08-JUN-1999  
 LOCUS  
 DEFINITION Fusarium oxysporum internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
 AF069310  
 ACCESSION AF069310.1 GI:5006327  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Fusarium oxysporum  
 Fusarium oxysporum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; mitosporic Hypocerales; Fusarium; Fusarium oxysporum complex.  
 1 (bases 1 to 506)  
 /organism="Fusarium oxysporum"  
 /mol\_type="rRNA"  
 /strain="93138"  
 /db\_xref="taxon:5507"  
 /country="Finland;Espoo"  
 /note="Isolated from barley root in 1986"  
 1. .138  
 /product="internal transcribed spacer 1"  
 139. .296  
 /product="5.8S ribosomal RNA"  
 297. .446  
 /product="internal transcribed spacer 2"  
 /note="ITS2"  
 447. .>506  
 /product="28S ribosomal RNA"

REFERENCE  
 AUTHORS Paavainen-Huhtala,S., Hyvonen,J., Bulat,S.A. and Yli-Mattila,T.  
 TITLE RAPD-PCR, isozyme, rDNA RFLP and rDNA sequence analyses in identification of Finnish Fusarium oxysporum isolates  
 JOURNAL Mycol. Res. 103 (5), 625-634 (1999)  
 REFERENCE  
 AUTHORS Yli-Mattila,T. and Paavainen-Huhtala,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-MAY-1998) Lab. of Plant Physiology and Molecular Biology, Dept. of Biology, Univ. of Turku, Turku 20014, Finland  
 FEATURES  
 source  
 1. .506  
 /organism="Fusarium oxysporum"  
 /mol\_type="rRNA"  
 /strain="93138"  
 /db\_xref="taxon:5507"  
 /country="Finland;Espoo"  
 /note="Isolated from barley root in 1986"  
 1. .138  
 /product="internal transcribed spacer 1"  
 139. .296  
 /product="5.8S ribosomal RNA"  
 297. .446  
 /product="internal transcribed spacer 2"  
 /note="ITS2"  
 447. .>506  
 /product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 506;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
 ||||||||||||||||  
 Db 350 CGTTAATTCGCGTTCCTC 367

RESULT 54  
 AY127698 506 bp DNA linear PLN 14-AUG-2002  
 LOCUS

Query Match 100.0%; Score 18; DB 8; Length 506;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
 ||||||||||||||||  
 Db 330 CGTTAATTCGCGTTCCTC 347

RESULT 53  
 AY127697 506 bp DNA linear PLN 14-AUG-2002  
 LOCUS  
 DEFINITION Fusarium oxysporum 40-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
 AY127697  
 ACCESSION AY127697.1 GI:22252968  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Fusarium oxysporum  
 Fusarium oxysporum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; mitosporic Hypocerales; Fusarium; Fusarium oxysporum complex.  
 1 (bases 1 to 506)  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /isolate="40-1"  
 /specific\_host="Gossypium hirsutum"  
 /db\_xref="taxon:5507"  
 /country="Australia"  
 <1. .20  
 /product="18S ribosomal RNA"  
 21. .158  
 /product="internal transcribed spacer 1"  
 159. .316  
 /product="5.8S ribosomal RNA"  
 317. .468  
 /product="internal transcribed spacer 2"  
 469. .>506  
 /product="28S ribosomal RNA"

REFERENCE  
 AUTHORS Becerra-Lopez Lavalley,L.A., Saleeba,J.A. and Lyon,B.R.  
 TITLE Molecular identification and classification of fungi isolated from stem tissue of cotton (Gossypium hirsutum L)  
 JOURNAL Unpublished  
 3 (bases 1 to 506)  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /isolate="40-1"  
 /specific\_host="Gossypium hirsutum"  
 /db\_xref="taxon:5507"  
 /country="Australia"  
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 21. .158  
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 159. .316  
 /product="5.8S ribosomal RNA"  
 317. .468  
 /product="internal transcribed spacer 2"  
 469. .>506  
 /product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 506;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
 ||||||||||||||||  
 Db 350 CGTTAATTCGCGTTCCTC 367

RESULT 54  
 AY127698 506 bp DNA linear PLN 14-AUG-2002  
 LOCUS

DEFINITION Fusarium oxysporum 48-2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AY127698 GI:22252969

VERSION

KEYWORDS

SOURCE Fusarium oxysporum

ORGANISM

REFERENCE 1 (bases 1 to 506)  
Becerra-Lopez Lavalle, L.A.  
Fusarium wilt of cotton: Molecular approaches towards durable disease resistance in *Gossypium hirsutum* L  
Thesis (2002) The University of Sydney, School of Biological Sciences, Macleay Building A12, Sydney, NSW, Australia, In press

REFERENCE 2 (bases 1 to 506)  
Becerra-Lopez Lavalle, L.A., Saleeba, J.A. and Lyon, B.R.  
Molecular identification and classification of fungi isolated from stem tissue of cotton (*Gossypium hirsutum* L)  
Unpublished

REFERENCE 3 (bases 1 to 506)  
Becerra-Lopez Lavalle, L.A., Saleeba, J.A. and Lyon, B.R.  
Direct Submission  
Submitted (27-JUN-2002) School of Biological Sciences, The University of Sydney, Macleay Building A12, Science Road, NSW 2006, Australia

FEATURES

source

1..506  
/organism="Fusarium oxysporum"  
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/isolate="48-2"  
/specific\_host="Gossypium hirsutum"  
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/country="Australia"  
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/product="18S ribosomal RNA"  
21..158  
/product="internal transcribed spacer 1"  
159..316  
/product="5.8S ribosomal RNA"  
317..468  
/product="internal transcribed spacer 2"  
469..>506  
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 506;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCTC 18  
|||||  
DB 350 CGTTAATTCGGCTTCCTC 367

RESULT 55  
AY127699 506 bp DNA linear PLN 14-AUG-2002

LOCUS Fusarium oxysporum 49-2 18S ribosomal RNA gene, partial sequence;  
DEFINITION internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AY127699 GI:22252970

VERSION

KEYWORDS

SOURCE Fusarium oxysporum

ORGANISM

REFERENCE 1 (bases 1 to 515)  
Becerra-Lopez Lavalle, L.A., Saleeba, J.A. and Lyon, B.R.  
Direct Submission  
Submitted (24-FEB-2004) Antioxidants Research Lab, Korea Research Institute of Bioscience and Biotechnology, Yuseong-Gu, Daejeon, Chungnam 305-333, South Korea  
Location/Qualifiers

REFERENCE 1 (bases 1 to 506)  
Becerra-Lopez Lavalle, L.A.  
Fusarium wilt of cotton: Molecular approaches towards durable disease resistance in *Gossypium hirsutum* L  
Thesis (2002) The University of Sydney, School of Biological Sciences, Macleay Building A12, Sydney, NSW, Australia, In press

REFERENCE 2 (bases 1 to 506)  
Becerra-Lopez Lavalle, L.A., Saleeba, J.A. and Lyon, B.R.  
Molecular identification and classification of fungi isolated from stem tissue of cotton (*Gossypium hirsutum* L)  
Unpublished

REFERENCE 3 (bases 1 to 506)  
Becerra-Lopez Lavalle, L.A., Saleeba, J.A. and Lyon, B.R.  
Direct Submission  
Submitted (27-JUN-2002) School of Biological Sciences, The University of Sydney, Macleay Building A12, Science Road, Sydney, NSW 2006, Australia

FEATURES

source

1..506  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/isolate="49-2"  
/specific\_host="Gossypium hirsutum"  
/db\_xref="taxon:5507"  
/country="Australia"  
<1..20  
/product="18S ribosomal RNA"  
21..158  
/product="internal transcribed spacer 1"  
159..316  
/product="5.8S ribosomal RNA"  
317..468  
/product="internal transcribed spacer 2"  
469..>506  
/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 506;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGGCTTCCTC 18  
|||||  
DB 350 CGTTAATTCGGCTTCCTC 367

RESULT 56  
AY555719 515 bp DNA linear PLN 20-MAR-2004

LOCUS Fusarium oxysporum strain F35 18S ribosomal RNA gene, partial  
DEFINITION sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AY555719 GI:45445262

VERSION

KEYWORDS

SOURCE Fusarium oxysporum

ORGANISM

REFERENCE 1 (bases 1 to 515)  
Li, C.-T., Wang, Q.-J., Mo, E.-K., Xu, B.-J., Fang, Z.-M. and Sung, C.-K.  
Taxol production by endophytes isolated from yew tree, *Taxus cuspidata*  
Unpublished

REFERENCE 2 (bases 1 to 515)  
Li, C.-T.  
Direct Submission  
Submitted (24-FEB-2004) Antioxidants Research Lab, Korea Research Institute of Bioscience and Biotechnology, Yuseong-Gu, Daejeon, Chungnam 305-333, South Korea  
Location/Qualifiers

source

1. 515

/organism="Fusarium oxysporum"

/mol\_type="genomic DNA"

/strain="F35"

/specific\_host="Taxus cuspidata"

/db\_xref="taxon:5507"

/country="South Korea: Kang-Won"

<1. .24

/product="18S ribosomal RNA"

25. .174

/product="internal transcribed spacer 1"

175. .332

/product="5.8S ribosomal RNA"

333. .482

/product="internal transcribed spacer 2"

483. .515

/product="28S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 515;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18

|||||

Db 365 CGTTAATTCGGCTTCCTC 382

RESULT 57

FOU34566

LOCUS FOU34566 530 bp DNA linear PLN 15-JUL-1998

DEFINITION Fusarium oxysporum NRRL 22902 Internal transcribed spacer RNA.

ACCESSION U34566

VERSION U34566.1 GI:1808932

KEYWORDS

SOURCE

ORGANISM

Fusarium oxysporum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;

Fusarium oxysporum complex.

1 (bases 1 to 520)

O'Donnell, K. and Cigelnik, E.

Two divergent intragenomic rDNA ITS2 types within a monophyletic

lineage of the fungus Fusarium are nonorthologous

Mol. Phylogenet. Evol. 7 (1), 103-116 (1997)

JOURNAL

MEDLINE

97159566

PUBMED

9007025

REFERENCE

2 (bases 1 to 520)

O'Donnell, K., Cigelnik, E. and Casper, H.H.

Molecular phylogenetic, morphological, and mycotoxin data support

reidentification of the Quorn mycoprotein fungus as Fusarium

venenatum

JOURNAL

MEDLINE

98162098

PUBMED

9501477

REFERENCE

3 (bases 1 to 520)

O'Donnell, K., Cigelnik, E. and Nirenberg, H.I.

Molecular systematics and phylogeography of the Gibberella

fujiokuroi species complex

Mycologia 90 (3), 465-493 (1998)

4 (bases 1 to 520)

O'Donnell, K. and Cigelnik, E.

Direct Submission

Submitted (21-AUG-1995) Kerry O'Donnell, NCAUR, USDA, 1815 N.

University St., Peoria, IL 61604, USA

JOURNAL

FEATURES

source

1. .520

/organism="Fusarium oxysporum"

/mol\_type="genomic DNA"

/strain="NRRL 22902"

/db\_xref="taxon:5507"

1. .520

/product="internal transcribed spacer"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 520;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18

|||||

Db 369 CGTTAATTCGGCTTCCTC 386

RESULT 58

AF176656

LOCUS AF176656 521 bp DNA linear PLN 17-SEP-2000

DEFINITION Fusarium oxysporum 18S ribosomal RNA gene, partial sequence;

internal transcribed spacer 1, 5.8S ribosomal RNA gene, and

internal transcribed spacer 2, complete sequence; and 28S ribosomal

RNA gene, partial sequence.

ACCESSION AF176656

VERSION AF176656.1 GI:10179438

KEYWORDS

SOURCE

ORGANISM

Fusarium oxysporum

Fusarium oxysporum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;

Fusarium oxysporum complex.

1 (bases 1 to 521)

Grundens, E., Chen, W. and Crane, J.L.

Fungi Colonizing Microclerotia of Verticillium dahliae

Unpublished

2 (bases 1 to 521)

Grundens, E., Chen, W. and Crane, J.L.

Direct Submission

Submitted (10-AUG-1999) Center for Biodiversity, Illinois Natural

History Survey, 607 E. Peabody Dr., Champaign, IL 61820, USA

JOURNAL

FEATURES

source

1. .521

/organism="Fusarium oxysporum"

/mol\_type="genomic DNA"

/db\_xref="taxon:5507"

<1. .521

/note="contains 18S ribosomal RNA, internal transcribed

spacer 1, 5.8S ribosomal RNA, internal transcribed spacer

2, and 28S ribosomal RNA"

misc\_RNA

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 521;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18

|||||

Db 345 CGTTAATTCGGCTTCCTC 362

RESULT 59

AF502841

LOCUS AF502841 523 bp DNA linear PLN 13-MAY-2002

DEFINITION leaf litter ascomycete strain ita330 isolate 1000501231 internal

transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,

complete sequence; and internal transcribed spacer 2, partial

sequence.

ACCESSION AF502841

VERSION AF502841.1 GI:20531648

KEYWORDS

SOURCE

ORGANISM

leaf litter ascomycete strain ita330

leaf litter ascomycete strain ita330

Eukaryota; Fungi; Ascomycota.

1 (bases 1 to 523)

Gilbert, G.S., Garbelotto, M., Chapela, I., Moeller, C. and

Dreyfuss, M.M.

Biogeography of leaf litter fungi

Unpublished

REFERENCE 2 (bases 1 to 523)  
 AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA  
 FEATURES  
 source  
 1..523  
 /organism="leaf litter ascomycete strain its330"  
 /mol\_type="genomic DNA"  
 /strain="its330"  
 /isolate="1000501231"  
 /specific\_host="Mammea americana"  
 /db\_xref="taxon:194113"  
 /country="Puerto Rico"  
 <1..163  
 /product="internal transcribed spacer 1"  
 164..318  
 /product="5.8S ribosomal RNA"  
 319..>523  
 /product="internal transcribed spacer 2"  
 ORIGIN  
 Query Match 100.0%; Score 18; DB 8; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 CGTTAATTCGGCTTCCTC 18  
 |||||  
 354 CGTTAATTCGGCTTCCTC 371  
 RESULT 60  
 AF242876 531 bp DNA linear PLN 12-APR-2000  
 LOCUS Fusarium oxysporum 18S ribosomal RNA gene, partial sequence;  
 DEFINITION internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal  
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA  
 gene, partial sequence.  
 AF242876  
 AF242876.1 GI:7542605  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Fusarium oxysporum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.  
 1 (bases 1 to 531)  
 Gomez-Ieyra,J.F., Ochoa-Sanchez,J.C., Loera-Quezada,M.,  
 Leal-Klvezas,D.S., Abeyratne,P., Nazari,R.N., Rodriguez-Garay,B.  
 and Martinez-Soriano,J.F.  
 Sensitive and specific PCR assay to detect the causal agent of the  
 Agave tequilana root rot  
 Unpublished  
 2 (bases 1 to 531)  
 Gomez-Ieyra,J.F., Ochoa-Sanchez,J.C., Leal-Klvezas,D.S. and  
 Martinez-Soriano,J.F.  
 Direct Submission  
 Submitted (08-MAR-2000) Biotechnology y Biocimica, Unidad de  
 Biotecnologia e Ingenieria Genetica de Plantas, CINVESTAV-IPN, km  
 9.6 Ibramleno norte, carr. Irapuato-Leon, Irapuato, Gto 36500,  
 Mexico  
 FEATURES  
 source  
 1..531  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /isolate="MMAVH13"  
 /specific\_host="Agave tequilana Weber var. Azul"  
 /db\_xref="taxon:5507"  
 <1..26  
 /product="18S ribosomal RNA"  
 27..174  
 /product="internal transcribed spacer 1"

RNA 175..331  
 /product="5.8S ribosomal RNA"  
 misc\_RNA 332..481  
 /product="internal transcribed spacer 2"  
 RNA 482..>531  
 /product="28S ribosomal RNA"  
 ORIGIN  
 Query Match 100.0%; Score 18; DB 8; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 CGTTAATTCGGCTTCCTC 18  
 |||||  
 365 CGTTAATTCGGCTTCCTC 382  
 RESULT 61  
 FOXYRNA 544 bp DNA linear PLN 14-JUN-2001  
 LOCUS Fusarium oxysporum 18S rRNA gene (partial), 5.8S rRNA gene, 28S  
 DEFINITION rRNA gene (partial), internal transcribed spacer 1 (ITS1) and  
 internal transcribed spacer 2 (ITS2).  
 X94173 X93902  
 X94173.1 GI:1122871  
 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;  
 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;  
 internal transcribed spacer 2; ITS1; ITS2.  
 SOURCE  
 Fusarium oxysporum  
 Fusarium oxysporum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.  
 1  
 Waalwijk,C., de Koning,J.R.A., Baayen,R.P. and Gams,W.  
 Discordant groupings of Fusarium spp. from sections Elegans,  
 lissolia and Diamina a based on ribosomal ITS1 and ITS2 sequences  
 Mycologia 88, 361-368 (1996)  
 2 (bases 1 to 544)  
 Waalwijk,C.  
 Direct Submission  
 Submitted (08-DEC-1995) C. Waalwijk, Research Inst. for Plant  
 Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS  
 On Jun 15, 2001 this sequence version replaced gi:1103570.  
 Overlaps with X78260.  
 FEATURES  
 source  
 1..544  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /strain="F101"  
 /specific\_host="carnation"  
 /db\_xref="taxon:5507"  
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 /gene="18S rRNA"  
 <1..30  
 /gene="18S rRNA"  
 /product="18S ribosomal RNA"  
 31..177  
 /note="internal transcribed spacer 1, ITS1"  
 178..335  
 /gene="5.8 rRNA"  
 178..335  
 /gene="5.8 rRNA"  
 /product="5.8 ribosomal RNA"  
 336..486  
 /note="internal transcribed spacer 2, ITS2"  
 487..544  
 /gene="28S rRNA"  
 487..>544  
 /gene="28S rRNA"  
 /product="28S ribosomal RNA"  
 ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18  
 |||||  
 Db 369 CGTTAATTCGGCTTCCTC 386

RESULT 62  
 FOVCB58 545 bp DNA linear PLN 16-JAN-1996  
 LOCUS F.oxysporum (f.sp.vasinflectum, BIE) 5.8S rRNA gene.  
 DEFINITION X78260.1 GI:467737  
 X78260 5.8S ribosomal RNA; 5.8S rRNA gene.  
 VERSION 5.8S ribosomal RNA; 5.8S rRNA gene.  
 KEYWORDS Fusarium oxysporum  
 SOURCE  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.

REFERENCE  
 AUTHORS Moricca,S., Kasuga,T., Mitchelson,K.R. and Ragazzi,A.  
 TITLE The sequence of the fusarium oxysporum f.s.p. vasinflectum 5.8S rRNA  
 and adjacent ITS 1 and ITS 2 regions  
 JOURNAL Fungal Genet. Newsl. 42, 53-55 (1995)  
 REFERENCE 2 (bases 1 to 545)  
 AUTHORS Mitchelson,K.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAR-1994) K.R. Mitchelson, Department of Molecular &  
 Cell Biology, University of Aberdeen, Aberdeen AB9 1AS, UK  
 FEATURES  
 source  
 1. 545  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /strain="BIE"  
 /sub\_species="f.sp.vasinflectum"  
 /db\_xref="taxon:5507"  
 /tissue\_type="Mycelium"  
 /clone\_lib="S.Moricca"  
 /lab\_host="Gossypium"  
 /note="host from Bie, Angola"  
 1. 545  
 /gene="5.8S rRNA"  
 1. 545  
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 /product="5.8S ribosomal RNA"

ORIGIN  
 Query Match 100.0%; Score 18; DB 8; Length 545;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18  
 |||||  
 Db 370 CGTTAATTCGGCTTCCTC 387

RESULT 63  
 FOVCB58 546 bp DNA linear PLN 16-JAN-1996  
 LOCUS F.oxysporum (f.sp.vasinflectum, Cuanza Bul) 5.8S rRNA gene.  
 DEFINITION X78259.1 GI:467738  
 X78259 5.8S ribosomal RNA; 5.8S rRNA gene.  
 VERSION 5.8S ribosomal RNA; 5.8S rRNA gene.  
 KEYWORDS Fusarium oxysporum  
 SOURCE  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.  
 REFERENCE 1 (bases 1 to 546)  
 AUTHORS Moricca,S., Kasuga,T., Mitchelson,K.R. and Ragazzi,A.  
 TITLE The sequence of the fusarium oxysporum f.s.p. vasinflectum 5.8S rRNA

JOURNAL  
 REFERENCE 2 (bases 1 to 546)  
 AUTHORS Mitchelson,K.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAR-1994) K.R. Mitchelson, Department of Molecular &  
 Cell Biology, University of Aberdeen, Aberdeen AB9 1AS, UK  
 FEATURES  
 source  
 1. 546  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /strain="Bul"  
 /sub\_species="f.sp.vasinflectum"  
 /db\_xref="taxon:5507"  
 /tissue\_type="Mycelium"  
 /clone\_lib="S.Moricca"  
 /lab\_host="Gossypium"  
 /note="host from Cuanza Bul, Angola"  
 1. 546  
 /gene="5.8S rRNA"  
 1. 546  
 /gene="5.8S rRNA"  
 /product="5.8S ribosomal RNA"

## ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 546;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18  
 |||||  
 Db 371 CGTTAATTCGGCTTCCTC 388

RESULT 64  
 FOVCN58 546 bp DNA linear PLN 16-JAN-1996  
 LOCUS F.oxysporum (f.sp.vasinflectum, Cuanza Norte) 5.8S rRNA gene.  
 DEFINITION X78258.1 GI:467739  
 X78258 5.8S ribosomal RNA; 5.8S rRNA gene.  
 VERSION 5.8S ribosomal RNA; 5.8S rRNA gene.  
 KEYWORDS Fusarium oxysporum  
 SOURCE  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.  
 REFERENCE 1 (bases 1 to 546)  
 AUTHORS Moricca,S., Kasuga,T., Mitchelson,K.R. and Ragazzi,A.  
 TITLE The sequence of the fusarium oxysporum f.s.p. vasinflectum 5.8S rRNA  
 and adjacent ITS 1 and ITS 2 regions  
 JOURNAL Fungal Genet. Newsl. 42, 53-55 (1995)  
 REFERENCE 2 (bases 1 to 546)  
 AUTHORS Mitchelson,K.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAR-1994) K.R. Mitchelson, Department of Molecular &  
 Cell Biology, University of Aberdeen, Aberdeen AB9 1AS, UK  
 FEATURES  
 source  
 1. 546  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /strain="Norte"  
 /sub\_species="f.sp.vasinflectum"  
 /db\_xref="taxon:5507"  
 /tissue\_type="Mycelium"  
 /clone\_lib="S.Moricca"  
 /lab\_host="Gossypium"  
 /note="host from Cuanza Norte, Italy"  
 1. 546  
 /gene="5.8S rRNA"  
 1. 546  
 /gene="5.8S rRNA"  
 /product="5.8S ribosomal RNA"

## ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 546;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
 |||||  
 Db 371 CGTTAATTCGCGTTCCTC 388

RESULT 65  
 AY147369 552 bp DNA linear PLN 15-FEB-2003  
 LOCUS Fusarium oxysporum 18S ribosomal RNA gene, partial sequence;  
 DEFINITION internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal  
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA  
 gene, partial sequence.  
 ACCESSION AY147369 GI:28394595  
 VERSION AY147369.1 GI:28394595  
 KEYWORDS Fusarium oxysporum  
 ORGANISM Fusarium oxysporum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 552)  
 Mishra, P.K.  
 Genomics and Evolutionary Biology of *Fusarium culmorum*  
 Thesis (2002) The University of Reading, Whiteknights, Reading,  
 Berkshire, United Kingdom

REFERENCE 2 (bases 1 to 552)  
 Mishra, P.K., Fox, R.T. and Culham, A.  
 Development of a PCR-based assay for rapid and reliable  
 identification of pathogenic *Fusaria*  
 FEMS Microbiol. Lett. 218 (2), 329-332 (2003)

JOURNAL MEDLINE 22474178  
 PUBMED 12586412  
 3 (bases 1 to 552)  
 Mishra, P.K., Fox, R.T.V. and Culham, A.  
 Direct Submission  
 Submitted (03-SEP-2002) School of Plant Sciences, The University of  
 Reading, Whiteknights, Reading, Berkshire RG6 6AS, United Kingdom

FEATURES  
 source  
 1..552  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:5507"  
 <1..>552  
 /note="contains 18S ribosomal RNA, internal transcribed  
 spacer 1, 5.8S ribosomal RNA, internal transcribed spacer  
 2, and 28S ribosomal RNA"

misc\_rna

ORIGIN  
 Query Match 100.0%; Score 18; DB 8; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
 |||||  
 Db 386 CGTTAATTCGCGTTCCTC 403

RESULT 66  
 AY462580 552 bp DNA linear PLN 06-DEC-2003  
 LOCUS Fusarium oxysporum f. sp. vasinfectum isolate PA3 18S ribosomal RNA  
 DEFINITION gene, partial sequence; internal transcribed spacer 1, 5.8S  
 ribosomal RNA gene, and internal transcribed spacer 2, complete  
 sequence; and 28S ribosomal RNA gene, partial sequence.  
 ACCESSION AY462580 GI:38569372  
 VERSION AY462580.1 GI:38569372  
 KEYWORDS Fusarium oxysporum f. sp. vasinfectum  
 SOURCE

ORGANISM Fusarium oxysporum f. sp. vasinfectum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 552)  
 Catal, M. and Schilder, A.M.C.  
 A PCR-based method to distinguish *Eutypa lata* and *Eutypella vitis*  
 from grapevine  
 Unpublished

JOURNAL 2 (bases 1 to 552)  
 Catal, M. and Schilder, A.M.C.  
 Direct Submission  
 Submitted (11-NOV-2003) Plant Pathology, Michigan State University,  
 Wilson Road, East Lansing, MI 48823, USA

FEATURES  
 source  
 1..552  
 /organism="Fusarium oxysporum f. sp. vasinfectum"  
 /mol\_type="genomic DNA"  
 /isolate="PA3"  
 /specific\_host="Vitis vinifera"  
 /db\_xref="taxon:61374"  
 /country="USA: PA"  
 /note="forma specialis: vasinfectum"  
 <1..54  
 /product="18S ribosomal RNA"  
 55..203  
 /product="internal transcribed spacer 1"  
 204..361  
 /product="5.8S ribosomal RNA"  
 362..511  
 /product="internal transcribed spacer 2"  
 512..>552  
 /product="28S ribosomal RNA"

misc\_rna

ORIGIN  
 Query Match 100.0%; Score 18; DB 8; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTAATTCGCGTTCCTC 18  
 |||||  
 Db 394 CGTTAATTCGCGTTCCTC 411

RESULT 67  
 AY462579 555 bp DNA linear PLN 06-DEC-2003  
 LOCUS Fusarium oxysporum f. sp. vasinfectum isolate PA1 18S ribosomal RNA  
 DEFINITION gene, partial sequence; internal transcribed spacer 1, 5.8S  
 ribosomal RNA gene, and internal transcribed spacer 2, complete  
 sequence; and 28S ribosomal RNA gene, partial sequence.  
 ACCESSION AY462579  
 VERSION AY462579.1 GI:38569371  
 KEYWORDS Fusarium oxysporum f. sp. vasinfectum  
 SOURCE  
 ORGANISM Fusarium oxysporum f. sp. vasinfectum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.

REFERENCE 1 (bases 1 to 555)  
 Catal, M. and Schilder, A.M.C.  
 A PCR-based method to distinguish *Eutypa lata* and *Eutypella vitis*  
 from grapevine  
 Unpublished

JOURNAL 2 (bases 1 to 555)  
 Catal, M. and Schilder, A.M.C.  
 Direct Submission  
 Submitted (11-NOV-2003) Plant Pathology, Michigan State University,  
 Wilson Road, East Lansing, MI 48823, USA

FEATURES  
 source  
 1..555  
 /organism="Fusarium oxysporum f. sp. vasinfectum"  
 /mol\_type="genomic DNA"

	/isolate="PA1"
	/specific_host="Vitis vinifera"
	/db_xref="taxon:61374"
	/country="USA; PA"
	/note="forma_specialis: vasinfectum"
rRNA	<1..53
	/product="18S ribosomal RNA"
misc_RNA	54..202
	/product="internal transcribed spacer 1"
rRNA	203..360
	/product="5.8S ribosomal RNA"
misc_RNA	361..510
	/product="internal transcribed spacer 2"
rRNA	511..>555
	/product="28S ribosomal RNA"
ORIGIN	
Query Match	100.0%; Score 18; DB 8; Length 555;
Best Local Similarity	100.0%; Pred. No. 27;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 CGTTAATCGCGTCTC 18       
Dd	392 CGTTAATCGCGTCTC 409
RESULT 68	
AF322074	616 bp DNA linear PLN 13-DEC-2000
LOCUS	Fusarium oxysporum f. sp. vasinfectum strain Ag149 18S ribosomal
DEFINITION	RNA gene, partial sequence; internal transcribed spacer 1, 5.8S
	ribosomal RNA gene and internal transcribed spacer 2, complete
	sequence; and 28S ribosomal RNA gene, partial sequence.
AF322074	AF322074.1 GI:11692812
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	Fusarium oxysporum f. sp. vasinfectum Fusarium oxysporum f. sp. vasinfectum Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex. 1 (bases 1 to 616) Ying,L., Hong,Y. and Guohua,G. 2 (bases 1 to 616) Comparison of ribosomal RNA gene sequences between a heterokaryon and two segregants of Fusarium oxysporum f.sp.vasinfectum Unpublished 2 (bases 1 to 616) Ying,L., Hong,Y. and Guohua,G. Submitted (20-Nov-2000) Department of Microbiology, College of Biological Sciences, China Agricultural University, No. 2, Yuanninguan West Road, Beijing 100094, P.R. China Location/Qualifiers 1..616 /organism="Fusarium oxysporum f. sp. vasinfectum" /mol_type="genomic DNA" /strain="Ag149" /db_xref="taxon:61374" /country="China; Henan Province, isolated from a cotton field" /note="forma_specialis: vasinfectum" <1..112 /product="18S ribosomal RNA" 113..250 /product="internal transcribed spacer 1" 251..408 /product="5.8S ribosomal RNA" 409..558 /product="internal transcribed spacer 2" 559..>616 /product="28S ribosomal RNA"
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	
ORIGIN	

Query Match	100.0%	Score 18	DB 8	Length 616
Best Local Similarity	100.0%	Pred. No. 27		
Matches	18	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
Oy	1	CGTTAATTCGCGTTCCCTC	18	
Db	441	CGTTAATTCGCGTTCCCTC	458	
RESULT 69				
AF322075				
LOCUS	616 bp	DNA	linear	PLN 13-DEC-2000
DEFINITION	Fusarium oxysporum f. sp. vasinfectum strain Ag149-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.			
ACCESSION	AF322075			
VERSION	AF322075.1	GI:11692813		
KEYWORDS				
SOURCE	Fusarium oxysporum f. sp. vasinfectum			
ORGANISM	Fusarium oxysporum f. sp. vasinfectum			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; microsporitic Hypocreales; Fusarium; Fusarium oxysporum complex.			
AUTHORS	1 (bases 1 to 616)			
TITLE	Ying,L., Hong,Y., and Guohua,G.			
REFERENCE	Comparison of ribosomal RNA gene sequences between a heterokaryon and two segregants of Fusarium oxysporum f.sp.vasinfectum			
REFERENCE	Unpublished			
REFERENCE	2 (bases 1 to 616)			
REFERENCE	Ying,L., Hong,Y. and Guohua,G.			
REFERENCE	Direct Submission			
REFERENCE	Submitted (20-NOV-2000) Department of Microbiology, College of Biological Sciences, China Agricultural University, No. 2, Yuanmingyuan West Road, Beijing 100094, P.R. China			
REFERENCE	Location/Qualifiers			
FEATURES	1..616			
source	/organism="Fusarium oxysporum f. sp. vasinfectum"			
	/mol_type="genomic DNA"			
	/strain="Ag149-1"			
	/db_xref="taxon:61374"			
	/note="nuclear type segregant"			
	/note="specialis: vasinfectum"			
	1..112			
	/product="18S ribosomal RNA"			
	113..250			
	/product="internal transcribed spacer 1"			
	251..408			
	/product="5.8S ribosomal RNA"			
	409..558			
	/product="internal transcribed spacer 2"			
	559..>616			
	/product="28S ribosomal RNA"			
ORIGIN				
Query Match	100.0%	Score 18	DB 8	Length 616
Best Local Similarity	100.0%	Pred. No. 27		
Matches	18	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
Oy	1	CGTTAATTCGCGTTCCCTC	18	
Db	441	CGTTAATTCGCGTTCCCTC	458	
RESULT 70				
AF322076				
LOCUS	616 bp	DNA	linear	PLN 13-DEC-2000
DEFINITION	Fusarium oxysporum f. sp. vasinfectum strain Ag149-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.			
ACCESSION	AF322076			
VERSION	AF322076.1	GI:11692814		

**KEYWORDS**  
**SOURCE** Fusarium oxysporum f. sp. vasinfectum  
**ORGANISM** Fusarium oxysporum f. sp. vasinfectum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.

**REFERENCE**  
**AUTHORS** Yang, L., Hong, Y., and Guohua, G.  
**TITLE** Comparison of ribosomal RNA gene sequences between a heterokaryon and two segregants of *Fusarium oxysporum* f. sp. vasinfectum  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 616)  
**AUTHORS** Yang, L., Hong, Y., and Guohua, G.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (20-NOV-2000) Department of Microbiology, College of Biological Sciences, China Agricultural University, No. 2, Yuanmingyuan West Road, Beijing 100094, P.R. China  
**FEATURES**  
**SOURCE** 1. 616  
 /organism="Fusarium oxysporum f. sp. vasinfectum"  
 /mol\_type="genomic DNA"  
 /strain="Ag149-111"  
 /db\_xref="taxon:61374"  
 /note="nuclear type segregant  
 forma specialis: vasinfectum"  
 <1..112  
 /product="18S ribosomal RNA"  
 113..250  
 /product="internal transcribed spacer 1"  
 251..408  
 /product="5.8S ribosomal RNA"  
 409..558  
 /product="internal transcribed spacer 2"  
 559..>616  
 /product="28S ribosomal RNA"

**ORIGIN**  
 Query Match 100.0%; Score 18; DB 8; Length 616;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Cy** 1 CGTTAATTCGCGTTCCTC 18  
 |||||  
**Db** 441 CGTTAATTCGCGTTCCTC 458

**RESULT 71**  
**AF443071/c** 636 bp DNA linear PLN 03-DEC-2001  
**LOCUS** Fusarium oxysporum 18S ribosomal RNA gene, partial sequence;  
**DEFINITION** internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal  
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA  
 gene, partial sequence.  
**ACCESSION** AF443071  
**VERSION** AF443071.1 GI:17227116  
**KEYWORDS** Fusarium oxysporum  
**SOURCE** Fusarium oxysporum  
**ORGANISM** Fusarium oxysporum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.  
**REFERENCE** 1 (bases 1 to 636)  
**AUTHORS** Quader, M. and Riley, I.T.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (06-NOV-2001) Applied and Molecular Ecology, Adelaide  
 University, Waite Campus, Glen Osmond, Adelaide, SA 5064, Australia  
**FEATURES**  
**SOURCE** 1..636  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3507"  
 /cissue\_type="galled roots"  
 complement(<1..>636)

**misc\_RNA**

**ORIGIN**  
 Query Match 100.0%; Score 18; DB 8; Length 636;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Cy** 1 CGTTAATTCGCGTTCCTC 18  
 |||||  
**Db** 200 CGTTAATTCGCGTTCCTC 183

**RESULT 72**  
**AY669120** 655 bp DNA linear PLN 20-JUL-2004  
**LOCUS** Fusarium oxysporum strain F-T.1.7-030520 18S ribosomal RNA gene,  
**DEFINITION** partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA  
 gene, and internal transcribed spacer 2, complete sequence; and 28S  
 ribosomal RNA gene, partial sequence.  
**ACCESSION** AY669120  
**VERSION** AY669120.1 GI:50313229  
**KEYWORDS** Fusarium oxysporum  
**SOURCE** Fusarium oxysporum  
**ORGANISM** Fusarium oxysporum  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
 Fusarium oxysporum complex.  
**REFERENCE** 1 (bases 1 to 655)  
**AUTHORS** Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.  
**TITLE** Comparison of ribosomal RNA gene sequences among the strains of  
 Fusarium oxysporum from different hosts  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 655)  
**AUTHORS** Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of  
 Agriculture Sciences, Wusi Road 247, Fuzhou, Fujian 350003, China  
**FEATURES**  
**SOURCE** 1..655  
 /organism="Fusarium oxysporum"  
 /mol\_type="genomic DNA"  
 /strain="F-T.1.7-030520"  
 /specific\_host="Cucumis melo L."  
 /db\_xref="taxon:5507"  
 /country="China: Fujian, Fuzhou, Yongtai"  
 <1..171  
 /product="18S ribosomal RNA"  
 172..310  
 /product="internal transcribed spacer 1"  
 311..468  
 /product="5.8S ribosomal RNA"  
 469..618  
 /product="internal transcribed spacer 2"  
 619..>655  
 /product="28S ribosomal RNA"

**ORIGIN**  
 Query Match 100.0%; Score 18; DB 8; Length 655;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Cy** 1 CGTTAATTCGCGTTCCTC 18  
 |||||  
**Db** 501 CGTTAATTCGCGTTCCTC 518

**RESULT 73**  
**AY667489** 666 bp DNA linear PLN 20-JUL-2004  
**LOCUS** Fusarium oxysporum isolate 12-152 internal transcribed spacer 1,  
**DEFINITION** partial sequence; 5.8S ribosomal RNA gene, complete sequence; and



internal transcribed spacer 2, partial sequence.

AY667489 internal transcribed spacer 2, partial sequence.  
AY667489.1 GI:50313404

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 666)  
Liu, B., Zhu, Y.J., Ling, Y.Z. and Cao, Y.  
Direct Submission  
Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of  
Agricultural Sciences, No. 247 Wusi Road, Fuzhou, Fujian 350003,  
P.R. China

FEATURES  
source  
Location/Qualifiers  
1..666  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/isolate="12-152"  
/specific\_host="cowpea plant"  
/db\_xref="taxon:5507"  
<1..319  
/product="internal transcribed spacer 1"  
320..477  
/product="5.8S ribosomal RNA"  
478..566  
/product="internal transcribed spacer 2"

ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 666;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18  
|||||  
Db 511 CGTTAATTCGGCTTCCTC 528

RESULT 74  
AY669122 671 bp DNA linear PLN 20-JUL-2004  
LOCUS  
DEFINITION  
Fusarium oxysporum strain F-W.6.2-030304 18S ribosomal RNA gene,  
internal transcribed spacer 1, 5.8S ribosomal RNA gene, and  
internal transcribed spacer 2, complete sequence; and 28S ribosomal  
RNA gene, partial sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 671)  
Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.  
Comparison of ribosomal RNA gene sequences among the strains of  
Fusarium oxysporum from different hosts  
Unpublished  
2 (bases 1 to 671)  
Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.  
Direct Submission  
Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of  
Agricultural Sciences, Wusi Road 247, Fuzhou, Fujian 350003, China

FEATURES  
source  
Location/Qualifiers  
1..671  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/strain="F-W.6.2-030304"  
/specific\_host="Pisum sativum L."  
/db\_xref="taxon:5507"  
/country="China: Fujian, Zhangzhou, Zhangpu"  
<1..186

/product="18S ribosomal RNA"  
187..325  
/product="internal transcribed spacer 1"  
326..483  
/product="5.8S ribosomal RNA"  
484..633  
/product="internal transcribed spacer 2"  
634..5671  
/product="28S ribosomal RNA"

ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 671;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18  
|||||  
Db 516 CGTTAATTCGGCTTCCTC 533

RESULT 75  
AY669125 678 bp DNA linear PLN 20-JUL-2004  
LOCUS  
DEFINITION  
Fusarium oxysporum strain F-X.1.7-030520-12 18S ribosomal RNA gene,  
partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA  
gene, and internal transcribed spacer 2, complete sequence; and 28S  
ribosomal RNA gene, partial sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 678)  
Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.  
Comparison of ribosomal RNA gene sequences among the strains of  
Fusarium oxysporum from different hosts  
Unpublished  
2 (bases 1 to 678)  
Cao, Y., Lin, Y., Ge, C., Xiao, R. and Liu, B.  
Direct Submission  
Submitted (28-JUN-2004) Biotechnology Center, Fujian Academy of  
Agricultural Sciences, Wusi Road 247, Fuzhou, Fujian 350003, China

FEATURES  
source  
Location/Qualifiers  
1..678  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/strain="F-X.1.7-030520-12"  
/specific\_host="Citrus limon (Thunb) Mansfeld"  
/db\_xref="taxon:5507"  
/country="China: Fujian, Fuzhou, Yongtai"  
<1..187  
/product="18S ribosomal RNA"  
188..326  
/product="internal transcribed spacer 1"  
327..484  
/product="5.8S ribosomal RNA"  
485..634  
/product="internal transcribed spacer 2"  
635..5678  
/product="28S ribosomal RNA"

ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 678;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGGCTTCCTC 18  
|||||  
Db 517 CGTTAATTCGGCTTCCTC 534

RESULT 76  
AY188919 1134 bp DNA linear PLN 30-NOV-2003  
LOCUS Fusarium oxysporum f. sp. melonis 18S ribosomal RNA gene, partial  
DEFINITION sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene  
and internal transcribed spacer 2, complete sequence; and 28S  
ribosomal RNA gene, partial sequence.  
ACCESSION AY188919  
VERSION AY188919.1 GI:37778811  
KEYWORDS  
SOURCE Fusarium oxysporum f. sp. melonis  
ORGANISM Fusarium oxysporum f. sp. melonis  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
REFERENCE 1 (bases 1 to 1134)  
Hatsch, D., Phalip, V. and Jeltsch, J.M.  
Study of the genes encoding cellobiohydrolase-C and topoisomerase  
II as target for phylogenetic analysis and identification of  
Fusarium at a species level  
Unpublished  
JOURNAL 2 (bases 1 to 1134)  
Hatsch, D., Phalip, V. and Jeltsch, J.M.  
REFERENCE Direct Submission  
AUTHORS Submitted (29-NOV-2002) Laboratoire de Phytopathologie, UMR 7100 -  
JOURNAL IFR 85 - ESBS - ULP, Boulevard Sebastien Brant,  
Illkirch-Graffenstaden, Alsace 67400, France  
FEATURES  
source location/Qualifiers  
1. .1134  
/organism="Fusarium oxysporum f. sp. melonis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:61369"  
/note="forma\_specialis: melonis"  
<1. .29  
/product="18S ribosomal RNA"  
30. .169  
/product="internal transcribed spacer 1"  
170. .326  
/product="5.8S ribosomal RNA"  
327. .474  
/product="internal transcribed spacer 2"  
475. .>1134  
/product="28S ribosomal RNA"  
ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 1134;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTTAATTCGCGTTCCTC 18  
|||||  
Db 369 CGTTAATTCGCGTTCCTC 386  
RESULT 77  
FOS88RNA 1471 bp DNA linear PLN 20-JAN-1997  
LOCUS F. oxysporum 5.8S rRNA, ITS2, and 26S rRNA.  
DEFINITION Y07991  
ACCESSION Y07991.1 GI:1805769  
KEYWORDS 26S ribosomal RNA; 5.8S ribosomal RNA; ITS2.  
SOURCE Fusarium oxysporum  
ORGANISM Fusarium oxysporum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.  
REFERENCE 1  
Iglesias, M. and Ballesta, J.P.G.  
JOURNAL Unpublished  
AUTHORS 2  
Ballesta, J.P.G.  
TITLE Direct Submission

JOURNAL Submitted (12-SEP-1996) J.P.G. Ballesta, Universidad Autonoma De  
Madrid, Centro De Biologia Molecular, Canto Blanco,, Madrid, 28049,  
SPAIN  
REMARK Revised by [3]  
REFERENCE 3 (bases 1 to 1471)  
AUTHORS Ballesta, J.P.G.  
TITLE Direct Submission  
JOURNAL Submitted (20-JAN-1997) J.P.G. Ballesta, Universidad Autonoma De  
Madrid, Centro De Biologia Molecular, Canto Blanco,, Madrid, 28049,  
SPAIN  
COMMENT On Jan 29, 1997 this sequence version replaced gi:1550626.  
FEATURES  
source location/Qualifiers  
1. .1471  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:5507"  
/clone\_11b="CA3"  
1. .144  
/gene="5.8S rRNA"  
<1. .144  
/gene="5.8S rRNA"  
/product="5.8S rRNA"  
145. .683  
/note="intergenic region ITS2"  
684. .1042  
/gene="26S rRNA"  
684. .1042  
/gene="26S rRNA"  
/product="26S rRNA"  
/product="26S ribosomal RNA"  
<1043. .>1471  
/codon\_start=3  
/product="hypothetical protein"  
/protein\_id="CAA69270.1"  
/db\_xref="GI:1805770"  
/db\_xref="EMBL:P78651"  
/translation="HSHQNRGHLIEIYQPEKQYPRAGIQPRSRNRHSKSLPIYVD  
ICIGQISKLAHVLRTPTPPVXSQSLASKTKPTVLEASQSEYLYRIRIRHQSSPE  
SILGALKSLAKGTAKIMHENVYLRAELREVRANILSRR"  
ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 1471;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGTTAATTCGCGTTCCTC 18  
|||||  
Db 178 CGTTAATTCGCGTTCCTC 195  
Search completed: December 7, 2004, 14:42:58  
Job time : 1413 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: December 8, 2004, 10:30:56 ; Search time 228 Seconds  
(without alignments)  
414.428 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgtatcgcgcgtcttc 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq238p04:\*

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	2	AAV83697
2	18	100.0	382	3	AAV72783
3	15.4	85.6	538	6	ABQ37055
4	15.4	85.6	538	6	ABQ37055
5	15	83.3	127	8	ACA13108
6	15	83.3	128	4	AA548419
7	15	83.3	250	4	AA547978
8	15	83.3	250	8	ACA12661
9	15	83.3	165	10	ADH82429
10	15	83.3	1467	8	ACA18462
11	15	83.3	9212	6	AA13271
12	15	83.3	9212	6	AB599066
13	14.8	82.2	207	10	ADG92275
14	14.8	82.2	554	6	ABQ14482
15	14.8	82.2	554	6	ABQ14483
16	14.8	82.2	650	5	AA505503
17	14.8	82.2	755	10	ACF65787
18	14.8	82.2	1200	4	AB116225
19	14.8	82.2	1231	6	ABQ28091
20	14.8	82.2	1231	6	ABQ28090
21	14.8	82.2	2457	10	ADH85065

C 22	14.8	82.2	3135	8	ACA32983	ACA32983 Prokaryot
C 23	14.8	82.2	3138	4	AA552883	AA552883 Enterococ
C 24	14.8	82.2	3257	4	AB112624	AB112624 Drosophill
C 25	14.8	82.2	4491	4	AB102050	AB102050 Drosophill
C 26	14.8	82.2	5864	4	AB103754	AB103754 Drosophill
C 27	14.8	82.2	10587	10	ACF72118	ACF72118 Phototriab
C 28	14.8	82.2	15428	4	AB102692	AB102692 Drosophill
C 29	14.8	82.2	110000	10	ACF67367	Continuation (54 o
C 30	14.8	82.2	110000	10	ACF65387	Continuation (6 of
C 31	14.4	80.0	65	6	AB226380	AB226380 Candida e
C 32	14.4	80.0	306	6	ABK79312	ABK79312 Bacillus
C 33	14.4	80.0	540	6	ABQ18322	ABQ18322 Oligonuc
C 34	14.4	80.0	540	6	ABQ18323	ABQ18323 Oligonuc
C 35	14.4	80.0	559	12	ACH74399	ACH74399 Human gen
C 36	14.4	80.0	601	6	ABQ34055	ABQ34055 Oligonuc
C 37	14.4	80.0	601	6	ABQ34054	ABQ34054 Oligonuc
C 38	14.4	80.0	939	6	AAH53833	AAH53833 S. epider
C 39	14.4	80.0	963	6	ABN91904	ABN91904 Staphyloc
C 40	14.4	80.0	2815	6	AAH54455	AAH54455 S. epider
C 41	14.4	80.0	5278	4	AB128982	AB128982 Drosophill
C 42	14.4	80.0	6711	9	AAH57212	AAH57212 Petunia R
C 43	14.4	80.0	8440	9	AAH57200	AAH57200 8.5 kb DN
C 44	14.4	80.0	110000	6	ABQ69245	Continuation (3 of
C 45	14.4	80.0	110000	6	ABQ67197	Continuation (2 of

## ALIGNMENTS

RESULT 1  
AAV83697  
ID AAV83697 standard; DNA; 18 BP.

XX AAV83697;

DT 26-FEB-1999 (first entry)

XX Species-specific probe targeted to the internal transcribed spacer 2.

XX Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger;  
XX A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;  
XX M. racemosus; M. plumbeus; M. indicus; A. fumigatus;  
XX M. circinelloides f. circinelloides; Rhizopus oryzae; R. microsporus;  
XX R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia chlamydosporum;  
XX Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiosporum;  
XX Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.

OS Synthetic.  
OS Fusarium oxysporum.

XX Key modified\_base 1 Location/Qualifiers  
XX FT /tag= a  
XX FT /note= "labelled with digoxigenin"

XX W09850564-A2.

XX 12-NOV-1998.

XX 01-MAY-1998; 98WO-US008926.

XX 02-MAY-1997; 97US-0045400P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Morrison CJ, Reiss E, Aidorevich L, Choi JS;

XX WPI; 1999-034737/03.

XX New nucleic acid probes for filamentous fungi - for detecting e.g.  
XX Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,  
XX Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix  
XX species.

```
XX Example 1; Page 22; 45bp; English.
PS
XX
CC Probes AAV83677-708 are derived from the internal transcribed spacer 2
CC (ITS2) region of various filamentous fungi (see AAV70845-73). The probes
CC are species-specific, and can be used for identifying a species selected
CC from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
CC Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
CC M. indicus, M. circinalioides f. circinalioides, Rhizopus oryzae, R.
CC microsporus, R. circinatus, R. stolonifer, Rhizomucor pusillus, Absetia
CC corymbifera, Cunninghamella elegans, Pseudallescheria boydii (teleomorph
CC of Scedosporium apiospermum), Penicillium notatum, or Sporothrix
CC schenkii. The probes can be used for differentiating filamentous fungal
CC species from each other and from other medically important fungi
XX
SQ Sequence 18 BP; 2 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGGCTTCCTC 18
DB 1 CGTTAATTCGGCTTCCTC 18
RESULT 2
AAAT2783
ID AAAA2783 standard; DNA; 382 BP.
XX
AC AAAA2783;
XX
DT 13-DEC-2000 (first entry)
XX
DE 5.8s rRNA gene sequence.
XX
KM Black spot disease; brown spot disease; fungi; fruit vegetable;
XX field crop; Alternaria; 5.8s rRNA; detection; ds.
XX
OS Fusarium oxysporum.
XX
PN WO20046397-A1.
XX
PD 10-AUG-2000.
XX
PF 24-JAN-2000; 2000WO-US001466.
XX
PR 02-FEB-1999; 99US-00241427.
XX
PA (TECR) TECHNION RES & DEV FOUND LTD.
XX (KASH) KASHI Y.
XX
PI Kashi Y, Zur G, Sharf R, Hallerman E,
XX
DR WPI; 2000-499381/44.
XX
PT Nucleic acid based assay and kit for detection of Alternaria
XX contamination in food products involves analyzing the sample of food
XX product for nucleic acid sequences unique to Alternaria.
XX
PS Example; Fig 1; 47bp; English.
XX
CC The invention relates to a nucleic acid based method for the detection of
CC Alternaria contamination in a food product. The method involves obtaining
CC and analyzing a food product sample for a nucleic acid sequence unique to
CC Alternaria. Detectable levels of the nucleic acid sequence can be used as
CC an indication of Alternaria contamination. Fungi from the genus
CC Alternaria are ubiquitous saprophytes and are economically important
CC pathogens affecting a wide range of plants. Alternaria are the causative
CC agents of black or brown spot disease in many fruits, vegetables and
CC field crops. The method is used for the detection of Alternaria
CC contamination in food products. The present sequence represents the
CC Fusarium oxysporum 5.8s rRNA gene, used in examples illustrating the
```

```
CC invention
XX
SQ Sequence 382 BP; 101 A; 99 C; 87 G; 95 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTAATTCGGCTTCCTC 18
DB 287 CGTTAATTCGGCTTCCTC 304
RESULT 3
ABQ37055/C
ID ABQ37055 standard; DNA; 538 BP.
XX
AC ABQ37055;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 23646.
XX
KM Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PR 05-SEP-2000; 2000DE-01045453.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
XX diagnosis and prognosis, comprises selective hybridization of amplicons
XX from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 538 BP; 256 A; 160 C; 61 G; 61 T; 0 U; 0 Other;
```

Query Match 85.6%; Score 15.4; DB 6; Length 538;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTATTGCGCTTCCTC 18  
|||||  
DB 105 GTTAATTCGCTTCCTC 89

## RESULT 4

ABQ37054  
ID ABQ37054 standard; DNA; 538 BP.

ABQ37054;

12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 23645.

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
drug; side effect; cancer; central nervous system; cardiovascular;  
gastrointestinal; respiratory system; single nucleotide polymorphism;  
SNP; cell differentiation; ds.

Homo sapiens.

WO200218632-A2.

07-MAR-2002.

01-SEP-2001; 2001WO-EP010074.

01-SEP-2000; 2000DE-01043826.

05-SEP-2000; 2000DE-01044543.

(EPG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K, Gietig D;

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for  
diagnosis and prognosis, comprises selective hybridization of amplicons  
from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of  
methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
genomic sample of DNA. The sample is treated chemically to convert  
cytosine (C) but not methylated C, to uracil, then part of the genomic  
DNA that contains the target C is amplified to form a labeled amplicon.  
The amplicon is hybridized to two classes, each with at least one member,  
of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
degree of hybridization to both classes is determined from the label on  
the amplicon. From the ratio of labels hybridized to the two classes of  
oligomers, the degree of methylation is calculated. The method is used:  
(i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
and of a wide range of diseases, e.g. cancer, disorders of the central  
nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
particularly by detecting mutations or single nucleotide polymorphisms  
(SNP's); and (ii) for differentiation of cell or tissue types and for  
investigating cell differentiation. The method allows the methylation  
status of many C residues to be determined simultaneously. AB013410-  
ABQ5121 represent genomic DNA sequences used to illustrate the method  
for determining the degree of cytosine methylation described in the  
disclosure of the invention

Sequence 538 BP; 61 A; 61 C; 160 G; 256 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 538;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTATTGCGCTTCCTC 18  
|||||  
DB 434 GTTAATTCGCTTCCTC 450

## RESULT 5

ACA13108/C  
ID ACA13108 standard; DNA; 127 BP.

ACA13108;

27-OCT-2003 (revised)

19-JUN-2003 (first entry)

Prokaryotic essential gene antisense oligonucleotide #978.

Antisense; ss; prokaryotic essential gene; cell proliferation;  
drug design.

Archaea.

WO200271183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW,  
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.

New antisense nucleic acids, useful for identifying proteins or screening  
for homologous nucleic acids required for cellular proliferation to  
isolate candidate molecules for rational drug discovery programs.

Claim 1; SEQ ID NO 978; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of  
the 6213 antisense sequences given in the specification where expression  
of the nucleic acid inhibits proliferation of a cell. Also included are:  
(1) a vector comprising a promoter operably linked to the nucleic acid  
encoding a polypeptide whose expression is inhibited by the antisense  
nucleic acid; (2) a host cell containing the vector; (3) an isolated  
polypeptide or its fragment whose expression is inhibited by the  
antisense nucleic acid; (4) an antibody capable of specifically binding  
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
proliferation; (7) identifying a gene in an operon required for  
proliferation; (8) identifying a compound that influences the activity of  
the gene product or that has an activity against a biological pathway  
required for proliferation, or that inhibits cellular proliferation; (9)  
identifying a gene required for cellular proliferation or its gene product lies  
pathway in which a proliferation-regulated gene or its gene product lies  
or a gene on which the test compound that inhibits proliferation of an  
organism acts; (9) manufacturing an antibiotic; (10) profiling a  
compound's activity; (11) a culture comprising strains in which the gene  
product is overexpressed or underexpressed; (12) determining the extent  
to which each of the strains is present in a culture or collection of  
strains; or (13) identifying the target of a compound that inhibits the  
proliferation of an organism. The antisense nucleic acids are useful for  
identifying proteins or screening for homologous nucleic acids required  
for cellular proliferation to isolate candidate molecules for rational  
drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the 6213  
CC antisense sequences of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 27-OCT-2003 to  
CC standardise OS field)

XX  
SQ Sequence 127 BP; 42 A; 31 C; 22 G; 32 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 8; Length 127;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATCGCGTTCC 16  
DB 117 GTTAATCGCGTTCC 103

RESULT 6  
AAS48419/C  
ID AAS48419 standard; DNA; 128 BP.

XX AAS48419;  
AC 13-FEB-2002 (first entry)  
XX  
XX Enterococcus faecalis cellular proliferation inhibitory sequence #989.  
DE Enterococcus faecalis cellular proliferation inhibitory sequence #989.  
XX  
XX Antisense; ss; prokaryotic cellular proliferation; antibiotic;  
KW antibacterial; drug design.  
XX  
XX Enterococcus faecalis.  
OS  
XX WO200170955-A2.  
FN  
XX  
XX 27-SEP-2001.  
PD  
XX  
XX 21-MAR-2001; 2001WO-US009180.  
PF  
XX  
XX 21-MAR-2000; 2000US-0191078P.  
PR  
XX 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
PR  
XX  
XX (ELIT-) ELITRA PHARM INC.  
PA  
XX  
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
PI WPI; 2001-611495/70.  
DR  
XX  
XX New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
XX  
XX Claim 1; SEQ ID NO 996; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*  
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,  
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety

CC of organisms. The present sequence is an antisense oligonucleotide of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 128 BP; 42 A; 31 C; 22 G; 33 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 4; Length 128;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATCGCGTTCC 16  
DB 118 GTTAATCGCGTTCC 104

RESULT 7  
AAS47978/C  
ID AAS47978 standard; DNA; 250 BP.

XX AAS47978;  
AC 13-FEB-2002 (first entry)  
XX  
XX Enterococcus faecalis cellular proliferation inhibitory sequence #548.  
DE Enterococcus faecalis cellular proliferation inhibitory sequence #548.  
XX  
XX Antisense; ss; prokaryotic cellular proliferation; antibiotic;  
KW antibacterial; drug design.  
XX  
XX Enterococcus faecalis.  
OS  
XX WO200170955-A2.  
FN  
XX  
XX 27-SEP-2001.  
PD  
XX  
XX 21-MAR-2001; 2001WO-US009180.  
PF  
XX  
XX 21-MAR-2000; 2000US-0191078P.  
PR  
XX 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-0207727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
PR  
XX  
XX (ELIT-) ELITRA PHARM INC.  
PA  
XX  
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
PI WPI; 2001-611495/70.  
DR  
XX  
XX New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.  
XX  
XX Claim 1; SEQ ID NO 555; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*  
CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,  
CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence is an antisense oligonucleotide of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 250 BP; 75 A; 53 C; 47 G; 75 T; 0 U; 0 Other;  
SQ  
Query Match 83.3%; Score 15; DB 4; Length 250;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2 GTTAATTCGCGTTCC 16  
|||||  
54 GTTAATTCGCGTTCC 40  
Db  
RESULT 8  
ACAI2661/c  
ID ACAI2661 standard; DNA; 250 BP.  
XX  
ACAI2661:  
XX  
27-OCT-2003 (revised)  
DT 19-JUN-2003 (first entry)  
XX  
XX Prokaryotic essential gene antisense oligonucleotide #531.  
XX Antisense; ss; prokaryotic essential gene; cell proliferation;  
XX drug design.  
XX  
XX Archaea.  
XX  
XX MO200277183-A2.  
XX  
XX 03-OCT-2002.  
XX  
XX 21-MAR-2002; 2002MO-US009107.  
XX  
XX 21-MAR-2001; 2001US-00815242.  
XX  
XX 06-SEP-2001; 2001US-00948993.  
XX  
XX 25-OCT-2001; 2001US-0342923P.  
XX  
XX 08-FEB-2002; 2002US-00072851.  
XX  
XX 06-MAR-2002; 2002US-0362699P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
XX  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KJ, Zyskind JW;  
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
XX for homologous nucleic acids required for cellular proliferation to  
XX isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 1; SEQ ID NO 531; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding  
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX proliferation or the activity of a gene in an operon required for  
XX proliferation; (7) identifying a compound that influences the activity of  
XX the gene product or that has an activity against a biological pathway;  
XX required for proliferation, or that inhibits cellular proliferation; (8)  
XX identifying a gene required for cellular proliferation or the biological  
XX pathway in which a proliferation-required gene or its gene product lies  
XX or a gene on which the test compound that inhibits proliferation of an  
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX compound's activity; (11) a culture comprising strains in which the gene  
XX product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the 6213  
CC antisense sequences of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 27-OCT-2003 to  
CC standardise OS field)  
XX  
XX Sequence 250 BP; 75 A; 53 C; 47 G; 75 T; 0 U; 0 Other;  
SQ  
Query Match 83.3%; Score 15; DB 8; Length 250;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
2 GTTAATTCGCGTTCC 16  
|||||  
54 GTTAATTCGCGTTCC 40  
Db  
RESULT 9  
ADH82429  
ID ADH82429 standard; DNA; 615 BP.  
XX  
XX ADH82429;  
XX  
XX 22-APR-2004 (first entry)  
XX  
XX Enterococcus faecalis polynucleotide #314.  
XX  
XX Enterococcus faecalis infection; transcription regulatory element;  
XX antibacterial; gene; ds.  
XX  
XX Enterococcus faecalis.  
XX  
XX US6617156-B1.  
XX  
XX 09-SEP-2003.  
XX  
XX 13-AUG-1998; 98US-00134000.  
XX  
XX 15-AUG-1997; 97US-0055778P.  
XX  
XX (DOUC/) DOUCETTE-STAMM L A.  
XX (BUSH/) BUSH D.  
XX  
XX Doucette-Stamm LA, Bush D;  
XX WPI; 2003-895394/82.  
XX  
XX P-PsDB; ADH85834.  
XX  
XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis  
XX polypeptide, useful for preparing a composition for diagnosing or  
XX treating *E. faecalis* infection.  
XX  
XX Disclosure; SEQ ID NO 314; 193pp; English.  
XX  
XX The invention relates to Enterococcus faecalis polynucleotides and  
XX polypeptides. The invention also relates to a recombinant expression  
XX vector comprising a polynucleotide operably linked to a transcription  
XX regulatory element, a cell comprising a recombinant vector, a method for  
XX producing an *E. faecalis* polypeptide, an isolated nucleic acid comprising  
XX a sequence not given in the specification, a recombinant vector  
XX comprising the nucleic acid and a cell comprising the recombinant vector.  
XX The polynucleotides can be used to detect the presence of *E. faecalis* in  
XX a sample. The sequences are useful for preparing a composition for  
XX diagnosing or treating Enterococcus faecalis infection. This sequence  
XX represents an *E. faecalis* polynucleotide of the invention.





XX Sequence 9212 BP, 3045 A, 1564 C, 2061 G, 2529 T, 0 U, 13 Other;  
SQ Query Match 83.3%; Score 15; DB 2; Length 9212;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GTTAATTCGCGTTCC 16  
DB 4989 GTTAATTCGCGTTCC 5003

RESULT 12  
ABS99066 standard; DNA; 9212 BP.  
XX ABS99066;  
AC  
XX 18-DEC-2002 (first entry)  
DT  
XX Enterococcus faecalis contig sequence #334.  
DE  
XX Computer readable medium; Enterococcus faecalis; microbe; growth;  
XX pathogenicity; vaccine; resistance; Enterococcal infection; commercial;  
KW therapeutic; industrial; fermenting; sugar source; metabolite; vaccine;  
KW biotech technology; antibacterial; modulator of nucleic acid expression;  
KW contig; ds.  
XX  
XX Enterococcus faecalis.  
OS  
XX US2002120116-A1.  
PN  
XX 29-AUG-2002.  
PD  
XX 04-MAY-1998; 98US-00070927.  
PF  
XX 04-MAY-1998; 98US-00070927.  
PR  
XX (KUNS/) KUNSCH C A.  
PA (DILL/) DILLON P J.  
PA (BARA/) BARASH S.  
XX  
XX Kunsch CA, Dillon PJ, Barash S;  
PI WPI; 2002-750065/81.  
XX  
XX Computer readable medium having recorded on it a Enterococcus faecalis  
PT nucleotide sequence useful for detecting diseases related to Enterococcus  
XX infections in animals.  
XX  
XX Claim 1; Page; 119pp; English.  
PS  
XX The present invention relates to a new computer readable medium with an  
CC Enterococcus faecalis nucleotide sequence. The invention is useful to  
CC diagnose the presence of E. faecalis in a sample or determining the  
CC presence of a specific microbe in a sample. The invention is also useful  
CC for modulating the growth or pathogenicity of E. faecalis, in a vaccine to  
CC confer resistance to Enterococcal infection, for commercial, therapeutic  
CC and industrial purposes, and for fermenting a particular sugar source or  
CC to produce a particular metabolite. The invention is useful for detecting  
CC diseases related to Enterococcus infections in animals, and for detecting  
CC E. faecalis using biotech technology. The present nucleic acid sequence  
CC represents an Enterococcus faecalis contig DNA sequence of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format directly from USPTO  
CC at http://seqdata.uspto.gov  
XX  
SQ Sequence 9212 BP, 3045 A, 1564 C, 2061 G, 2529 T, 0 U, 13 Other;  
QY Query Match 83.3%; Score 15; DB 6; Length 9212;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCC 16  
DB 4989 GTTAATTCGCGTTCC 5003

RESULT 13  
ADC92275/C  
ID ADC92275 standard; DNA; 207 BP.  
XX ADC92275;  
AC  
XX 01-JAN-2004 (first entry)  
DT  
XX E. faecium DNA sequence SEQ ID 1902.  
DE  
XX ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;  
KW abdominal-pelvic infection.  
KW Enterococcus faecium.  
OS  
XX US6583275-B1.  
PN  
XX 24-JUN-2003.  
PD  
XX 30-JUN-1998; 98US-00107532.  
PF  
XX 02-JUL-1997; 97US-0051571P.  
PR 14-MAY-1998; 98US-0085598P.  
XX  
XX (GENO-) GENOME THERAPEUTICS CORP.  
PA  
XX Doucette-Stamm LA, Bush D;  
PI WPI; 2003-799836/75.  
DR P-PSDB; ADC95929.  
XX  
XX New isolated nucleic acid derived from Enterococcus faecium encoding an  
PT Enterococcus faecium polypeptide useful for detection, prevention and  
PT treatment of a pathological condition resulting from a bacterial  
PT infection.  
XX  
XX Example 1; SEQ ID NO 1902; 243pp; English.  
PS  
XX The invention relates to an isolated nucleic acid derived from  
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having  
CC one of 10 fully defined sequences given in the (or comprising 40  
CC sequential nucleotides chosen from any of the nucleic acids, its  
CC complement or sequences hybridising to it). Also included are a  
CC recombinant vector comprising the nucleic acid operably linked to  
CC transcription regulatory element, a cell comprising the vector and a  
CC single-stranded probe comprising the nucleic acid. The nucleic acids are  
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.  
CC The nucleic acids are useful for diagnosing pathological conditions  
CC resulting from E. faecium bacterial infection (e.g. urinary tract  
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic  
CC infection), and for screening drugs such as agonists and antagonists. The  
CC nucleic acid is useful for recombinant production of Candida albicans -  
CC derived peptides or antisense polypeptides. Pharmaceutical compositions  
CC and vaccines containing the nucleic acid are useful for preventing or  
CC treating Enterococcus faecium infections. The present sequence represents  
CC one if the disclosed E. faecium nucleic acids.  
XX  
SQ Sequence 207 BP, 68 A, 36 C, 47 G, 55 T, 0 U, 1 Other;  
QY Query Match 82.2%; Score 14.8; DB 10; Length 207;  
Best Local Similarity 88.9%; Pred. No. 4.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CGTTAATTCGCGTTCTC 18  
DB 84 CGTTAATTCGCGTTCTC 67

RESULT 14  
ABQ14482 ID ABQ14482 standard; DNA; 554 BP.  
XX  
AC ABQ14482;  
XX  
DT 12-JUL-2002 (first entry)  
XX  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1073.  
XX  
KW Human; cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;  
KM drug; side effect; cancer; central nervous system; cardiovascular;  
KM gastrointestinal; respiratory system; single nucleotide polymorphism;  
SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX  
FN WO200218632-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 01-SEP-2001; 2001WO-EP010074.  
XX  
PR 01-SEP-2000; 2000DE-01043826.  
XX  
PR 05-SEP-2000; 2000DE-01044543.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
DR WPI; 2002-371829/40.  
XX  
PT Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
PS  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CPG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C<sub>5</sub> to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNPs); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ1410-ABQ1412 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention

Sequence 554 BP; 76 A; 67 C; 169 G; 242 T; 0 U; 0 Other;  
XX  
SO

Query Match 82.2%; Score 14.8; DB 6; Length 554;  
Best Local Similarity 88.9%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 113 CGTTAATTCGCCTTATC 130  
1 CGTTAATTCGCCTTCTC 18  
|||||  
|||

RESULT 15  
ABQ14483/C  
ID ABQ14483 standard; DNA; 554 BP.

XX AB014483;  
 AC  
 XX 12-JUL-2002 (first entry)  
 DT  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1074.  
 XX  
 XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; dr.  
 XX  
 XX Homo sapiens.  
 OS  
 PN WO200218632-A2.  
 PD  
 PD 07-MAR-2002.  
 PF  
 PF 01-SEP-2001; 2001WO-EP010074.  
 PR 01-SEP-2000; 2000DE-01043826.  
 PR 05-SEP-2000; 2000DE-01044543.  
 PA (EPIC-) EPIDENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
 XX  
 XX WPI; 2002-371829/40.  
 DR  
 PT Determining the degree of cytosine methylation in genomic DNA, useful for  
 PT diagnosis and prognosis, comprises selective hybridization of amplicons  
 PT from chemically treated DNA.  
 XX  
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
 CC This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one member,  
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 CC degree of hybridisation to both classes is determined from the label on  
 CC the amplicon. From the ratio of labels hybridised to the two classes of  
 CC oligomers, the degree of methylation is calculated. The method is used:  
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 CC particularly by detecting mutations or single nucleotide polymorphisms  
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
 CC investigating cell differentiation. The method allows the methylation  
 CC status of many C residues to be determined simultaneously. AB013410-  
 CC AB013411 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the  
 CC disclosure of the invention  
 XX  
 XX Sequence 554 BP; 242 A; 169 C; 67 G; 76 T; 0 U; 0 Other;  
 SQ  
 Query Match 82.2%; Score 14.8; DB 6; Length 554;  
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CGTTAATTCGCGTTCTC 18  
 |||  
 DB 442 CGTTAATTCGCGTTATC 425

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 10:28:40 ; Search time 60 Seconds  
(without alignments)  
213.237 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 CGTAAATCGCGTCTC 18

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	US-09-423-233-50	Sequence 50, Appl
2	15	83.3	615	US-08-134-000C-314	Sequence 314, App
3	14.8	82.2	207	US-09-107-532A-1902	Sequence 1902, Ap
4	14.8	82.2	650	US-09-669-751-103	Sequence 103, App
5	14.8	82.2	2457	US-09-134-000C-2950	Sequence 2950, Ap
6	14.4	80.0	939	US-09-710-279-3059	Sequence 3059, Ap
7	14.4	80.0	963	US-09-134-001C-1367	Sequence 1367, Ap
8	14.4	80.0	2815	US-09-710-279-3819	Sequence 3819, Ap
9	14	77.8	3208	US-07-972-791-3	Sequence 3, Appl
10	14	77.8	3345	US-07-972-791-7	Sequence 7, Appl
11	14	77.8	3346	US-07-972-791-5	Sequence 5, Appl
12	14	77.8	3347	US-07-972-791-2	Sequence 2, Appl
13	14	77.8	3347	US-07-972-791-8	Sequence 8, Appl
14	14	77.8	3361	US-07-972-791-6	Sequence 6, Appl
15	14	77.8	3434	US-05-543-681A-4125	Sequence 4125, Ap
16	13.8	76.7	702	US-09-328-352-1886	Sequence 1886, Ap
17	13.8	76.7	1386	US-09-134-001C-984	Sequence 984, App
18	13.8	76.7	5679	US-08-844-274-10	Sequence 10, Appl
19	13.8	76.7	5679	US-08-844-274-10	Sequence 10, Appl
20	13.8	76.7	6642	US-09-809-665A-80	Sequence 80, Appl
21	13.8	76.7	6642	US-08-844-274-13	Sequence 13, Appl
22	13.8	76.7	6723	US-08-844-274-13	Sequence 14, Appl
23	13.8	76.7	6723	US-09-598-421-13	Sequence 13, Appl
24	13.8	76.7	6723	US-09-598-421-14	Sequence 14, Appl
25	13.8	76.7	7560	US-08-844-274-20	Sequence 20, Appl
26	13.8	76.7	7560	US-09-598-421-20	Sequence 20, Appl
27	13.8	76.7	7560	US-09-598-421-20	Sequence 20, Appl

28	13.8	76.7	9423	US-09-377-066-6	Sequence 6, Appl
29	13.8	76.7	9704	US-09-814-951A-3	Sequence 3, Appl
30	13.8	76.7	9717	US-09-251-645-1	Sequence 1, Appl
31	13.8	76.7	12666	US-08-961-527-137	Sequence 137, App
32	13.8	76.7	49795	US-08-453-702B-60	Sequence 60, Appl
33	13.6	75.6	3378	US-07-972-791-1	Sequence 1, Appl
34	13.4	74.4	341	US-09-270-767-8188	Sequence 8188, Ap
35	13.4	74.4	341	US-09-270-767-23470	Sequence 23470, A
36	13.4	74.4	350	US-09-270-767-1708	Sequence 1708, Ap
37	13.4	74.4	350	US-09-270-767-16990	Sequence 16990, A
38	13.4	74.4	492	US-09-248-796A-4921	Sequence 4921, Ap
39	13.4	74.4	549	US-09-328-352-3243	Sequence 3243, Ap
40	13.4	74.4	720	US-09-134-000C-1003	Sequence 1003, Ap
41	13.4	74.4	1293	US-09-489-039A-409	Sequence 409, App
42	13.4	74.4	1411	US-09-270-767-11617	Sequence 11617, A
43	13.4	74.4	2430	US-09-620-312D-176	Sequence 176, App
44	13.4	74.4	2967	US-09-185-501B-12	Sequence 12, Appl
45	13.4	74.4	10144	US-10-204-708-94	Sequence 94, Appl

## ALIGNMENTS

RESULT 1  
US-09-423-233-50  
; Sequence 50, Application US/09423233  
; Patent No. 6372430  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America as  
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
; FILE REFERENCE: 03063-0341WP  
; CURRENT APPLICATION NUMBER: US/09/423,233  
; CURRENT FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 50  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Fusarium oxysporum  
US-09-423-233-50

Query Match 100.0%; Score 18; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.84;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTAAATCGCGTCTC 18  
Db 1 CGTAAATCGCGTCTC 18

RESULT 2  
US-09-134-000C-314  
; Sequence 314, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 314  
; LENGTH: 615  
; TYPE: DNA  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-314

Query Match 83.3%; Score 15; DB 4; Length 615;

Best Local Similarity 100.0%; Pred. No. 49;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATCGGCTTC 16  
DB 172 GTTAATCGGCTTC 186

## RESULT 3

US-09-107-532A-1902/c  
; Sequence 1902, Application US/09107532A  
; Patent No. 6583275

## GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinlele, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 1902:

SEQUENCE CHARACTERISTICS:

LENGTH: 207 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

MOLECULE TYPE: circular

HYPOTHEICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...207

SEQUENCE DESCRIPTION: SEQ ID NO: 1902:

US-09-107-532A-1902

Query Match 82.2%; Score 14.8; DB 4; Length 207;

Best Local Similarity 88.9%; Pred. No. 56;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATCGGCTTC 18

DB 84 CGTTAATCGGCTTC 67

## RESULT 4

US-09-669-751-103  
; Sequence 103, Application US/09669751

Patent No. 6551575  
; GENERAL INFORMATION:

APPLICANT: Greenspan, Ralph J.

TITLE OF INVENTION: Methods for Identifying Compounds for

TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to

TITLE OF INVENTION: Balance and the Perception of Gravity

FILE REFERENCE: P-NI 3864

CURRENT APPLICATION NUMBER: US/09/669,751

CURRENT FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US 60/168,579

PRIOR FILING DATE: 1999-12-02

NUMBER OF SEQ ID NOS: 261

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 103

LENGTH: 650

TYPE: DNA

ORGANISM: Drosophila

US-09-669-751-103

Query Match 82.2%; Score 14.8; DB 4; Length 650;

Best Local Similarity 88.9%; Pred. No. 63;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATCGGCTTC 18

DB 69 CGTTAATCGGCTTC 86

## RESULT 5

US-09-134-000C-2950/c  
; Sequence 2950, Application US/09134000C  
; Patent No. 6617156

## GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2950

LENGTH: 2457

TYPE: DNA

ORGANISM: Enterococcus faecalis

US-09-134-000C-2950

Query Match 82.2%; Score 14.8; DB 4; Length 2457;

Best Local Similarity 88.9%; Pred. No. 71;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTAATCGGCTTC 18

DB 963 CGTTAATCGGCTTC 946

## RESULT 6

US-09-710-279-3059/c  
; Sequence 3059, Application US/09710279  
; Patent No. 6703492

## GENERAL INFORMATION:

APPLICANT: KIMMERLY WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PUS48005

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3059

LENGTH: 939  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-710-279-3059

Query Match 80.0%; Score 14.4; DB 4; Length 939;  
Best Local Similarity 93.8%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTAATTCGCGTTCCTC 18  
|||||  
DB 616 TTAATTCGCGTTCCTC 601

RESULT 7  
US-09-134-001C-1367/c  
Sequence 1367, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 1367  
LENGTH: 963  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-1367

Query Match 80.0%; Score 14.4; DB 3; Length 963;  
Best Local Similarity 93.8%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTAATTCGCGTTCCTC 18  
|||||  
DB 640 TTAATTCGCGTTCCTC 625

RESULT 8  
US-09-710-279-3819  
Sequence 3819, Application US/09710279  
Patent No. 6703492  
GENERAL INFORMATION:  
APPLICANT: KIMBERLY, WILLIAM JOHN  
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
FILE REFERENCE: P03480US  
CURRENT APPLICATION NUMBER: US/09/710,279  
CURRENT FILING DATE: 2000-11-09  
PRIOR APPLICATION NUMBER: 60/164,258  
PRIOR FILING DATE: 1999-11-09  
NUMBER OF SEQ ID NOS: 4472  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 3819  
LENGTH: 2815  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-710-279-3819

Query Match 80.0%; Score 14.4; DB 4; Length 2815;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTAATTCGCGTTCCTC 18  
|||||  
DB 792 TTAATTCGCGTTCCTC 807

RESULT 9  
US-07-972-791-3/c  
Sequence 3, Application US/07972791  
Patent No. 5348857  
GENERAL INFORMATION:  
APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAYEL, GAMBRELL, HEMITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3208 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella abortus  
STRAIN: biovar 1 (S2308)  
US-07-972-791-3

Query Match 77.8%; Score 14; DB 1; Length 3208;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 15  
|||||  
DB 1488 GTTAATTCGCGTTC 1475

RESULT 10  
US-07-972-791-7/c  
Sequence 7, Application US/07972791  
Patent No. 5348857  
GENERAL INFORMATION:  
APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:

ADDRESSEE: PRAVEL, GAMRELL, HEWITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: IBM PC compatible  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3345 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella melitensis  
STRAIN: biovar 1  
US-07-972-791-7

Query Match 77.8%; Score 14; DB 1; Length 3345;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTAATCGCGTTC 15  
|||||  
DB 1487 GTTAATCGCGTTC 1474

RESULT 11  
US-07-972-791-5/c  
Sequence 5, Application US/07972791  
Patent No. 5348857  
GENERAL INFORMATION:  
APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAVEL, GAMRELL, HEWITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909

TELEFAX: 713-850-0165  
TELEX: 792026  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3346 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella neotomae  
US-07-972-791-5

Query Match 77.8%; Score 14; DB 1; Length 3346;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTAATCGCGTTC 15  
|||||  
DB 1488 GTTAATCGCGTTC 1475

RESULT 12  
US-07-972-791-2/c  
Sequence 2, Application US/07972791  
Patent No. 5348857  
GENERAL INFORMATION:  
APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAVEL, GAMRELL, HEWITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3347 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella abortus  
STRAIN: biovar 5  
US-07-972-791-2

Query Match 77.8%; Score 14; DB 1; Length 3347;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTAATCGCGTTC 15  
|||||

Db 1488 GTTAATTCGCGTTC 1475

RESULT 13

US-07-972-791-8/c  
Sequence 8, Application US/07972791  
Patent No. 5348857

GENERAL INFORMATION:

APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77027

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3347 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella suis  
STRAIN: biovar 1  
US-07-972-791-8

Query Match 77.8%; Score 14; DB 1; Length 3347;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 15  
Db 1488 GTTAATTCGCGTTC 1475

RESULT 14

US-07-972-791-6/c  
Sequence 6, Application US/07972791  
Patent No. 5348857

GENERAL INFORMATION:

APPLICANT: Ficht, Thomas A.  
APPLICANT: Sowa, Blair A.  
APPLICANT: Adams, L. Gary  
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING  
TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER  
STREET: 1177 West Loop South, 10th Floor  
CITY: Houston  
STATE: Texas

COUNTRY: USA  
ZIP: 77027

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,791  
FILING DATE: 19921106  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kettelberger, Denise M.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-850-0909  
TELEFAX: 713-850-0165  
TELEX: 792026

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3361 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Brucella ovis  
US-07-972-791-6

Query Match 77.8%; Score 14; DB 1; Length 3361;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 15  
Db 1503 GTTAATTCGCGTTC 1490

RESULT 15

5310649-1/c  
Patent No. 5310649  
APPLICANT: Ficht, Thomas A.; Sowa, Blair A.; Adams, Garry L.  
TITLE OF INVENTION: METHOD OF DETECTING SPECIES AND BIOVARS  
OF BRUCELLA  
NUMBER OF SEQUENCES: 11  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/527,017  
FILING DATE: 22-MAY-1990  
SEQ ID NO: 1;  
LENGTH: 3434  
5310649-1

Query Match 77.8%; Score 14; DB 6; Length 3434;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTC 15  
Db 1692 GTTAATTCGCGTTC 1679

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 10:31:11 ; Search time 257 Seconds  
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Title: US-10-046-955-50  
Perfect score: 18  
Sequence: 1 cgttaattccgcgttcctc 18

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

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Maximum Match 100%  
Listing first 45 summaries

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Published Applications\_NA.\*  
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18: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
19: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
20: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
21: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-046-955-50	Sequence 50, Appl
2	15.4	85.6	538	US-10-363-345A-23645	Sequence 23645, A
3	15.4	85.6	538	US-10-363-345A-23646	Sequence 23646, A
4	15.4	85.6	4461	US-10-437-963-93618	Sequence 93618, A
5	15	83.3	127	US-10-282-122A-978	Sequence 978, App
6	15	83.3	128	US-09-815-242-996	Sequence 996, App
7	15	83.3	250	US-09-815-242-555	Sequence 555, App
8	15	83.3	250	US-10-282-122A-531	Sequence 531, App
9	15	83.3	1467	US-10-282-122A-6332	Sequence 6332, Ap
10	15	83.3	9212	US-09-070-972A-334	Sequence 334, App
11	14.8	82.2	262	US-09-535-459-1371	Sequence 1371, Ap
12	14.8	82.2	438	US-10-424-599-43896	Sequence 43896, A

13	14.8	82.2	554	18	US-10-363-345A-1073	Sequence 1073, Ap
14	14.8	82.2	554	18	US-10-363-345A-1074	Sequence 1074, Ap
15	14.8	82.2	585	17	US-10-437-963-81762	Sequence 81762, A
16	14.8	82.2	650	14	US-10-255-536-103	Sequence 103, App
17	14.8	82.2	816	18	US-10-425-115-60210	Sequence 60210, A
18	14.8	82.2	1231	18	US-10-363-345A-14681	Sequence 14681, A
19	14.8	82.2	1231	18	US-10-363-345A-14682	Sequence 14682, A
20	14.8	82.2	1445	18	US-10-425-115-145901	Sequence 145901, A
21	14.8	82.2	3135	16	US-10-282-122A-20853	Sequence 20853, A
22	14.8	82.2	3138	9	US-09-815-242-6520	Sequence 6520, Ap
23	14.8	82.2	2731748	17	US-10-287-465A-1	Sequence 1, Appli
24	14.4	80.0	65	15	US-10-032-585-259	Sequence 259, App
25	14.4	80.0	230	16	US-10-242-535A-247	Sequence 247, App
26	14.4	80.0	230	16	US-10-085-783A-247	Sequence 247, App
27	14.4	80.0	306	9	US-09-974-300-6603	Sequence 6603, Ap
28	14.4	80.0	540	18	US-10-363-345A-4913	Sequence 4913, Ap
29	14.4	80.0	540	18	US-10-363-345A-4914	Sequence 4914, Ap
30	14.4	80.0	559	15	US-10-029-386-7594	Sequence 7594, Ap
31	14.4	80.0	601	18	US-10-363-345A-20645	Sequence 20645, A
32	14.4	80.0	601	18	US-10-363-345A-20646	Sequence 20646, A
33	14.4	80.0	651	13	US-10-027-632-266929	Sequence 266929, A
34	14.4	80.0	651	15	US-10-027-632-266929	Sequence 266929, A
35	14.4	80.0	914	15	US-10-369-493-35000	Sequence 35000, A
36	14.4	80.0	948	16	US-10-424-599-78398	Sequence 78398, A
37	14.4	80.0	1520	16	US-10-424-599-116221	Sequence 116221, A
38	14.4	80.0	6711	15	US-10-341-200-42	Sequence 42, Appl
39	14.4	80.0	8440	15	US-10-341-200-19	Sequence 19, Appl
40	14.4	80.0	1163020	16	US-10-398-221-10	Sequence 10, Appl
41	14.4	80.0	3011208	16	US-10-398-221-2058	Sequence 2058, A
42	14	77.8	549	14	US-10-363-345A-15973	Sequence 15973, A
43	14	77.8	549	18	US-10-363-345A-15974	Sequence 15974, A
44	14	77.8	704	18	US-10-363-345A-23187	Sequence 23187, A
45	14	77.8	704	18	US-10-363-345A-23188	Sequence 23188, A

#### ALIGNMENTS

RESULT 1  
US-10-046-955-50  
; Sequence 50, Application US/10046955  
; Publication No. US20030129600A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as Represented by the  
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Di.  
; APPLICANT: Control and Prevention  
; APPLICANT: Morrison, Christine J.  
; APPLICANT: Reis, Etrol  
; APPLICANT: Aidorevich, Lilliana  
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
; TITLE OF INVENTION: Other Filamentous Fungi  
; FILE REFERENCE: 6395-62064  
; CURRENT APPLICATION NUMBER: US/10/046,955  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 09/423,233  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: PCT/US98/08926  
; PRIOR FILING DATE: 1998-05-01  
; PRIOR APPLICATION NUMBER: US 60/045,400  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 50  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Fusarium oxysporum  
US-10-046-955-50  
Query Match 100.0%; Score 18; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CCTAATTCGCGTTCCTC 18  
|||||  
Db 1 CCTAATTCGCGTTCCTC 18

## RESULT 2

US-10-363-345A-23645  
; Sequence 23645, Application US/10363345A  
; Publication No. US20040234960A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Method for determining the degree of methylation of defined  
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3  
; FILE REFERENCE: E01/1227  
; CURRENT APPLICATION NUMBER: US/10/363,345A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 23645  
; LENGTH: 538  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: CpG-island No: 23645  
US-10-363-345A-23645

Query Match 85.6%; Score 15.4; DB 18; Length 538;  
Best Local Similarity 94.1%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCCTC 18  
|||||  
Db 434 GTTAATTCGCGTTCCTC 450

## RESULT 3

US-10-363-345A-23646/c  
; Sequence 23646, Application US/10363345A  
; Publication No. US20040234960A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Method for determining the degree of methylation of defined  
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3  
; FILE REFERENCE: E01/1227  
; CURRENT APPLICATION NUMBER: US/10/363,345A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 23646  
; LENGTH: 538  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: CpG-island No: 23646  
US-10-363-345A-23646

Query Match 85.6%; Score 15.4; DB 18; Length 538;  
Best Local Similarity 94.1%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCCTC 18  
|||||  
Db 105 GTTAATTCGCGTTCCTC 89

## RESULT 4

US-10-437-963-93618/c  
; Sequence 93618, Application US/10437963  
; Publication No. US20040123343A1

; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 93618  
; LENGTH: 4461  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_91986C.1  
US-10-437-963-93618

Query Match 85.6%; Score 15.4; DB 17; Length 4461;  
Best Local Similarity 94.1%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCCTC 18  
|||||  
Db 1209 GTTAATTCGCGTTCCTC 1193

## RESULT 5

US-10-282-122A-978/c  
; Sequence 978, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16

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Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 978
; LENGTH: 127
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-978
```

```
Query Match      83.3%; Score 15; DB 16; Length 127;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 GTTAATTCGGCTTCC 16
      |||||
Db      117 GTTAATTCGGCTTCC 103
```

```
RESULT 6
US-09-815-242-996/c
; Sequence 996, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 996
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-996
```

```
Query Match      83.3%; Score 15; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 GTTAATTCGGCTTCC 16
      |||||
Db      118 GTTAATTCGGCTTCC 104
```

```
RESULT 7
US-09-815-242-555/c
; Sequence 555, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
```

```
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 555
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-555
```

```
Query Match      83.3%; Score 15; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 GTTAATTCGGCTTCC 16
      |||||
Db      54 GTTAATTCGGCTTCC 40
```

```
RESULT 8
US-10-282-122A-531/c
; Sequence 531, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Mang, Lianguu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
```

PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 531  
LENGTH: 250  
TYPE: DNA  
ORGANISM: Enterococcus faecalis  
US-10-282-122A-531

Query Match  
Best Local Similarity 83.3%; Score 15; DB 16; Length 250;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCC 16  
DB 54 GTTAATTCGCGTTCC 40

RESULT 9  
US-10-282-122A-6332  
Sequence 6332, Application US/10282122A  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zykkind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Foreyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282.122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1

SEQ ID NO: 6332  
LENGTH: 1467  
TYPE: DNA  
ORGANISM: Enterococcus faecalis  
US-10-282-122A-6332

Query Match  
Best Local Similarity 83.3%; Score 15; DB 16; Length 1467;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCC 16  
DB 1027 GTTAATTCGCGTTCC 1041

RESULT 10  
US-09-070-927A-334  
Sequence 334, Application US/09070927A  
Patent No. US20020120116A1  
GENERAL INFORMATION:  
APPLICANT: Charles A. Kunsch  
Patrick J. Dillon  
Steven Barash  
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
NUMBER OF SEQUENCES: 982  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,927A  
FILING DATE: 04-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/046,655  
FILING DATE: 1997-05-16  
APPLICATION NUMBER: 60/044,031  
FILING DATE: 1997-05-06  
APPLICATION NUMBER: 60/066,009  
FILING DATE: 1997-11-14  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB369  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 334:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9212 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 334:  
US-09-070-927A-334

Query Match  
Best Local Similarity 83.3%; Score 15; DB 9; Length 9212;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCC 16  
DB 4989 GTTAATTCGCGTTCC 5003

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RESULT 11
US-09-535-459-1371/C
; Sequence 1371, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuve, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1371
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: m13c_feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01153717
US-09-535-459-1371

Query Match      82.2%; Score 14.8; DB 10; Length 262;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCTC 18
DB      102 CTTAATTCGCGTTCTC 85

RESULT 12
US-10-424-599-43896
; Sequence 43896, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 43896
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139637C.1
US-10-424-599-43896

Query Match      82.2%; Score 14.8; DB 16; Length 438;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCTC 18
DB      297 CGTTAATTCGCGTTCTC 314

RESULT 13
US-10-363-345A-1073
; Sequence 1073, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 1073
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 1073
US-10-363-345A-1073

Query Match      82.2%; Score 14.8; DB 18; Length 554;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCTC 18
DB      113 CGTTAATTCGCGTTATC 130

RESULT 14
US-10-363-345A-1074/C
; Sequence 1074, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 1074
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 1074
US-10-363-345A-1074

Query Match      82.2%; Score 14.8; DB 18; Length 554;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATTCGCGTTCTC 18
DB      442 CGTTAATTCGCGTTATC 425

RESULT 15
US-10-437-963-81762
; Sequence 81762, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
```

```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 81762
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81256C.1
US-10-437-963-81762

Query Match      82.2%; Score 14.8; DB 17; Length 585;
Best Local Similarity 88.9%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGTTAATCGCGCTCTC 18
        |||||
Db      230 CGTTCATTGCGCTCCAC 247

Search completed: December 8, 2004, 11:18:07
Job time : 261 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 10:26:55 ; Search time 1781 Seconds  
(without alignments)  
368.285 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaatcgcgtccccc 18

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	91.1	667	5	BQ483402 WHE3508_B
2	16.4	91.1	949	9	CL460875 SAT1.11
3	16.4	88.9	685	9	CL707833 OR_BBA002
4	16.4	88.9	701	9	CL708823 OR_BBA003
5	16.4	88.9	750	9	CL714278 OR_BBA003
6	16.4	88.9	750	9	CL788163 OR_BBA010
7	15.4	85.6	262	8	AZ359925 1M0103B02
8	15.4	85.6	277	8	AZ359925 1M0103B02
9	15.4	85.6	367	7	BM452985 BOHGA60TF
10	15.4	85.6	402	9	CN746869 SAL_US027
11	15.4	85.6	493	8	CG858920 ZMMBC026
12	15.4	85.6	499	8	AZ498171 1M0335P13
13	15.4	85.6	547	7	BH144783 TDEB091TH
14	15.4	85.6	588	8	BH144783 TDEB091TH
15	15.4	85.6	669	3	BZ508556 BONS38TF
16	15.4	85.6	740	9	AY440797 Armigeres
17	15.4	85.6	753	3	AG042918 Pan trogl
18	15.4	85.6	819	3	AY440799 Armigeres
19	15.4	85.6	902	6	CG810640 FSA082TF
20	15.4	85.6	921	6	CA278228 SCBSFD03
21	15.4	85.6	968	7	CK288913 EST751635
22	15.4	85.6	1000	5	CK286745 EST749467
23	15.4	85.6	1278	5	BP512280 BP512280
24	15.4	83.3	311	2	BM543811 AGERCORT
					AM833312 RC2-TT000

25	15	83.3	543	4	BI881942 fm89g12.x
26	15	83.3	547	6	CB406133 OSTR064C7
27	15	83.3	563	6	CB406152 OSTR064C7
28	15	83.3	611	9	CR257810 Forward s
29	15	83.3	636	2	BE557132 Forward s
30	15	83.3	728	4	BE557132 Forward s
31	15	83.3	870	7	CG200815 Forward s
32	15	83.3	928	9	CG200815 Forward s
33	15	83.3	1057	9	AG081712 Pan trogl
34	14.8	82.2	140	6	CB066245
35	14.8	82.2	147	4	BM616169
36	14.8	82.2	206	8	AZ991070 2M0275N03
37	14.8	82.2	206	8	AZ991080 2M0275P03
38	14.8	82.2	239	6	CR203507 Forward s
39	14.8	82.2	282	6	CR066239 PVBE11E04
40	14.8	82.2	296	9	CR066239 Forward s
41	14.8	82.2	298	9	CR045992 Forward s
42	14.8	82.2	299	9	CR180215 Forward s
43	14.8	82.2	303	1	AA785231 5th08a1.f
44	14.8	82.2	322	9	BM543811 AGERCORT
45	14.8	82.2	338	1	AJ502973 AJ502973

## ALIGNMENTS

RESULT 1  
BQ483402/c 667 bp mRNA linear EST 03-JUN-2002  
LOCUS WHE3508\_B09\_D18ZS wheat unstressed root cDNA library Triticum  
DEFINITION aetivum cDNA clone WHE3508\_B09\_D18, mRNA sequence.

ACCESSION BQ483402 GI:21319338  
VERSION BQ483402.1  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum

REFERENCE  
AUTHORS Anderson, O.D., Zhao, S., Close, T.J., Crossman, C., Fenton, R.D.,  
Lazo, G.R., Nguyen, H.T., Rauech, C.J., Wilson, C., Woo, J., and Zhang, D.  
TITLE The structure and function of the expressed portion of the wheat  
JOURNAL Unpublished (2002)  
COMMENT Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: oanderson@pw.usda.gov

FEATURES  
source  
Seq primer: SK primer.  
Location/Qualifiers  
1. 667  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cui="taxon:4565"  
/db\_xref="taxon:4565"  
/clone="WHE3508\_B09\_D18"  
/tissue\_type="Roots"  
/dev\_stage="Full tillering"  
/lab\_host="E. coli SOLR"  
/clone\_lib="wheat unstressed root cDNA library"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid  
pBluescript SK(-), Site 1: EcoRI, Site 2: XhoI. Plants  
were grown until full tillering stage and root tissue was  
collected at Texas Tech University (Zhang, H.T. Nguyen  
lab). Total RNA and poly(A) RNA were prepared, a cDNA  
library was made, and the cDNA clones were in vivo  
excised to give pBluescript SK(-) phagemids in the T7

Close lab (Close, Fenton) at the University of California, Riverside. Colony plating, plasmid preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

## ORIGIN

Query Match 91.1%; Score 16.4; DB 5; Length 667;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18  
|||||  
Db 243 CGTTAATTCGGCTTCCTC 226

## RESULT 2

LOCUS CL708823 949 bp DNA linear GSS 31-MAR-2004  
DEFINITION SAIL\_111\_C06.v1 SAIL Collection Arabidopsis thaliana genomic clone  
CL708823  
VERSION CL708823  
KEYWORDS GI:45863780  
ACCESSION

ORGANISM Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis;

REFERENCE 1 (bases 1 to 949)  
Sessions, A., Burke, E., Presting, G., Aux, G., McEliver, J., Patton, D., Dietrich, B., Ho, P., Bacwarden, J., Ko, C., Clarke, J.D., Cotton, D., Bullis, D., Snell, J., Miguel, T., Hutchinson, D., Kimmery, B., Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A.  
A high-throughput Arabidopsis reverse genetics system  
Plant Cell 14 (12), 2985-2994 (2002)

JOURNAL  
MEDLINE  
PubMed  
12356987  
12468722

COMMENT  
Applied Trait Genetics  
Contact: Sessions A  
Syngenta Biotechnology Inc.  
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA  
Email: allen.sessions@syngenta.com  
ABRC Stock Number CS805419; T-DNA left border flanking sequences of  
Syngenta Arabidopsis Insertion Library (SAIL) lines are available  
through the Arabidopsis Biological Resource Center (ABRC).  
Sequences represent a pool of amplified genomic regions and not  
single contiguous sequences.  
Class: T-DNA tagged.

FEATURES  
source  
Location/Qualifiers  
1..949  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Columbia"  
/db\_xref="taxon:3702"  
/clone="SAIL\_111\_C06.v1"  
/note="T-DNA left border sequences were isolated using a  
modified TAIL-PCR strategy"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 9; Length 949;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18  
|||||  
Db 578 CGTTAATTCGGCTTCGC 595

RESULT 3  
LOCUS CL707833/c 665 bp DNA linear GSS 26-JUL-2004  
DEFINITION OR\_BB40027F10.r OR\_BB4 Oryza rufipogon genomic clone OR\_BB40027F10

ORIGIN  
Query Match 91.1%; Score 16.4; DB 9; Length 949;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGTTAATTCGGCTTCCTC 18  
|||||  
Db 578 CGTTAATTCGGCTTCGC 595

RESULT 4  
LOCUS CL708823/c 701 bp DNA linear GSS 26-JUL-2004  
DEFINITION OR\_BB80030B15.r OR\_BB8 Oryza rufipogon genomic clone OR\_BB80030B15  
CL708823  
VERSION CL708823  
KEYWORDS GI:50595861  
ACCESSION

ORGANISM Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 701)  
Kim H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
OAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259

3', genomic survey sequence.

ACCESSION CL707833  
VERSION CL707833.1 GI:50594871  
KEYWORDS GSS.

## SOURCE

Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 685)  
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
OAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: http://genome.arizona.edu

## ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 685;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATTCGGCTTCCT 17  
|||||  
Db 32 GTTAATTCGGCTTCCT 17

RESULT 4  
LOCUS CL708823 701 bp DNA linear GSS 26-JUL-2004  
DEFINITION OR\_BB80030B15.r OR\_BB8 Oryza rufipogon genomic clone OR\_BB80030B15  
CL708823  
VERSION CL708823  
KEYWORDS GI:50595861  
ACCESSION

ORGANISM Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 701)  
Kim H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
OAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: http://genome.arizona.edu

PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert Length: 161 Std Error: 0.00  
Plate: 0027 row: F column: 10  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

FEATURES  
source  
Location/Qualifiers  
1..685  
/organism="Oryza rufipogon"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4529"  
/clone="OR\_BB80027F10"  
/tissue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_id="OR\_BB8"  
/note="Vector: pGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

ORIGIN  
Query Match 88.9%; Score 16; DB 9; Length 685;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATTCGGCTTCCT 17  
|||||  
Db 32 GTTAATTCGGCTTCCT 17

RESULT 4  
LOCUS CL708823 701 bp DNA linear GSS 26-JUL-2004  
DEFINITION OR\_BB80030B15.r OR\_BB8 Oryza rufipogon genomic clone OR\_BB80030B15  
CL708823  
VERSION CL708823  
KEYWORDS GI:50595861  
ACCESSION

ORGANISM Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 701)  
Kim H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
OAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259

ORIGIN  
Query Match 88.9%; Score 16; DB 9; Length 685;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATTCGGCTTCCT 17  
|||||  
Db 32 GTTAATTCGGCTTCCT 17

RESULT 4  
LOCUS CL708823 701 bp DNA linear GSS 26-JUL-2004  
DEFINITION OR\_BB80030B15.r OR\_BB8 Oryza rufipogon genomic clone OR\_BB80030B15  
CL708823  
VERSION CL708823  
KEYWORDS GI:50595861  
ACCESSION

ORGANISM Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 701)  
Kim H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
OAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259



Email: http://genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert length: 161 Std Error: 0.00  
Plate: 0030 row: B column: 15  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

FEATURES  
source Location/Qualifiers

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/organism="Oryza rufipogon"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4529"  
/clone="OR\_BBa0030B15"  
/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_lib="OR\_BBa"  
/note="Vector: pAGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

## ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 701;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATTCGCGTTCT 17  
|||||  
32 GTTAATTCGCGTTCT 17

Db

RESULT 5 740 bp DNA linear GSS 26-JUL-2004  
CL714278/c OR\_BBa0038P08.r OR\_BBa Oryza rufipogon genomic clone OR\_BBa0038P08  
LOCUS  
DEFINITION  
3' genomic survey sequence.  
CL714278  
CL714278.1 GI:50601316  
GSS.  
Oryza rufipogon  
Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriactoidae; Oryzaceae; Oryza.  
1 (bases 1 to 740)

REFERENCE  
AUTHORS Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
TITLE OMAP Project  
JOURNAL Unpublished (2004)  
COMMENT Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: http://genome.arizona.edu

PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert length: 161 Std Error: 0.00  
Plate: 0030 row: B column: 08  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

FEATURES  
source Location/Qualifiers

1..740  
/organism="Oryza rufipogon"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4529"  
/clone="OR\_BBa0038P08"  
/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_lib="OR\_BBa"  
/note="Vector: pAGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 740;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATTCGCGTTCT 17  
|||||  
32 GTTAATTCGCGTTCT 17

Db

RESULT 6 750 bp DNA linear GSS 30-JUL-2004  
CL788163/c OR\_BBa0106112.r OR\_BBa Oryza rufipogon genomic clone OR\_BBa0106112  
LOCUS  
DEFINITION  
3' genomic survey sequence.  
CL788163  
CL788163.1 GI:50867814  
GSS.  
Oryza rufipogon  
Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriactoidae; Oryzaceae; Oryza.  
1 (bases 1 to 750)

REFERENCE  
AUTHORS Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
TITLE OMAP Project  
JOURNAL Unpublished (2004)  
COMMENT Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: http://genome.arizona.edu

PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert length: 161 Std Error: 0.00  
Plate: 0106 row: I column: 12  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

FEATURES  
source Location/Qualifiers

1..750  
/organism="Oryza rufipogon"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4529"  
/clone="OR\_BBa0106112"  
/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_lib="OR\_BBa"  
/note="Vector: pAGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

## ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 750;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GTTAATTCGCGTTCT 17  
|||||  
34 GTTAATTCGCGTTCT 19

Db

RESULT 7 262 bp DNA linear GSS 02-OCT-2000  
AZ359925/c IM0103B02F Mouse 10kb plasmid UGCIIM library Mus musculus genomic  
LOCUS  
DEFINITION  
clone UGCIIM0103B02 F, genomic survey sequence.  
AZ359925  
AZ359925.1 GI:10473625  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

FEATURES  
source Location/Qualifiers

1..10473625  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="IM0103B02F"  
/issue\_type="genomic survey sequence"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_lib="OR\_BBa"  
/note="Vector: pAGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

ORIGIN

REFERENCE 1 (bases 1 to 262)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0103 row: B column: 02  
 Seq primer: CGTTGTAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 262.  
 Location/Qualifiers  
 1..262  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UTGCM1013B02"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42ny: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 8; Length 262;  
 Best Local Similarity 94.1%; Pred. No. 6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 2 GTTATTGGCTTCTC 18  
 |||||  
 Db 214 GTTAATCGCCTTCTC 198

RESULT 8  
 BH452985/c  
 LOCUS BH452985 277 bp DNA linear GSS 12-DEC-2001  
 DEFINITION BOHGA60TF BOHG Brassica oleracea genomic clone BOHGA60, genomic survey sequence.  
 ACCESSION BH452985  
 VERSION BH452985.1 GI:17638696  
 KEYWORDS GSS  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 277)  
 AUTHORS Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Fraser,C.M.  
 TITLE Whole genome shotgun sequencing of Brassica oleracea  
 JOURNAL Unpublished (2001)  
 COMMENT Other GSSs: BOHGA60TR  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 Seq primer: TFC  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Class: sheared ends.  
 Location/Qualifiers  
 1..277  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BOHGA60"  
 /note="Vector: pHOSt; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOSt using BstXI linkers"

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 8; Length 277;  
 Best Local Similarity 94.1%; Pred. No. 6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 1 CGTTAATTCGGCTTCT 17  
 |||||  
 Db 94 CGTTAATTCGGCTTCT 78

RESULT 9  
 CN746869 367 bp mRNA linear EST 19-MAY-2004  
 LOCUS SAL\_US027xg21f1.ab1 SAL\_US N. Benthamenia benthamiana cDNA  
 DEFINITION SAL\_US027xg21f1.ab1 SAL\_US N. Benthamenia benthamiana cDNA  
 ACCESSION CN746869  
 VERSION CN746869.1 GI:47511866  
 KEYWORDS EST.  
 SOURCE Nicotiana benthamiana  
 ORGANISM Nicotiana benthamiana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Nicotiana.  
 1 (bases 1 to 367)  
 Opperman,C.H., Lommel,S.A., Burke,M., Feulner,G., Carlson,J., George,C., Gove,S., Houfek,T.D., Jefferys,S.R., Kalat,S., King,R., Levin,J., Little,P.C., Lumpkin,A., Ross,T., Salestead,A., Scholl,E.H., Sosinski,B.R., Stephens,P.J. and Zekans,S.H.  
 Tobacco Genome Initiative (TGI) Nicotiana benthamiana ESTs  
 Unpublished (2004)  
 CONTACT: Dr. Steven A. Lommel  
 Tobacco Genome Initiative  
 North Carolina State University  
 Box 7253, NCSU, Raleigh, NC 27606, USA  
 Tel: 9195130006  
 Fax: 9195159500  
 Email: Steve.Lommel@ncsu.edu  
 Homology: e-val = 7.0e-022. Description = asparaginyl-tRNA synthetase, cytoplasmic (asparagine-tRNA ligase), putative [Arabidopsis thaliana] g120140327|sp|Q9SSK1|SYN1\_ARATH Asparaginyl-tRNA synthetase, cytoplasmic 3 (Asparaginyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)]) e-val = 2.4e-022. Description = putative asparaginyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)] g114587206|dbj|BAB61140.1| putative asparaginyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)]



QY 2 GTTAATTCGCGTTCCTC 18  
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 Db 383 GTTAATTCGCGTTCCTC 367

RESULT 12  
 BH144783 499 bp DNA linear GSS 16-AUG-2001  
 LOCUS TDG8091TH CTG Lycopersicon esculentum genomic clone CTG030P13,  
 DEFINITION genomic survey sequence.  
 ACCESSION BH144783  
 VERSION BH144783.1 GI:15200046  
 KEYWORDS GSS.  
 SOURCE Lycopersicon esculentum (tomato)  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
 1 (bases 1 to 499)  
 van der Hoeven, R., Sun, H., Cho, J., Utterback, T., Romning, C. and  
 Tanksley, S.  
 Tomato Demethylated Genomic DNA Sequences  
 Unpublished (2001)  
 CONTACT: CUGI  
 CLEMSON UNIVERSITY GENOMICS INSTITUTE  
 CLEMSON UNIVERSITY  
 100 JORDAN HALL, CLEMSON, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 tomato demethylated genomic DNA  
 Insert length: 1270 Std Error: 0.00  
 Seq primer: M13-F-R  
 Class: shotgun.

FEATURES  
 source Location/Qualifiers  
 1..499  
 /organism="Lycopersicon esculentum"  
 /mol\_type="genomic DNA"  
 /cultivar="R6203"  
 /db\_xref="taxon:4081"  
 /clone="CTG030P13"  
 /tissue\_type="young leaves"  
 /dev\_stage="12-14 weeks post harvest"  
 /lab\_host="E.coli JM109"  
 /clone\_lib="CTG"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
 XhoI; This library was made from short EcoRI digested  
 fragments of the genome of Lycopersicon esculentum ligated  
 into pBS (SK-). The fragments were cloned into the  
 methylation restrictive E.coli strain JM109 with the  
 purpose of enriching the library for non-methylated DNA  
 fragments. This procedure may enrich the pool of cloned  
 fragments in JM109 cells for sequences representing  
 expressed genes. Average insert size 1.27 Kb."

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 8; Length 499;  
 Best Local Similarity 94.1%; Pred. No. 6.3e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCCTC 18  
 |||||  
 Db 116 GTTAATTCGCGTTCCTC 132

RESULT 13  
 CK701447 547 bp mRNA linear EST 09-FEB-2004  
 LOCUS CK701447/c  
 DEFINITION USDA-FP 4707 Ridge pineapple sweet orange entire seedling Citrus  
 sinensis cDNA clone RSE3JA08 5', mRNA sequence.  
 ACCESSION CK701447  
 VERSION CK701447.1 GI:42477392  
 KEYWORDS EST.  
 SOURCE Citrus sinensis

ORGANISM Citrus sinensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosids; eurosids II; Sapindales; Rutaceae; Citrus.  
 1 (bases 1 to 547)  
 Bausher, M., Shatters, R., Chaparro, J., Dang, P., Hunter, W. and  
 Niedz, R.  
 An expressed sequence tag (EST) set from Citrus sinensis L. Osbeck  
 whole seedlings and the implications of further perennal source  
 investigations  
 Plant Sci. 165, 415-422 (2003)  
 CONTACT: Michael Bausher  
 US Horticultural Research  
 USDA - ARS  
 2001 South Rock Rd., Fort Pierce, FL 34945, USA  
 Tel: (772) 462-5918  
 Fax: (772) 462-5961  
 Email: [mBausher@usnr1.ars.usda.gov](mailto:mBausher@usnr1.ars.usda.gov)  
 Seq primer: T3 Universal.

FEATURES  
 source Location/Qualifiers  
 1..547  
 /organism="Citrus sinensis"  
 /mol\_type="mRNA"  
 /cultivar="Ridge Pineapple"  
 /db\_xref="taxon:2711"  
 /clone="RSE3JA08"  
 /tissue\_type="entire seedling"  
 /dev\_stage="50 days after germination"  
 /lab\_host="X11-Blue"  
 /clone\_lib="Ridge pineapple sweet orange entire seedling"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
 XhoI; A high quality EST with at least 200 contiguous  
 bases at Trace Tuner score of 20 or better"

ORIGIN  
 Query Match 85.6%; Score 15.4; DB 7; Length 547;  
 Best Local Similarity 94.1%; Pred. No. 6.3e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTAATTCGCGTTCCTC 18  
 |||||  
 Db 491 GTTAATTCGCGTTCCTC 475

RESULT 14  
 BZ508556/c 588 bp DNA linear GSS 16-DEC-2002  
 LOCUS BZ508556  
 DEFINITION BZ508556 BO\_1.6\_2\_KB\_tot Brassica oleracea genomic clone BZ508556,  
 genomic survey sequence.  
 ACCESSION BZ508556  
 VERSION BZ508556.1 GI:27031477  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 588)  
 Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Frazer, C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other GSSs: BZ508556R  
 CONTACT: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: [cdtown@tigr.org](mailto:cdtown@tigr.org)  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TP  
 Class: shared ends.

FEATURES  
 source Location/Qualifiers  
 1..588

ORIGIN

/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="T0100DH3"  
/db\_xref="taxon:3712"  
/clone="BONSH38"  
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/note="Vector: PHOS1, Site 1: BstXI, 1.6-2 kb sheared  
total DNA inserted into PHOS1 using BstXI linkers"

Query Match 85.6%; Score 15.4; DB 8; Length 588;  
Best Local Similarity 94.1%; Pred. No. 6.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCT 17  
|||||  
Db 445 CGTTAATTCGCGTTCT 429

RESULT 15  
AY440797 669 bp mRNA linear HTC 24-JUN-2004  
LOCUS Armigeres subalbatus ASAP ID: 40469 putative: alanine  
DEFINITION aminotransferase mRNA sequence.  
ACCESSION AY440797 GI:42765826  
VERSION AY440797.1 GI:42765826  
KEYWORDS HTC.  
SOURCE Armigeres subalbatus  
ORGANISM Armigeres subalbatus  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
Armigeres.  
1 (bases 1 to 669)  
Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,  
Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,  
Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,  
Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and  
Christensen,B.M.  
Description of the Transcriptomes of Immune Response-Activated  
Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres  
subalbatus  
JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)  
PUBMED 15213157  
REFERENCE 2 (bases 1 to 669)  
Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,  
Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,  
Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,  
Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.  
TITLE Direct Submission  
JOURNAL Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,  
University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI  
53706, USA  
COMMENT More information about this sequence is available in ASAP (A  
Systematic Annotation Package for community analysis of genomes)  
from the University of Wisconsin-Madison at  
<https://asap.ahabs.wisc.edu/annotation/pnp/logon.php>.  
FEATURES  
source  
1..669  
/organism="Armigeres subalbatus"  
/mol\_type="mRNA"  
/isolation\_source="perfused hemolymph of  
bacteria-inoculated organisms at 1, 3, 6, 12, and 24  
hours post-inoculation"  
/db\_xref="taxon:124917"  
/sex="female"  
/cell\_type="hemocyte"  
/tissue\_type="hemolymph"  
/dev\_stage="adult"  
/note="ASAP-UW Feature ID: 40468"  
1..669  
/note="putative: alanine aminotransferase; similar to  
Anopheles gambiae ENSANGP0000017843 v14.2.1 at Ensembl;  
ASAP-UW Feature ID: 40469"

## ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 669;  
Best Local Similarity 94.1%; Pred. No. 6.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTAATTCGCGTTCT 17  
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Db 32 CGTTAATTCGCGTTCT 48

Search completed: December 8, 2004, 11:08:40  
Job time : 1785 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 171.043 Seconds

(without alignments)  
5321.503 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21  
Sequence: 1 ctaccacctgcgaactggaga 21Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_stb: *
12: gb_sv: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_stb: *
28: em_un: *
29: em_vi: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rsd: *
36: em_hcg_mam: *
37: em_hcg_vrt: *
38: em_by: *
39: em_hcgo_hum: *
40: em_hcgo_mus: *
41: em_hcgo_other: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	6 AR206445	AR206445 Sequence
2	21	100.0	21	6 BD083636	BD083636 Nucleic a
3	21	100.0	298	8 AY226096	AY226096 Nectria h
4	21	100.0	319	6 AR206400	AR206400 Sequence
5	21	100.0	319	6 BD083591	BD083591 Nucleic a
6	21	100.0	319	6 AF117921	AF117921 Nectria h
7	21	100.0	468	8 AY426972	AY426972 Fusarium
8	21	100.0	471	8 AF161222	AF161222 Nectria h
9	21	100.0	471	8 AY043472	AY043472 Nectria h
10	21	100.0	471	8 AY043473	AY043473 Nectria h
11	21	100.0	477	8 AY043478	AY043478 Nectria h
12	21	100.0	477	8 FSU38558	FSU38558 Fusarium bo
13	21	100.0	478	8 AF132801	AF132801 Nectria h
14	21	100.0	478	8 AF150459	AF150459 Nectria h
15	21	100.0	478	8 AF150460	AF150460 Nectria h
16	21	100.0	478	8 AF150461	AF150461 Nectria h
17	21	100.0	478	8 AF150462	AF150462 Nectria h
18	21	100.0	478	8 AF150463	AF150463 Nectria h
19	21	100.0	478	8 AF150464	AF150464 Nectria h
20	21	100.0	478	8 AF150465	AF150465 Nectria h
21	21	100.0	479	8 AF150469	AF150469 Nectria h
22	21	100.0	479	8 AF150470	AF150470 Nectria h
23	21	100.0	479	8 AF150475	AF150475 Nectria h
24	21	100.0	480	8 AF150466	AF150466 Nectria h
25	21	100.0	480	8 AF150467	AF150467 Nectria h
26	21	100.0	480	8 AF150477	AF150477 Nectria h
27	21	100.0	480	8 AF150478	AF150478 Nectria h
28	21	100.0	480	8 AF150479	AF150479 Nectria h
29	21	100.0	480	8 AF150480	AF150480 Nectria h
30	21	100.0	480	8 AF440567	AF440567 Nectria h
31	21	100.0	480	8 FSU38557	FSU38557 Fusarium bo
32	21	100.0	481	8 AY210327	AY210327 Nectria s
33	21	100.0	483	8 AY043477	AY043477 Nectria h
34	21	100.0	501	8 AY273332	AY273332 Unculture
35	21	100.0	502	8 AY210323	AY210323 Nectria s
36	21	100.0	505	8 AY043470	AY043470 Nectria h
37	21	100.0	509	8 AF165874	AF165874 Nectria h
38	21	100.0	544	8 NEXITS	L36627 Neocosmospo
39	21	100.0	546	8 AF178413	AF178413 Neocosmos
40	21	100.0	547	8 AF178412	AF178412 Neocosmos
41	21	100.0	547	8 NECTISA	L36619 Nectria hae
42	21	100.0	548	8 AF178397	AF178397 Fusarium
43	21	100.0	548	8 AF178402	AF178402 Fusarium
44	21	100.0	549	8 AF178398	AF178398 Nectria i
45	21	100.0	550	8 AF178394	AF178394 Nectria h

## ALIGNMENTS

```
RESULT 1
LOCUS AR206445
DEFINITION Sequence 51 from patent US 6372430.
ACCESSION AR206445
VERSION AR206445.1 GI:21505049
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 21)
TITLE Morrison,C.J., Reies,E., Aidorevich,L. and Choi,J.Soo.
JOURNAL Nucleic acids for detecting Aspergillus species and other
Patent: US 6372430-A 51 16-APR-2002;
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FEATURES	source	Location/Qualifiers
		1..21
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		/mol_type="unassigned DNA"
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QY		
	1 CTACACCTCGCAACTGGAGA 21	
	1 CTACACCTCGCAACTGGAGA 21	
Db		
	1 CTACACCTCGCAACTGGAGA 21	
RESULT 2		
LOCUS	BD083636	
DEFINITION	Nucleic acids for detecting <i>Aspergillus</i> species and other filamentous fungi.	
ACCESSION	BD083636	
VERSION	BD083636.1	
KEYWORDS	JP 2001525665-A/51.	
SOURCE	Fusarium solani	
ORGANISM	Fusarium solani	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.	
AUTHORS	1 (bases 1 to 21)	
TITLE	Morrison C.J., Reiss E., Aldorevich L. and Choi J.S.	
JOURNAL	Nucleic acids for detecting <i>Aspergillus</i> species and other filamentous fungi	
	Patent: JP 2001525665-A 51 11-DEC-2001;	
	THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE	
COMMENT		
	OS Fusarium solani	
	PN JP 2001525665-A/51	
	PD 11-DEC-2001	
	PF 01-MAY-1998 JP 1998548275	
	PR 02-MAY-1997 US 60/045400	
	PI CHRISTINE J MORRISON,ERROL REISS,LILIANA ALDOREVICH,JONG SOO	
	PI CHOI	
	PC C12Q1/68	
	CC Strandedness: Single;	
	CC Topology: linear;	
FEATURES		
source		Location/Qualifiers.
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	/organism="Fusarium solani"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:169388"	
	/note="Fusarium solani"	
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Best Local Similarity		100.0%; Pred. No. 13;
Matches	21; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY		
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Db		
	1 CTACACCTCGCAACTGGAGA 21	
RESULT 3		
LOCUS	AY226096	
DEFINITION	Nectria haematococca 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence.	
ACCESSION	AY226096	
VERSION	AY226096.1	
	GI:29293692	

KEYWORDS	
SOURCE	Nectria haematococca
ORGANISM	Nectria haematococca Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE	1 (bases 1 to 298)
AUTHORS	Millar,B.C., Xu,J. and Moore,J.E.
TITLE	Direct Submission
JOURNAL	Submitted (28-JUN-2003) Department of Bacteriology, Northern Ireland Public Health Laboratory, Belfast City Hospital, Lisburn Road, Belfast, Co. Antrim BT9 7AD, Northern Ireland, UK
FEATURES	
source	1..298 /organism="Nectria haematococca" /mol_type="genomic DNA" /strains="260499/24" /db_xref="taxon:140110" <1..132 /product="5.8S ribosomal RNA" 133..245 /product="internal transcribed spacer 2" 246..>298 /product="28S ribosomal RNA"
ORIGIN	
Query Match	100.0%; Score 21; DB 8; Length 298;
Best Local Similarity	100.0%; Pred. No. 10;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy	1 CTACACCTCGCAACTGAGA 21 
Db	195 CTACACCTCGCAACTGAGA 215
RESULT 4	
LOCUS	AR206400 319 bp DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 6 from patent US 6372430.
ACCESSION	AR206400
VERSION	AR206400.1 GI:21504990
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified. 1 (bases 1 to 319) Morrison,C.J., Reiss,E., Aidrevich,L. and Choi,J.Soo. Nucleic acids for detecting Aspergillus species and other filamentous fungi Patent: US 6372430-A 6 16-Apr-2002; Location/Qualifiers 1..319 /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Query Match	100.0%; Score 21; DB 6; Length 319;
Best Local Similarity	100.0%; Pred. No. 10;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy	1 CTACACCTCGCAACTGAGA 21 
Db	222 CTACACCTCGCAACTGAGA 242
RESULT 5	
LOCUS	BD083591 319 bp DNA linear PAT 27-AUG-2002
DEFINITION	Nucleic acids for detecting Aspergillus species and other filamentous fungi.
ACCESSION	BD083591
VERSION	BD083591.1 GI:22629201
KEYWORDS	JP 2001525665-A/6. Fusarium solani
SOURCE	



ORGANISM Fusarium solani  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 319)  
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.  
Nucleic acids for detecting *Asergillus* species and other filamentous fungi  
Patent: JP 2001525665-A 6 11-DEC-2001;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE

COMMENT OS Fusarium solani  
PN JP 2001525665-A/6  
PD 11-DEC-2001  
PF 01-MAY-1998 JP 1998548275  
PR 02-MAY-1997 US 60/045400  
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO PI CHOI  
PC C1201/68  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.

FEATURES  
source 1..319  
/organism="Fusarium solani"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:169388"  
/note="Fusarium solani"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAACACCTCGCACTGGAGA 21  
|||||  
Db 222 CTAACACCTCGCACTGGAGA 242

RESULT 6  
AF117921 319 bp DNA linear PLN 17-UN-2000  
LOCUS Nectria haematococca 5.8S ribosomal RNA gene, partial sequence;  
DEFINITION internal transcribed spacer 2, complete sequence; and 28S ribosomal  
RNA gene, partial sequence.  
AF117921  
ACCESSION AF117921  
VERSION AF117921.1 GI:8570107  
KEYWORDS  
SOURCE Fusarium solani  
ORGANISM Fusarium solani  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
REFERENCE 1 (bases 1 to 319)  
Choi,J.S., Westerman,J.M. and Morrison,C.J.  
Rapid differentiation of filamentous fungi using species-specific  
DNA probes.  
Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)  
2 (bases 1 to 319)  
Choi,J.S., Westerman,J.M. and Morrison,C.J.  
Direct Submission  
Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA  
30333, USA

FEATURES  
source 1..319  
/organism="Fusarium solani"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:169388"  
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/product="5.8S ribosomal RNA"  
160..272  
/product="internal transcribed spacer 2"

RNA  
/note="ITS2"  
273..>319  
/product="28S ribosomal RNA"

ORIGIN  
Query Match 100.0%; Score 21; DB 8; Length 319;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAACACCTCGCACTGGAGA 21  
|||||  
Db 222 CTAACACCTCGCACTGGAGA 242

RESULT 7  
AY426972 468 bp DNA linear PLN 03-NOV-2003  
LOCUS Fusarium sp. MU-2-1 internal transcribed spacer 1, partial  
DEFINITION sequence; 5.8S ribosomal RNA gene, complete sequence; and internal  
transcribed spacer 2, partial sequence.  
AY426972  
ACCESSION AY426972.1 GI:38018121  
VERSION AY426972.1  
KEYWORDS  
SOURCE Fusarium sp. MU-2-1  
ORGANISM Fusarium sp. MU-2-1  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
REFERENCE 1 (bases 1 to 468)  
Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y.  
and Zhang,Z.Q.  
Genetic analysis of pathogenic and nonpathogenic *Fusarium* sp. from  
vanilla plantation  
Unpublished  
REFERENCE 2 (bases 1 to 468)  
Wang,Y.Y., Whitehead,M., Zhu,Y.Y., Burns,A., Hocking,T., Ruan,X.Y.  
and Zhang,Z.Q.  
Direct Submission  
Submitted (02-OCT-2003) Department of Plant Pathology, Yunnan  
Agricultural University, Longtuo Street, Kunming, Yunnan 650201, P.  
R. China

FEATURES  
source 1..468  
/organism="Fusarium sp. MU-2-1"  
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<1..136  
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137..295  
/product="5.8S ribosomal RNA"  
296..>468  
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Query Match 100.0%; Score 21; DB 8; Length 468;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTAACACCTCGCACTGGAGA 21  
|||||  
Db 408 CTAACACCTCGCACTGGAGA 428

RESULT 8  
AF161222 471 bp DNA linear PLN 09-FEB-2000  
LOCUS Fusarium solani internal transcribed spacer 1, partial sequence;  
DEFINITION 5.8S ribosomal RNA gene, complete sequence; internal transcribed  
spacer 2, and 28S ribosomal RNA gene, partial sequence.  
AF161222  
ACCESSION AF161222.1 GI:6941832  
VERSION AF161222.1  
KEYWORDS

SOURCE  
ORGANISM Fusarium solani  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
AUTHORS 1 (bases 1 to 471)  
TITLE Grunden, E., Chen, W. and Crane, J. L.  
JOURNAL Fungi Colonizing Microclerotia of Verticillium dahliae  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 471)  
TITLE Grunden, E., Chen, W. and Crane, J. L.  
JOURNAL Direct Submission  
TITLE Submitted (21-JUN-1999) Center for Biodiversity, Illinois Natural  
History Survey, IL Dept. Natural Resources, 607 E. Peabody Dr.,  
Champaign, IL 61820, USA  
LOCATION/Qualifiers  
1. .471  
/organism="Fusarium solani"  
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118. .276  
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277. .450  
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451. .2471  
/product="28S ribosomal RNA"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCACTGGAGA 21  
Db 390 CTAACACCTCGCACTGGAGA 410

RESULT 9  
LOCUS AY043472/c 471 bp DNA linear PLN 14-JUN-2002  
DEFINITION Nectria haematococca strain 35 internal transcribed spacer 1, 5.8S  
ribosomal RNA gene, and internal transcribed spacer 2, complete  
sequence.  
ACCESSION AY043472  
VERSION AY043472.1 GI:15450333  
KEYWORDS  
SOURCE  
ORGANISM Fusarium solani (anamorph: Fusarium solanii)  
REFERENCE Fusarium solani  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
AUTHORS 1 (bases 1 to 471)  
TITLE Miller, R.N.G. and Lopes, C.A.  
JOURNAL rDNA sequence variability in Fusarium solani populations associated  
with eumartii wilt and dry rot of potato in Brazil  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 471)  
TITLE Miller, R.N.G. and Lopes, C.A.  
JOURNAL Submitted (03-JUN-2001) Genomic Biotechnology, Universidade  
Catolica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,  
Brazil  
LOCATION/Qualifiers  
1. .471  
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/strain="35"  
/db\_xref="taxon:169388"  
/note="anamorph: Fusarium solanii"  
complement(1. .471)  
/note="contains internal transcribed spacer 1, 5.8S  
rDNA sequence variability in Fusarium solani populations associated  
with eumartii wilt and dry rot of potato in Brazil"

FEATURES  
source  
misc\_RNA

ORIGIN ribosomal RNA, and internal transcribed spacer 2"

Query Match 100.0%; Score 21; DB 8; Length 471;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCACTGGAGA 21  
Db 59 CTAACACCTCGCACTGGAGA 39

RESULT 10  
LOCUS AY043473/c 471 bp DNA linear PLN 14-JUN-2002  
DEFINITION Nectria haematococca strain 39 internal transcribed spacer 1, 5.8S  
ribosomal RNA gene, and internal transcribed spacer 2, complete  
sequence.  
ACCESSION AY043473  
VERSION AY043473.1 GI:15450334  
KEYWORDS  
SOURCE  
ORGANISM Fusarium solani (anamorph: Fusarium solanii)  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
AUTHORS 1 (bases 1 to 471)  
TITLE Miller, R.N.G. and Lopes, C.A.  
JOURNAL rDNA sequence variability in Fusarium solani populations associated  
with eumartii wilt and dry rot of potato in Brazil  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 471)  
TITLE Miller, R.N.G. and Lopes, C.A.  
JOURNAL Submitted (03-JUN-2001) Genomic Biotechnology, Universidade  
Catolica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,  
Brazil  
LOCATION/Qualifiers  
1. .471  
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/db\_xref="taxon:169388"  
/note="anamorph: Fusarium solanii"  
complement(1. .471)  
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ribosomal RNA, and internal transcribed spacer 2"

FEATURES  
source  
misc\_RNA

with eumartii wilt and dry rot of potato in Brazil

JOURNAL  
REFERENCE 2 (bases 1 to 471)  
AUTHORS Miller, R.N.G. and Lopes, C.A.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUL-2001) Genomic Biotechnology, Universidade  
Catoica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,  
Brazil

FEATURES  
source  
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/note="contains internal transcribed spacer 1, 5.8S  
ribosomal RNA, and internal transcribed spacer 2"

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Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCACTGGAGA 21  
|||||  
Db 59 CTAACACCTCGCACTGGAGA 39

RESULT 12  
FSU38558 477 bp DNA linear **PLN 08-NOV-1995**  
LOCUS Fusarium solani 5.8S ribosomal RNA gene, complete sequence and  
DEFINITION internal transcribed spacers 1 and 2.  
ACCESSION U38558  
VERSION U38558.1 GI:1054930  
KEYWORDS  
SOURCE  
ORGANISM Fusarium solani  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
REFERENCE 1 (bases 1 to 477)  
AUTHORS Duggal, A.  
TITLE Direct Submission  
JOURNAL Submitted (13-OCT-1995) Arti Duggal, Forestry, Univ. of Toronto, 33  
Willcocks St., Toronto, Ont. M5S 3B3, Canada

FEATURES  
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Location/Qualifiers  
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/organism="Fusarium solani"  
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307..477  
/note="internal transcribed spacer 2; ITS2"

ORIGIN  
Query Match 100.0%; Score 21; DB 8; Length 477;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCACTGGAGA 21  
|||||  
Db 418 CTAACACCTCGCACTGGAGA 438

RESULT 13  
AF132801 478 bp DNA linear PLN 20-JAN-2000  
LOCUS Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal  
DEFINITION RNA, and internal transcribed spacer 2, complete sequence.

ACCESSION AF132801  
VERSION AF132801.1 GI:4803015  
KEYWORDS  
SOURCE  
ORGANISM Fusarium solani  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
REFERENCE 1 (bases 1 to 478)  
AUTHORS Harrington, T.C., Steimel, J.P., Workneh, F. and Yang, X.B.  
TITLE Molecular Identification of Fungi Associated with Vascular  
Discoloration of Soybean in the North Central United States  
JOURNAL Plant Dis. 84 (1), 83-89 (2000)  
2 (bases 1 to 478)  
Harrington, T.C., Steimel, J.P., Workneh, F. and Yang, X.B.  
TITLE Direct Submission  
JOURNAL Submitted (03-MAR-1999) Plant Pathology, Iowa State University,  
Room 351 Bessey Hall, Ames, IA 50011, USA

FEATURES  
source  
Location/Qualifiers  
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/organism="Fusarium solani"  
/mol\_type="genomic DNA"  
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/tissue\_type="mycelium"  
/country="USA; Iowa, Lee County"  
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150..306  
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307..478  
/product="internal transcribed spacer 2"  
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ORIGIN  
Query Match 100.0%; Score 21; DB 8; Length 478;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAACACCTCGCACTGGAGA 21  
|||||  
Db 419 CTAACACCTCGCACTGGAGA 439

RESULT 14  
AF150459 478 bp DNA linear PLN 05-JAN-2001  
LOCUS Nectria haematococca strain K-1 internal transcribed spacer 1, 5.8S  
DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete  
sequence.  
ACCESSION AF150459  
VERSION AF150459.1 GI:7650157  
KEYWORDS  
SOURCE  
ORGANISM Nectria haematococca  
Nectria haematococca  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
REFERENCE 1 (bases 1 to 478)  
AUTHORS Suga, H., Hasegawa, T., Mitsui, H., Kageyama, K. and Hyakumachi, M.  
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani  
based on the rDNA-ITS region  
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)  
2 (bases 1 to 478)  
Suga, H., Hyakumachi, M. and Kageyama, K.  
TITLE Direct Submission  
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu  
University, Gifu 501-1112, Japan

FEATURES  
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Location/Qualifiers  
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 308..478  
 /product="internal transcribed spacer 2"

## ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 9.6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAGA 21  
 |||||  
 Db 419 CTACACCTCGCACTGGAGA 439

## RESULT 15

AF150460 478 bp DNA linear PLN 05-JAN-2001  
 LOCUS Nectria haematococca strain FI internal transcribed spacer 1, 5.8S  
 DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete  
 sequence.

ACCESSION AF150460  
 VERSION AF150460  
 KEYWORDS AF150460.1 GI:7650158

SOURCE Nectria haematococca  
 ORGANISM Nectria haematococca  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 478)  
 Suga, H., Hasegawa, T., Mitsui, H., Kageyama, K. and Hyakumachi, M.  
 TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani  
 based on the rDNA-ITS region  
 JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)  
 AUTHORS Suga, H., Hyakumachi, M. and Kageyama, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu  
 University, Gifu 501-1112, Japan  
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## ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 9.6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAGA 21  
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 Db 419 CTACACCTCGCACTGGAGA 439

Search completed: October 1, 2004, 05:17:03  
 Job time : 172.543 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 23:11:57 ; Search time 37.2571 Seconds  
(without alignments)  
2394.501 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctaacactgcgaactggaga 21

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	2	AAV83698 Species-s
2	21	100.0	319	2	AAV70850 Internal
3	19	90.5	502	3	AA61893 Fusarium
4	19	90.5	561	2	AAV59009 F. avenac
5	19	90.5	659	6	ABV78724 C. sinens
6	17	81.0	510	3	AAV37182 Arabidops
7	17	81.0	2706	3	AAV45891 Arabidops
8	16.2	77.1	1144	5	ABV44826 Rat gene
9	16.2	77.1	33769	5	ABA82622 Human HBM
10	16.2	77.1	33769	7	ABK22781 Human hlg
11	16.2	77.1	33769	7	ACC45363 Human HBM
12	16.2	77.1	33769	9	ADB82432 Human HBM
13	16.2	77.1	33769	9	ADB82432 Human HBM
14	16.2	77.1	33769	9	ADB82432 Human HBM
15	16.2	77.1	33769	9	ADB82432 Human HBM
16	16.2	77.1	33769	9	ADB82432 Human HBM
17	16.2	77.1	33769	9	ADB82432 Human HBM
18	16.2	77.1	33769	9	ADB82432 Human HBM
19	16.2	77.1	33769	9	ADB82432 Human HBM
20	16.2	77.1	33769	9	ADB82432 Human HBM
21	16.2	77.1	33769	9	ADB82432 Human HBM
22	16.2	77.1	33769	9	ADB82432 Human HBM
23	16.2	77.1	33769	9	ADB82432 Human HBM

24	15.8	75.2	4763	4	ABL08780 Drosophill
25	15.4	73.3	989	4	ABL18503 Drosophill
26	15.4	73.3	1110	7	ACA37427 Prokaryot
27	15.4	73.3	1260	4	ABL11645 Drosophill
28	15.4	73.3	1388	9	ADDS8528 Human gen
29	15.4	73.3	1388	9	ADD47423 Human gen
30	15.4	73.3	1884	4	AAV55358 Staphyloc
31	15.4	73.3	2034	7	ABV73338 M. sexta
32	15.4	73.3	2310	4	AAV52105 Staphyloc
33	15.4	73.3	2787	7	ACF73619 Staphyloc
34	15.4	73.3	2790	4	AAV54538 Staphyloc
35	15.4	73.3	2790	4	AAV55168 Staphyloc
36	15.4	73.3	2790	4	ACA19827 Prokaryot
37	15.4	73.3	2853	4	ABL15238 Drosophill
38	15.4	73.3	3061	4	ABL18502 Drosophill
39	15.4	73.3	3433	4	ABL11644 Drosophill
40	15.4	73.3	3713	4	ABL15001 Drosophill
41	15.4	73.3	4676	4	ABL08318 Drosophill
42	15.4	73.3	6325	4	ABL06620 Drosophill
43	15.4	73.3	29555	2	AAV74517 Staphyloc
44	15.4	73.3	36181	9	ADB74371 Mycobacte
45	15.4	73.3	38494	9	ADB74275 Mycobacte

## ALIGNMENTS

RESULT 1	AAV83698 standard; DNA; 21 BP.
ID	AAV83698
XX	AAV83698;
XX	26-FEB-1999 (first entry)
DT	Species-specific probe targeted to the internal transcribed spacer 2.
DE	Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger;
XX	A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;
XX	M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
XX	M. circinellioideus f. circinellioideus; Rhizopus oryzae; R. microsporus;
XX	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
XX	Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
XX	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX	Synthetic.
OS	Fusarium solani.
OS	Fusarium solani.
FT	Key modified_base 1 location/Qualifiers
FT	/*tag= a /note= "labelled with digoxigenin"
XX	MO9850584-A2.
XX	12-NOV-1998.
XX	01-MAY-1998; 98WO-US008926.
XX	02-MAY-1997; 97US-0045400P.
XX	(USHS ) US DEPT HEALTH & HUMAN SERVICES.
XX	Morrison CJ, Reiss E, Aldorevich L, Choi JS;
XX	WPI, 1999-034737/03.
XX	New nucleic acid probes for filamentous fungi - for detecting e.g.
XX	Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
XX	Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
XX	species.
XX	Example 1; Page 22; 45pp; English.

XX Probes AAV83677-708 are derived from the internal transcribed spacer 2 (ITS2) region of various filamentous fungi (see AAV70845-73). The probes are species-specific, and can be used for identifying a species selected from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*, *M. circinellus*, *Rhizopus oryzae*, *R. microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix schenckii*. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi

XX Sequence 21 BP; 7 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 21; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.6; Mismatches 0; Gaps 0;  
Matches 21; Conservative 0; Indels 0; Gaps 0;

Db 1 CTAACACCTCGCAACTGAGG 21  
1 CTAACACCTCGCAACTGAGG 21

RESULT 2  
ID AAV70850 standard; DNA; 319 BP.  
XX AAV70850;  
XX 26-FEB-1999 (first entry)

XX Internal transcribed spacer 2 (ITS2) and adjacent regions.

XX Internal transcribed spacer 2; ITS2; probe: *Aspergillus flavus*; *A. niger*; *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*; *Mucor rouxii*; *M. racemosus*; *M. plumbeus*; *M. indicus*; *A. fumigatus*; *M. circinelloides* f. *circinelloides*; *Rhizopus oryzae*; *R. microsporus*; *R. circinans*; *R. stolonifer*; *Rhizomucor pusillus*; *Abidia corymbifera*; *Cunninghamella elegans*; *Pseudallescheria boydii*; *Scedosporium apiospermum*; *Penicillium notatum*; *Sporothrix schenckii*; filamentous fungus; ss.

XX *Fusarium solani*.  
XX WO9850584-A2.  
XX 12-NOV-1998.  
XX 01-MAY-1998; 98WO-US008926.  
XX 02-MAY-1997; 97US-0045400P.  
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX Morrison CJ, Reiss E, Aidorevich L, Choi JS;  
XX MPI; 1999-034737/03.  
XX New nucleic acid probes for filamentous fungi - for detecting e.g. *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Abidia*, *Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix* species.  
XX Claim 1; Page 12; 45pp; English.

XX The present sequence represents an internal transcribed spacer 2 (ITS2) and adjacent regions. Probes can be derived from the present sequence which are species-specific. The specification also describes ITS2 sequence-derived probes for identifying a species selected from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*, *M. circinelloides* f. *circinelloides*, *Rhizopus oryzae*, *R. microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia*

CC *corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix schenckii*. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi

XX Sequence 319 BP; 77 A; 96 C; 84 G; 62 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 21; DB 2; Length 319;  
Best Local Similarity 100.0%; Pred. No. 0.777; Mismatches 0; Gaps 0;  
Matches 21; Conservative 0; Indels 0; Gaps 0;

Db 1 CTAACACCTCGCAACTGAGG 21  
222 CTAACACCTCGCAACTGAGG 242

RESULT 3  
ID AAA61893 standard; DNA; 502 BP.  
XX AAA61893;  
XX 15-SEP-2003 (revised)  
XX 14-NOV-2000 (first entry)

XX *Fusarium* sp. MF6381 rDNA internal transcribed spacer (ITS) region.  
XX Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469; HIV integrase inhibitor; steroid compound; human immunodeficiency virus; acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex; symptomatic infection; asymptomatic infection; potential HIV exposure; combination therapy; ds.

XX *Fusarium* sp. MF6381.  
XX WO200036132-A1.  
XX 22-JUN-2000.  
XX 09-DEC-1999; 99WO-US029356.  
XX 14-DEC-1998; 98US-0112168P.  
XX (MERI) MERCK & CO INC.  
XX Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;  
XX Dombrowski AW;  
XX MPI; 2000-431606/37.  
XX New steroid compounds are HIV integrase inhibitors used for treating HIV infection and AIDS.  
XX Disclosure; Page 14; 113pp; English.

XX The invention relates to novel steroid compounds derived from the African soil fungus *Fusarium* sp. MF6381 (ATCC 74469) which act as inhibitors of HIV integrase. The invention encompasses cultures of *Fusarium* sp. MF6381. The invention also relates to a composition comprising a compound of the invention in combination with an AIDS antiviral agent, an immunomodulator and an anti-infective agent. The compounds of the invention may be used in the inhibition of HIV integrase and in the prevention and treatment of HIV infection. A wide range of state of HIV infection may be treated: AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex); both symptomatic and asymptomatic HIV infection; and actual or potential exposure to HIV. The compounds may be used to isolate HIV integrase mutants which are potentially useful as screening tools for antiviral compounds. The compounds may also be used to establish or determine the site at which other antivirals bind to HIV integrase (e.g., by competitive inhibition). The present sequence represents the ribosomal DNA (rDNA) internal transcribed spacer (ITS) region of *Fusarium* sp. MF6381, which may be used to characterize MF6381. (Updated on 15-SEP-2003 to standardise OS field)

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XX SQ Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 U; 0 Other;
Query Match 90.5%; Score 19; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAACACCTCGCAACTGGA 19
Db 410 CTAACACCTCGCAACTGGA 428

RESULT 4
AAV59009
ID AAV59009 standard; DNA; 561 BP.
XX
AC AAV59009;
XX
AC 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE F. avenaceum internal transcribed spacer.
XX
KW Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
KW fungal pathogen identification; infection identification; ss.
XX
OS Gibberella avenacea.
XX
XX
XX Key Location/Qualifiers
FH misc_feature 31..181
FT /*tag= a
FT /note= "ITS1"
FT misc_feature 339..504
FT /*tag= b
FT /note= "ITS2"
XX
XX US5827695-A.
XX
XX 27-OCT-1998.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JI;
XX
XX WPI; 1998-593995/50.
XX
XX Wheat pathogen internal transcribed spacer sequences - used as a basis
XX for primers for the species-specific polymerase chain reaction detection
XX of the pathogens.
XX
XX Claim 1; Col 29-30; 20pp; English.
XX
XX This sequence represents an internal transcribed spacer (ITS) sequence of
XX the invention. The primer pairs, based on the ITS sequences, are used for
XX the PCR amplification detection of wheat Microdochium and Fusarium fungal
XX pathogens, especially M. nivale, F. graminearum, F. culmorum, F.
XX avenaceum, F. poae, F. moniliforme or F. roseum. The two different
XX strains of fungi show different symptoms during infection, which may or
XX may not be due to infection. Early identification of the strain causing
XX the infection allows early, and more specific fungicidal treatment.
XX (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
XX correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 561 BP; 145 A; 152 C; 135 G; 126 T; 0 U; 3 Other;
Query Match 90.5%; Score 19; DB 2; Length 561;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 CTAACACCTCGCAACTGGA 19
Db 445 CTAACACCTCGCAACTGGA 463

RESULT 5
ABV78724
ID ABV78724 standard; rRNA; 659 BP.
XX
AC ABV78724;
XX
XX 14-JAN-2003 (first entry)
DT
XX
DE C. sinensis rRNA sequence #23.
XX
XX Ribosome ribonucleic acid; rRNA; Cordyceps crassispora; classification;
KW Cordyceps sinensis; ss.
XX
OS Cordyceps sinensis.
XX
XX JP2002204696-A.
XX
XX 23-JUL-2002.
PD
XX
PF 12-JAN-2001; 2001JP-00004805.
XX
PR 12-JAN-2001; 2001JP-00004805.
XX
XX (HEAL-) HEALTHWAY KK.
XX (KANE/) KANESHIRO N.
PA
XX WPI; 2002-639075/69.
XX
XX Ribosome RNA gene base sequence of Cordyceps sinensis for classification
XX of seeds of Cordyceps sinensis.
XX
XX 26; Page 25; 33pp; Japanese.
XX
XX The invention relates to a novel base sequence which is part of a fully
XX defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassispora.
XX The base sequences can be used for the classification of Cordyceps
XX sinensis. The sequence represents a C. sinensis rRNA sequence of the
XX invention
XX
XX SQ Sequence 659 BP; 183 A; 173 C; 160 G; 143 T; 0 U; 0 Other;
Query Match 90.5%; Score 19; DB 6; Length 659;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAACACCTCGCAACTGGA 19
Db 473 CTAACACCTCGCAACTGGA 491

RESULT 6
AAC37182
ID AAC37182 standard; DNA; 510 BP.
XX
AC AAC37182;
XX
XX 17-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 16470.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX EPI033405-A2.
PN

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XX	06-SEP-2000.	
PD		
XX	25-FEB-2000;	2000EP-00301439.
PR		
XX	25-FEB-1999;	99US-0121825P.
PR	05-MAR-1999;	99US-0123180P.
PR	09-MAR-1999;	99US-0123548P.
PR	23-MAR-1999;	99US-0125768P.
PR	25-MAR-1999;	99US-0126264P.
PR	29-MAR-1999;	99US-0126785P.
PR	01-APR-1999;	99US-0127462P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
PR	19-APR-1999;	99US-0130077P.
PR	21-APR-1999;	99US-0130449P.
PR	23-APR-1999;	99US-0130510P.
PR	28-APR-1999;	99US-0130891P.
PR	30-APR-1999;	99US-0132048P.
PR	04-MAY-1999;	99US-0132407P.
PR	05-MAY-1999;	99US-0132484P.
PR	06-MAY-1999;	99US-0132485P.
PR	07-MAY-1999;	99US-0132487P.
PR	11-MAY-1999;	99US-0134256P.
PR	14-MAY-1999;	99US-0134218P.
PR	14-MAY-1999;	99US-0134219P.
PR	14-MAY-1999;	99US-0134221P.
PR	18-MAY-1999;	99US-0134370P.
PR	19-MAY-1999;	99US-0134941P.
PR	20-MAY-1999;	99US-0135124P.
PR	21-MAY-1999;	99US-0135353P.
PR	24-MAY-1999;	99US-0135629P.
PR	25-MAY-1999;	99US-0136021P.
PR	27-MAY-1999;	99US-0136392P.
PR	28-MAY-1999;	99US-0136782P.
PR	01-JUN-1999;	99US-0137222P.
PR	03-JUN-1999;	99US-0137528P.
PR	04-JUN-1999;	99US-0137502P.
PR	07-JUN-1999;	99US-0137724P.
PR	08-JUN-1999;	99US-0138094P.
PR	10-JUN-1999;	99US-0138540P.
PR	14-JUN-1999;	99US-0138847P.
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PR	18-JUN-1999;	99US-0139750P.
PR	18-JUN-1999;	99US-0139763P.
PR	21-JUN-1999;	99US-0139817P.
PR	22-JUN-1999;	99US-0139899P.
PR	23-JUN-1999;	99US-0140353P.
PR	23-JUN-1999;	99US-0140354P.
PR	24-JUN-1999;	99US-0140695P.
PR	28-JUN-1999;	99US-0140823P.
PR	29-JUN-1999;	99US-0140991P.
PR	30-JUN-1999;	99US-0141287P.
PR	01-JUL-1999;	99US-0141842P.
PR	01-JUL-1999;	99US-0142354P.
PR		
PR	02-JUL-1999;	99US-0142055P.
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PR	23-JUL-1999;	99US-0145192P.
PR	23-JUL-1999;	99US-0145145P.
PR	23-JUL-1999;	99US-0145181P.
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PR	23-AUG-1999;	99US-0149930P.
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PR	26-AUG-1999;	99US-0150884P.
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PR	27-AUG-1999;	99US-0151080P.
PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
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PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
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PR	20-SEP-1999;	99US-0154779P.



PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
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PR 06-OCT-1999; 99US-0157865P.  
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PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 81.0%; Score 17; DB 3; Length 510;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CACCTCGCACTGGAGA 21  
Db 37 CACCTCGCACTGGAGA 53

RESULT 7

ID AAC45891 standard; DNA; 2706 BP.

XX AAC45891;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 48143.

KW Hybridization assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-012180P.

PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126284P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 28-APR-1999; 99US-0130891P.  
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PR 04-MAY-1999; 99US-0132407P.  
PR 05-MAY-1999; 99US-0132484P.  
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PR 14-MAY-1999; 99US-0134256P.  
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PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
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PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137228P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
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PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
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PR 18-JUN-1999; 99US-0139459P.  
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PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139753P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 23-JUN-1999; 99US-0140355P.  
PR 24-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140605P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142380P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.

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PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144008P.
PR 16-JUL-1999; 99US-0144008P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145066P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-014512P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147182P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.

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PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

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Query Match      81.0%; Score 17; DB 3; Length 2706;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 CACCTGCACTGGAGA 21
Db 20 CACCTGCACTGGAGA 36

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RESULT 8
ADD44826
ID ADD44826 standard; DNA; 1144 Bp.
XX AC ADD44826;
XX DT 29-JAN-2004 (first entry)
XX DE Rat gene Y00311, SEQ ID NO 10257.
XX KW Rat; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN W02003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GENO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX

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DR WPI: 2003-268312/26.  
 DR GENBANK; Y00311.  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page: 1017pp; English.  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNR)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat DNA (shown in Table 2 of the  
 CC specification) which encodes one of the polypeptides of the invention  
 CC which is differentially expressed during pain. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 SQ Sequence 1144 BP; 310 A; 256 C; 291 G; 287 T; 0 U; 0 Other;  
 Query Match 77.1%; Score 16.2; DB 9; Length 1144;  
 Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTACACCTCGCACTGAGAGA 21  
 Db 33 CTACACCTCGCACTGAGAGA 53

RESULT 9  
 ID ABA82622 standard; DNA; 33769 BP.  
 AC ABA82622;  
 DT 25-JAN-2002 (first entry)  
 XX  
 DE Human HBM gene region b527d12-h\_contig308G.  
 XX  
 KW Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;  
 KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;  
 KW antisense therapy; vaccine; bone disorder; Paget's disease; sclerostosis;  
 KW osteomalacia; fibrous dysplasia; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO20017737-A1.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 21-JUN-2000; 2000WO-US016951.  
 XX  
 PR 05-APR-2000; 2000US-00543771.  
 PR 05-APR-2000; 2000US-00544398.

XX  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 XX  
 PI Carulli JP, Little RD, Recker RR, Johnson ML;  
 XX  
 DR WPI: 2001-657171/75.  
 XX  
 PT New high bone mass (HBM) and Zmax1 gene and proteins useful for  
 PT modulating bone mass for the treatment of e.g. osteoporosis.  
 XX  
 PS Claim 51; Page 237-257; 443pp; English.  
 CC The present invention describes the human Zmax1 gene and the high bone  
 CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM  
 CC genes have osteopathic activities. The genes can be used in gene therapy,  
 CC antisense therapy and in the production of vaccines. They can be used in  
 CC the diagnosis and treatment of bone disorders including osteoporosis,  
 CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.  
 CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in  
 CC the exemplification of the present invention  
 CC  
 SQ Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 0 U; 3 Other;  
 Query Match 77.1%; Score 16.2; DB 5; Length 33769;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTACACCTCGCACTGAGAGA 21  
 Db 25831 CTACACCTCGCACTGAGAGA 25851

RESULT 10  
 ID ABR22781 standard; CDNA; 33769 BP.  
 AC ABR22781;  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human high bone mass (HBM) polynucleotide clone #4.  
 XX  
 KW Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;  
 KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;  
 KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;  
 KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;  
 KW bone development disorder; antiarteriosclerotic; cardiovascular;  
 KW osteopathic; cerebroprotective.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200192891-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US016946.  
 XX  
 PR 26-MAY-2000; 2000US-00578900.  
 XX  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.  
 XX  
 PI Carulli JP, Little RD, Recker RR, Johnson ML;  
 XX  
 DR WPI: 2002-097784/13.  
 XX  
 PT Identifying molecules involved in lipid regulation, useful for  
 PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises  
 PT identifying a molecule that binds to high bone mass gene or its  
 PT corresponding wild type gene.  
 XX  
 PS Example 2; Page 259-283; 409pp; English.

CC The invention relates to a method for identifying a molecule involved in  
CC lipid regulation comprising identifying a molecule that binds to or  
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type  
CC gene, Zmax1. Compounds identified by the method are useful for treating,  
CC diagnosing, preventing or screening for normal and abnormal lipid-  
CC associated conditions, including arteriosclerosis, cardiovascular  
CC disease, stroke, and osteoporosis. The compounds may also be used in the  
CC treatment or prevention of diabetic atherosclerosis, neurovascular  
CC conditions caused by plaque build-up, poor circulation due to plaque  
CC build-up and associated poor wound healing. The methods may be used in  
CC gene therapy, pharmaceutical development, and diagnostic assays for bone  
CC development disorders. Molecules identified by comparison of Zmax1 and  
CC HBM systems can be used as surrogate markers in pharmaceutical  
CC development in diagnosis of human or animal bone disease, and in the  
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA  
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers  
CC and adapters of the invention  
XX

SQ Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 0 U; 3 Other;

Query Match 77.1%; Score 16.2; DB 6; Length 33769;

Best Local Similarity 85.7%; Pred. No. 3.4e+02; Mismatches 0; Gaps 0;

Matches 18; Conservative 0; Indels 0; Gaps 0;

OY 1 CTACACCTCGCACTGAGA 21

DB 25831 CTAGCACCCTCTCACTGACA 25851

RESULT 11  
ACCA5363

ID ACCA5363 standard; DNA; 33769 BP.

AC ACC45363;

02-JUN-2003 (first entry)

DE Human HBM gene fragment #4.

XX Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;  
XX gene therapy; bone density modulation; bone strength; trabecular number;  
XX bone size; bone tissue connectivity; bone disease; osteoporosis;  
XX osteomalacia; rickets; Paget's disease; neoplasm of the bone; gene; ds.

OS Homo sapiens.

XX

PN WO200292764-A2.

21-NOV-2002.

PF 13-MAY-2002; 2002WO-US014876.

PR 11-MAY-2001; 2001US-0290071P.

PR 17-MAY-2001; 2001US-0291311P.

PR 01-FEB-2002; 2002US-0353058P.

PR 04-MAR-2002; 2002US-0361293P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PA (AMHP) WYETH.

PI Babi J P, Bex FJ, Yaworsky PJ, Bodine PV;

XX WPI; 2003-129278/12.

XX New transgenic animals (e.g. mice), useful as models for studying bone  
XX density modulation, developing drugs for treating or preventing bone  
XX diseases (e.g. osteoporosis), or diagnosing diseases characterized by  
XX reduced bone density.

PS Example 2; Page 323-334; 603pp; English.

XX The invention relates to novel transgenic animals expressing the high  
XX bone mass (HBM) gene, expressing the corresponding wild type HBM gene,

CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing  
CC an LRP5 that is modulated by an altered gene control sequence introduced  
CC by homologous or non-homologous recombination. The transgenic animals are  
CC for the study of bone density modulation or bone mass modulation. The  
CC invention has osteopathic and cytostatic activity. The polynucleotides of  
CC the invention may have a use in gene therapy. The transgenic animals and  
CC nucleic acids are for the study of bone density modulation, where the  
CC bone mass is modulated relative to non-transgenic animals of the same  
CC species in more than one parameter selected from bone density, bone  
CC strength, trabecular number, bone size, or bone tissue connectivity. The  
CC transgenic animals, nucleic acids and methods are useful for identifying  
CC molecules involved in bone development, and for developing pharmaceutical  
CC compositions, which may be employed for treating or preventing bone  
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or  
CC neoplasms of the bone. The transgenic animals and nucleic acids are also  
CC useful in methods for diagnosing diseases involved in bone development,  
CC or characterised by reduced bone density or mass. The present sequence is  
CC used in the exemplification of the invention  
XX

SQ Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 0 U; 3 Other;

Query Match 77.1%; Score 16.2; DB 7; Length 33769;

Best Local Similarity 85.7%; Pred. No. 3.4e+02; Mismatches 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTACACCTCGCACTGAGA 21

DB 25831 CTAGCACCCTCTCACTGACA 25851

RESULT 12  
ADB98063

ID ADB98063 standard; DNA; 33769 BP.

AC ADB98063;

04-DEC-2003 (first entry)

DE HBM-related clone contig b527d12-h contig308G.

XX Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;  
XX bone mass modulation; osteoporosis; human; ds.

OS Homo sapiens.

XX

PN WO200292000-A2.

21-NOV-2002.

PF 13-MAY-2002; 2002WO-US014877.

PR 11-MAY-2001; 2001US-0290071P.

PR 17-MAY-2001; 2001US-0291311P.

PR 01-FEB-2002; 2002US-0353058P.

PR 04-MAR-2002; 2002US-0361293P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PA (AMHP) WYETH.

PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;

XX WPI; 2003-129214/12.

XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for  
XX diagnosing a HBM-like phenotype in a subject and for preparing a  
XX composition for modulating bone mass and/or lipid levels in a subject  
XX suffering from e.g. osteoporosis.

PS Example 3; SEQ ID NO 8; 629pp; English.

XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and  
XX LRP6 mutants, which results in a HBM-like phenotype when expressed in a  
XX cell. The HBM-like phenotype results in bone mass modulation and/or lipid

CC level modulation. The invention is useful for diagnosing a HBM-like  
CC phenotype in a subject and for preparing a composition for modulating  
CC bone mass and/or lipid levels in a subject suffering from e.g.  
CC osteoporosis. The present sequence was used to illustrate the invention.

XX Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 0 U; 3 Other;

Query Match 77.1%; Score 16.2; DB 9; Length 33769;

Best Local Similarity 85.7%; Pred. No. 3.4e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTAACACCTCGCACTGAGAGA 21

DB 25831 CTAGCACCCTCTCACTGAGACA 25851

#### RESULT 13

ID ADE82432 standard; DNA; 33769 BP.

XX AC ADE82432;

XX DT 29-JAN-2004 (first entry)

XX DE Human DNA sequence related to the invention #4.

XX KW LRP5; LRP6; HBM; Dkk activity; Osteopathic; Antiinflammatory;

XX KW Antiarthritic; bone mass disorders; osteoporosis; hypercalcaemia;

XX KW hyperostosis; osteogenesis; Wnt signaling; ds.

XX OS Homo sapiens.

XX PN WO200292015-A2.

XX PF 17-MAY-2002; 2002WO-US015982.

XX PR 17-MAY-2001; 2001US-0291311P.

XX PR 01-FEB-2002; 2002US-0353058P.

XX PR 04-MAR-2002; 2002US-0361293P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PA (AMHP) WYETH.

XX PI Allen K, Anisowicz A, Bhat BM, Damagnez V, Robinson JA;

XX PI Yaworsky PJ;

XX DR WPI; 2003-129219/12.

XX PT Regulating LRP5, LRP6 or HBM activity in a subject, useful for modulating

XX PT lipid levels and/or bone mass, and for in treating bone mass disorders,

XX PT e.g. osteoporosis, comprises administering a composition which modulates

XX PT a Dkk activity.

XX PS Disclosure; SEQ ID NO 8; 173pp; English.

XX CC The present invention relates to regulating LRP5, LRP6 or HBM activity in

XX CC a subject comprising administering a composition which modulates a Dkk

XX CC activity. The method is useful for modulating lipid levels and/or bone

XX CC mass, and is useful in treating or diagnosing abnormal lipid levels and

XX CC bone mass disorders, such as osteoporosis, bone fracture, age-related

XX CC turnover, hypercalcaemia, hyperostosis, osteogenesis, imperforata,

XX CC osteomalacia, osteomyelitis, Paget's disease, osteoarthritis, and

XX CC rickets. Modulators of Dkk activity are useful for as reagents in

XX CC studying bone mass and lipid level modulation, in modulating Wnt

XX CC signaling, or treating Dkk-mediated disorders. The present sequence

XX CC represents a human DNA sequence related to the invention.

XX SQ Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 0 U; 3 Other;

Query Match 77.1%; Score 16.2; DB 9; Length 33769;

Best Local Similarity 85.7%; Pred. No. 3.4e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTAACACCTCGCACTGAGAGA 21

DB 25831 CTAGCACCCTCTCACTGAGACA 25851

#### RESULT 14

ID ABQ45159 standard; DNA; 1118 BP.

XX AC ABQ45159;

XX DT 12-JUL-2002 (first entry)

XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 31750.

XX KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

XX KW drug; side effect; cancer; central nervous system; cardiovascular;

XX KW gastrointestinal; respiratory system; single nucleotide polymorphism;

XX KW SNP; cell differentiation; ds.

XX OS Homo sapiens.

XX PN WO200218632-A2.

XX PF 07-MAR-2002.

XX PR 01-SEP-2001; 2001WO-EP010074.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PR 05-SEP-2000; 2000DE-01044543.

XX PA (EPIC-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX DR WPI; 2002-371829/40.

XX PT Determining the degree of cytosine methylation in genomic DNA, useful for

XX PT diagnosis and prognosis, comprises selective hybridization of amplicons

XX PT from chemically treated DNA.

XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX CC This invention describes a novel method for determining the degree of

XX CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a

XX CC genomic sample of DNA. The sample is treated chemically to convert

XX CC cytosine (C) but not methylated C, to uracil, then part of the genomic

XX CC DNA that contains the target C is amplified to form a labeled amplicon.

XX CC The amplicon is hybridised to two classes, each with at least one member,

XX CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the

XX CC degree of hybridisation to both classes is determined from the label on

XX CC the amplicon. From the ratio of labels hybridised to the two classes of

XX CC oligomers, the degree of methylation is calculated. The method is used:

XX CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs

XX CC and of a wide range of diseases, e.g. cancer, disorders of the central

XX CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,

XX CC particularly by detecting mutations or single nucleotide polymorphisms

XX CC (SNP's), and (ii) for differentiation of cell or tissue types and for

XX CC investigating cell differentiation. The method allows the methylation

XX CC status of many C residues to be determined simultaneously. ABQ13410-

XX CC ABQ54121 represent genomic DNA sequences used to illustrate the method

XX CC for determining the degree of cytosine methylation described in the

XX CC disclosure of the invention

XX SQ Sequence 1118 BP; 389 A; 464 C; 144 G; 121 T; 0 U; 0 Other;

Query Match 76.2%; Score 16; DB 6; Length 1118;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTAACACCTCGCAACT 16  
 |||||  
 DB 396 CTAACACCTCGCAACT 411

Search completed: October 1, 2004, 03:41:21  
 Job time : 42.2571 secs

RESULT 15  
 ABQ45158/c  
 ID ABQ45158 standard; DNA; 1118 BP.  
 XX  
 AC ABQ45158;  
 XX

DT 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 31749.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; ds.  
 XX

OS Homo sapiens.

PN WO200218632-A2.

PD 07-MAR-2002.

PF 01-SEP-2001; 2001WO-EP010074.

PR 01-SEP-2000; 2000DE-01043826.

PR 05-SEP-2000; 2000DE-01044543.

XX (EPIC-) EPICENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful for  
 PT diagnosis and prognosis, comprises selective hybridization of amplicons  
 PT from chemically treated DNA.

PS Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one member,  
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 CC degree of hybridisation to both classes is determined from the label on  
 CC the amplicon. From the ratio of labels hybridised to the two classes of  
 CC oligomers, the degree of methylation is calculated. The method is used:  
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 CC particularly by detecting mutations or single nucleotide polymorphisms  
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
 CC investigating cell differentiation. The method allows the methylation  
 CC status of many C residues to be determined simultaneously. ABQ13410-  
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the  
 CC disclosure of the invention

CC Sequence 1118 BP; 121 A; 144 C; 464 G; 389 T; 0 U; 0 Other;

CC Query Match 76.2%; Score 16; DB 6; Length 1118;

CC Best Local Similarity 100.0%; Pred. No. 3.1e+02;

OY 1 CTAACACCTCGCAACT 16  
 |||||  
 DB 723 CTAACACCTCGCAACT 708

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:09:43 / Search time 6.92045 Seconds  
(without alignments)  
1683.989 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctaccactctgcacactgagaga 21

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTCUTS.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	US-09-423-233-51	Sequence 51, Appl
2	21	100.0	319	US-09-423-233-6	Sequence 6, Appl
3	19	90.5	561	US-08-905-314A-24	Sequence 24, Appl
4	15.4	73.3	29555	US-08-956-171E-206	Sequence 206, App
5	15.4	73.3	36181	US-08-311-731A-120	Sequence 120, App
6	15.4	73.3	38494	US-08-311-731A-24	Sequence 134, Appl
7	15.4	73.3	38675	US-08-311-731A-135	Sequence 135, App
8	15.2	72.4	1173	US-09-398-858-13	Sequence 13, Appl
9	14.8	70.5	927	US-09-252-991A-6522	Sequence 6522, Ap
10	14.8	70.5	41171	US-08-311-731A-122	Sequence 122, App
11	14.8	70.5	1230025	US-09-198-452A-1	Sequence 1, Appl
12	14.8	70.5	4403765	US-09-103-840A-2	Sequence 2, Appl
13	14.8	70.5	4411529	US-09-103-840A-1	Sequence 1, Appl
14	14.6	69.5	357	US-09-489-039A-5642	Sequence 5642, App
15	14.6	69.5	517	US-09-276-031-122	Sequence 122, App
16	14.6	69.5	525	US-09-621-976-2520	Sequence 2520, App
17	14.6	69.5	535	US-09-833-381-881	Sequence 881, App
18	14.6	69.5	804	US-09-833-381-1461	Sequence 1461, App
19	14.6	69.5	1661	US-09-149-476-246	Sequence 246, App
20	14.6	69.5	1766	PCT-US93-00601-1	Sequence 1, Appl
21	14.6	69.5	1766	PCT-US94-07107A-1	Sequence 1, Appl
22	14.6	69.5	1767	US-08-083-945C-1	Sequence 1, Appl
23	14.6	69.5	1784	US-08-554-612C-13	Sequence 13, Appl
24	14.6	69.5	2201	US-09-149-476-245	Sequence 245, App
25	14.6	69.5	2264	US-09-833-381-883	Sequence 883, App
26	14.6	69.5	2337	US-09-489-039A-1284	Sequence 1284, App
27	14.6	69.5	2636	US-08-554-612C-12	Sequence 12, Appl

C 28	14.6	69.5	2898	1	US-08-554-612C-51	Sequence 51, Appl
C 29	14.6	69.5	2909	1	US-08-554-612C-10	Sequence 10, Appl
C 30	14.6	69.5	2909	1	US-08-554-612C-11	Sequence 11, Appl
C 31	14.6	69.5	5613	4	US-09-562-702A-13	Sequence 13, Appl
C 32	14.6	69.5	5613	4	US-09-561-818A-13	Sequence 13, Appl
C 33	14.6	69.5	5613	4	US-09-561-709B-10	Sequence 10, Appl
C 34	14.6	69.5	5843	4	US-08-554-612C-2	Sequence 2, Appl
C 35	14.4	68.6	7796	4	US-09-521-511C-12	Sequence 12, Appl
C 36	14.2	67.6	20	4	US-09-198-452A-4305	Sequence 4305, App
C 37	14.2	67.6	402	4	US-09-252-991A-6809	Sequence 6809, App
C 38	14.2	67.6	519	4	US-09-252-991A-8273	Sequence 8273, App
C 39	14.2	67.6	644	3	US-09-386-493-9	Sequence 9, Appl
C 40	14.2	67.6	654	4	US-09-543-681A-2368	Sequence 2368, App
C 41	14.2	67.6	738	4	US-09-252-991A-13238	Sequence 13238, A
C 42	14.2	67.6	837	4	US-09-252-991A-5983	Sequence 5983, App
C 43	14.2	67.6	1001	4	US-09-671-317-284	Sequence 284, App
C 44	14.2	67.6	1095	3	US-08-928-383B-3	Sequence 3, Appl
C 45	14.2	67.6	1104	4	US-09-252-991A-6759	Sequence 6759, App

## ALIGNMENTS

RESULT 1  
US-09-423-233-51  
Sequence 51, Application US/09423233  
Patent No. 6372430  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America as  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
FILE REFERENCE: 03063-0341WP  
CURRENT APPLICATION NUMBER: US/09/423,233  
CURRENT FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 51  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Fusarium solani  
US-09-423-233-51  
Query Match 100.0%; Score 21; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.042;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CTAACCTCGCACTGAGA 21  
Db 1 CTAACCTCGCACTGAGA 21  
RESULT 2  
US-09-423-233-6  
Sequence 6, Application US/09423233  
Patent No. 6372430  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America as  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
FILE REFERENCE: 03063-0341WP  
CURRENT APPLICATION NUMBER: US/09/423,233  
CURRENT FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 319  
TYPE: DNA  
ORGANISM: Fusarium solani  
US-09-423-233-6  
Query Match 100.0%; Score 21; DB 4; Length 319;  
Best Local Similarity 100.0%; Pred. No. 0.062;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGAGA 21  
Db 222 CTACACCTCGCACTGAGA 242

## RESULT 3

US-08-905-314A-24  
; Sequence 24, Application US/08905314A  
; Patent No. 5827695  
; GENERAL INFORMATION:  
; APPLICANT: Beck, James J.  
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: No. 5827695artis Corporation Patent Department  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 20779-2257  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/905,314A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC 1944  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8587  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 561 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE: DNA  
; STRAIN: Fusarium avenaceum  
; INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..30  
; OTHER INFORMATION: /note= "3' end of small subunit  
; OTHER INFORMATION: rRNA gene"  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 31..181  
; OTHER INFORMATION: /note= "ITS 1"  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 182..338  
; OTHER INFORMATION: /note= "5.8S rRNA gene"  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 339..504  
; OTHER INFORMATION: /note= "ITS 2"  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 505..561  
; OTHER INFORMATION: /note= "5' end of large subunit  
; OTHER INFORMATION: rRNA gene"  
US-08-905-314A-24

Query Match 90.5%; Score 19; DB 1; Length 561;

Best Local Similarity 100.0%; Pred. No. 0.76;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGA 19  
Db 445 CTACACCTCGCACTGGA 463

## RESULT 4

US-08-956-171E-206/c  
; Sequence 206, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; Gil H. Choi  
; Patrick S. Dillon  
; Craig A. Rosen  
; Steven C. Barash  
; Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,171E  
; FILING DATE: 20-Oct-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB248P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 206:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29555 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:  
US-08-956-171E-206

Query Match 73.3%; Score 15.4; DB 4; Length 29555;  
Best Local Similarity 94.1%; Pred. No. 1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAACACCTCGCACTGG 18  
Db 1809 TAACACCTCGCACTGG 1793

## RESULT 5

US-08-311-731A-120/c  
; Sequence 120, Application US/08311731A  
; Patent No. 6583266  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, DOUGLAS



APPLICANT: MAO, JEN-I  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36181 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MYCOBACTERIUM LEPRAE  
US-08-311-731A-120

Query Match 73.3%; Score 15.4; DB 4; Length 36181;  
Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AACACCTGCAACTGGA 19  
|||||  
Db 28405 AACACCGCGCAACTGGA 28389

RESULT 6  
US-08-311-731A-24/c  
Sequence 24, Application US/08311731A  
Patent No. 6583266  
GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
APPLICANT: MAO, JEN-I  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38494 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MYCOBACTERIUM LEPRAE  
US-08-311-731A-24

Query Match 73.3%; Score 15.4; DB 4; Length 38494;  
Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CACCTGCAACTGGAGA 21  
|||||  
Db 23279 CACCTGCAACTGGAGA 23263

RESULT 7  
US-08-311-731A-135/c  
Sequence 135, Application US/08311731A  
Patent No. 6583266  
GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
APPLICANT: MAO, JEN-I  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38675 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mycobacterium leprae  
US-08-311-731A-135

Query Match 73.3%; Score 15.4; DB 4; Length 38675;  
Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CACCTCGCACTGGAGA 21  
|||||  
Db 3801 CACCTCGCACTGGCGA 3785

RESULT 8  
US-09-398-858-13  
Sequence 13, Application US/09398858  
Patent No. 6518487  
GENERAL INFORMATION:  
APPLICANT: Lowe, Keith S.  
APPLICANT: Tao, Yumai  
APPLICANT: Gordon-Kamm, William J.  
APPLICANT: Gregory, Carolyn A.  
APPLICANT: McElver, John A.  
APPLICANT: Hoelter, George J.  
TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides  
FILE REFERENCE: 0926  
CURRENT APPLICATION NUMBER: US/09/398,858  
CURRENT FILING DATE: 1999-09-20  
PRIOR APPLICATION NUMBER: 60/101,551  
PRIOR FILING DATE: 1998-09-23  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 13  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1173)  
US-09-398-858-13

Query Match 72.4%; Score 15.2; DB 4; Length 1173;  
Best Local Similarity 85.0%; Pred. No. 84;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTAACACTCGCACTGGAG 20  
|||||  
Db 550 CTAACACTCGCACTGGAG 569

RESULT 9  
US-09-252-991A-6522  
Sequence 6522, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 3142  
SEQ ID NO 6522  
LENGTH: 927  
TYPE: DNA

ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6522

Query Match 70.5%; Score 14.8; DB 4; Length 927;  
Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AACACTCGCACTGGAGA 21  
|||||  
Db 875 AACACTCGCACTGGAGA 892

RESULT 10  
US-08-311-731A-122  
Sequence 122, Application US/08311731A  
Patent No. 6583266  
GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
APPLICANT: MAO, JEN-I  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 122:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41171 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MYCOBACTERIUM LEPRAE  
US-08-311-731A-122

Query Match 70.5%; Score 14.8; DB 4; Length 41171;  
Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACACTCGCACTGGAG 20  
|||||  
Db 30961 AACACTCGCACTGGAG 30978

RESULT 11  
US-09-198-452A-1  
Sequence 1, Application US/09198452A  
Patent No. 6559294  
GENERAL INFORMATION:

APPLICANT: Grifais, R.  
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
FILE REFERENCE: 9710-003-999  
CURRENT APPLICATION NUMBER: US/09/198,452A  
CURRENT FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6849  
SEQ ID NO 1  
LENGTH: 1230025  
TYPE: DNA  
ORGANISM: Chlamydia pneumoniae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1) .. (15000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
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OTHER INFORMATION: n=a or c or g or t  
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NAME/KEY: misc feature  
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NAME/KEY: misc feature





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:20:11 ; Search time 85.5213 Seconds  
(without alignments)  
1244.847 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctacacactcgcaactgagaga 21

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
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- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10C\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	US-10-046-955-51	Sequence 51, Appl
2	21	100.0	319	US-10-046-955-6	Sequence 123319,
3	16.2	77.1	403	US-10-424-599-123319	Sequence 123319,
4	16.2	77.1	499	US-10-027-632-136133	Sequence 136133,
5	16.2	77.1	499	US-10-027-632-136134	Sequence 136134,
6	16.2	77.1	499	US-10-027-632-136133	Sequence 136133,
7	16.2	77.1	499	US-10-027-632-136134	Sequence 136134,
8	16.2	77.1	894	US-10-437-963-41403	Sequence 41403, A
9	16.2	77.1	1037	US-10-027-632-259445	Sequence 259445,
10	16.2	77.1	1037	US-10-027-632-259446	Sequence 259446,
11	16.2	77.1	1037	US-10-027-632-259447	Sequence 259447,
12	16.2	77.1	1037	US-10-027-632-259445	Sequence 259445,
13	16.2	77.1	1037	US-10-027-632-259446	Sequence 259446,
14	16.2	77.1	1037	US-10-027-632-259447	Sequence 259447,

15	16.2	77.1	2985	17	US-10-437-963-99074	Sequence 99074, A
16	16.2	77.1	33769	13	US-10-182-936A-8	Sequence 8, Appl1
17	16.2	77.1	33769	17	US-10-374-979-8	Sequence 8, Appl1
18	16.2	77.1	33769	17	US-10-731-739-8	Sequence 8, Appl1
19	16.2	77.1	152759	17	US-10-322-281-10	Sequence 10, Appl
20	16.2	77.1	156843	13	US-10-087-192-1408	Sequence 1408, Ap
21	15.8	75.2	879	16	US-10-369-493-29617	Sequence 29617, A
22	15.8	75.2	879	13	US-10-282-122A-33226	Sequence 33226, A
23	15.8	75.2	1858	13	US-10-087-192-656	Sequence 656, App
24	15.8	75.2	2571	13	US-10-424-599-95510	Sequence 95510, A
25	15.8	75.2	2811	15	US-10-156-761-6673	Sequence 6673, Ap
26	15.8	75.2	5822	17	US-10-437-963-3726	Sequence 3726, Ap
27	15.8	75.2	5822	17	US-10-437-963-3724	Sequence 3724, Ap
28	15.8	75.2	71678	13	US-10-087-192-655	Sequence 655, App
29	15.8	75.2	9025608	15	US-10-156-761-1	Sequence 1, Appl1
30	15.4	73.3	1110	13	US-10-282-122A-25297	Sequence 25297, A
31	15.4	73.3	1884	9	US-09-815-242-8995	Sequence 8995, Ap
32	15.4	73.3	2034	9	US-09-815-223-11	Sequence 11, Appl
33	15.4	73.3	2310	9	US-09-815-242-8995	Sequence 4687, Ap
34	15.4	73.3	2790	9	US-09-815-242-8175	Sequence 8175, Ap
35	15.4	73.3	2790	9	US-09-815-242-8805	Sequence 8805, Ap
36	15.4	73.3	2790	13	US-10-282-122A-7697	Sequence 7697, Ap
37	15.4	73.3	2941	17	US-10-437-963-16977	Sequence 16977, A
38	15.4	73.3	29555	8	US-08-781-986A-206	Sequence 206, App
39	15.4	73.3	29555	13	US-10-329-624-206	Sequence 206, App
40	15.2	72.4	39	13	US-10-252-155-724	Sequence 724, App
41	15.2	72.4	39	13	US-10-252-155-725	Sequence 725, App
42	15.2	72.4	598	13	US-10-027-632-224405	Sequence 224405,
43	15.2	72.4	630	16	US-10-027-632-224405	Sequence 224405,
44	15.2	72.4	630	15	US-10-061-043A-32	Sequence 32, Appl
45	15.2	72.4	630	16	US-10-060-634C-32	Sequence 32, Appl

#### ALIGNMENTS

RESULT 1  
US-10-046-955-51  
Sequence 51, Application US/10046955  
Publication No. US20030129600A1  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America, as Represented by the  
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease Control and Prevention  
APPLICANT: Morrison, Christine J.  
APPLICANT: Reiss, Errol  
APPLICANT: Amdorovich, Liliana  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
FILE REFERENCE: 6395-62064  
CURRENT FILING DATE: US/10/046,955  
CURRENT FILING DATE: 2002-06-04  
PRIOR APPLICATION NUMBER: US 09/423,233  
PRIOR FILING DATE: 2000-06-27  
PRIOR APPLICATION NUMBER: PCT/US98/08926  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: US 60/045,400  
PRIOR FILING DATE: 1997-05-02  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 51  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Fusarium solani  
US-10-046-955-51

Query Match 100.0%; Score 21; DB 15; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CTACACCTCGCACTGAGAG 21  
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Db 1 CTAACCTCGCACTGGAGA 21

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RESULT 2
US-10-046-955-6
; Sequence 6, Application US/10046955
; Publication No. US20030128600A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Etrol
; APPLICANT: Aldorevich, Liliانا
; APPLICANT: Choi, Jong Seo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-10-046-955-6
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Query Match 100.0%; Score 21; DB 15; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTAACCTCGCACTGGAGA 21  
Db 222 CTAACCTCGCACTGGAGA 242

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RESULT 3
US-10-424-599-123319
; Sequence 123319, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 123319
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_82365C.1
US-10-424-599-123319
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Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CTAACCTCGCACTGGAGA 21  
Db 107 CTAACGACACCACTGGAGA 127

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RESULT 4
US-10-027-632-136133
; Sequence 136133, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136133
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136133
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Query Match 77.1%; Score 16.2; DB 13; Length 499;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 55 CTAACCTCGCCCACTGGAGA 75

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RESULT 5
US-10-027-632-136134
; Sequence 136134, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136134
; LENGTH: 499
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TYPE: DNA  
ORGANISM: Human  
US-10-027-632-136134

Query Match 77.1%; Score 16.2; DB 13; Length 499;  
Best Local Similarity 85.7%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAGA 21  
DB 55 CTAACCTCTCCCACTGGAGA 75

RESULT 6  
US-10-027-632-136133

Sequence 136133, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 136133

LENGTH: 499

TYPE: DNA

ORGANISM: Human

US-10-027-632-136133

Query Match 77.1%; Score 16.2; DB 16; Length 499;  
Best Local Similarity 85.7%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAGA 21  
DB 55 CTAACCTCTCCCACTGGAGA 75

RESULT 7  
US-10-027-632-136134

Sequence 136134, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 136134  
LENGTH: 499  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-136134

Query Match 77.1%; Score 16.2; DB 16; Length 499;  
Best Local Similarity 85.7%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAGA 21  
DB 55 CTAACCTCTCCCACTGGAGA 75

RESULT 8  
US-10-437-963-41403/C

Sequence 41403, Application US/10437963  
Publication No. US20040123345A1  
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 41403

LENGTH: 894

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT4530\_44751C.1

US-10-437-963-41403

Query Match 77.1%; Score 16.2; DB 17; Length 894;  
Best Local Similarity 85.7%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAGA 21  
DB 763 CTAACCTCTCGCACTGGAGA 743

RESULT 9  
US-10-027-632-259445

Sequence 259445, Application US/10027632  
Publication No. US20020198371A1  
GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

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; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259445
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259445
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Query Match
Best Local Similarity 77.1%; Score 16.2; DB 13; Length 1037;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 CTAACACCTGCAACTGAGGA 21
      |||||
Db      496 CTTACCCCTTGCAACTGAGGA 516
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RESULT 10
US-10-027-632-259446
; Sequence 259446, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259446
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259446
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```

Query Match
Best Local Similarity 77.1%; Score 16.2; DB 13; Length 1037;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```

QY      1 CTAACACCTGCAACTGAGGA 21
      |||||
Db      496 CTTACCCCTTGCAACTGAGGA 516
```

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RESULT 11
US-10-027-632-259447
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; Sequence 259447, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259447
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259447
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```

Query Match
Best Local Similarity 77.1%; Score 16.2; DB 13; Length 1037;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```

QY      1 CTAACACCTGCAACTGAGGA 21
      |||||
Db      496 CTTACCCCTTGCAACTGAGGA 516
```

```

RESULT 12
US-10-027-632-259445
; Sequence 259445, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259445
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259445
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 : Search time 294 Seconds

(without alignments)  
213.013 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctcaactcgcactgcagaga 21

Scoring table: IDENTITY\_NUC

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estrov:\*  
6: em\_estrpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estlum:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrt:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.8	84.8	762	29	CE746752 tigr-gss
2	17.4	82.9	540	28	B2896386 NARP9_013
3	17	81.0	606	14	CB256360 81-E01166
4	16.8	80.0	313	29	AG225492 Locust cor

Result No.	Score	Query Match	Length	DB ID	Description
5	16.8	80.0	362	10	BE070797 RC3-BR050
6	16.8	80.0	458	28	AO681735 SP_2142_A
7	16.8	80.0	552	28	AZ191211 SP_1019_A
8	16.8	80.0	586	9	AL955976 AL955976
9	16.8	80.0	610	12	BM440563 PPR1n.pko
10	16.8	80.0	639	29	CG294089 CG1B182TH
11	16.8	80.0	646	13	BU407567 604140848
12	16.8	80.0	668	13	BU235239 603793039
13	16.8	80.0	679	13	BU482142 603841434
14	16.8	80.0	784	13	BU311672 603541288
15	16.8	80.0	811	13	BU303091 603870435
16	16.8	80.0	829	29	CG14705 PUFMO83TD
17	16.8	80.0	883	13	BU142471 603135611
18	16.8	80.0	907	28	B2659389 OCAME36TC
19	16.8	80.0	951	29	CG14704 PUFMO83TB
20	16.8	80.0	972	29	CNS0777Y T7 end of
21	16.8	80.0	973	28	CC396411 PPHOT80TB
22	16.8	80.0	1321	12	B1490849 603031810
23	16.4	78.1	174	9	AT001540 AT001540
24	16.4	78.1	300	9	AV179460 AV179460
25	16.4	78.1	376	9	AV191390 AV191390
26	16.4	78.1	380	12	BU154339 BU154339
27	16.4	78.1	394	12	BU125969 BU125969
28	16.4	78.1	469	10	AW582687 RCO-ST029
29	16.4	78.1	586	9	AU218666 AU218666
30	16.4	78.1	587	10	BF619904 HYSMEC000
31	16.4	78.1	713	29	BH064238 RPT1-24-3
32	16.4	78.1	771	29	CC546447 CH240_429
33	16.4	78.1	787	28	BH061459 RPT1-24-3
34	16.4	78.1	819	28	BH061403 RPT1-24-3
35	16.2	77.1	252	28	AZ468148 IM0281F02
36	16.2	77.1	266	9	AV043034 AV043034
37	16.2	77.1	293	10	BB089128 BB089128
38	16.2	77.1	293	10	BB572305 BB572305
39	16.2	77.1	326	28	AQ260963 CITBI-E1-
40	16.2	77.1	349	28	AQ013861 RPT11-23
41	16.2	77.1	384	29	CC930150 ZMMBC053
42	16.2	77.1	430	28	AQ836420 HS_5367_A
43	16.2	77.1	437	9	AA840330 vW91d02_F
44	16.2	77.1	439	9	AW081834 XB55903.X
45	16.2	77.1	452	10	BF320988 uz58a02.Y

## ALIGNMENTS

RESULT 1  
LOCUS CE746752 762 bp DNA linear GSS 30-SEP-2003  
DEFINITION tigr-gss-dog-17000369563878 Dog Library Canis familiaris genomic,  
genomic survey sequence.  
ACCESSION CE746752  
VERSION CE746752.1 GI:37087099  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE Ruskch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
JOURNAL MEDLINE 22875432  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org

VERSION	CR256360.1	GI:32881133
KEYWORDS	EST.	
SOURCE	Arabidopsis thaliana (thale cress)	
ORGANISM	Arabidopsis thaliana	
REFERENCE	Bukarczyk, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie. 1 (bases 1 to 606)	
AUTHORS	Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.	
TITLE	Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)	
JOURNAL		
MEDLINE	22683290	
PUBMED	12799357	
COMMENT	Contact: Weisshaar B AIDS DNA core facility at MPZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weisshaar@mpiz-koeln.mpg.de Insert Length: 606 Std Error: 0.00 Plate: 6 row: A column: 22 Seq primer: T7R: CTAATGACCTCATCATGGCA. Location/Qualifiers 1..606 /organism="Arabidopsis thaliana" /mol_type="mRNA" /cultivar="Eifel-2 (Ei-2)" /db_xref="GABI:593758" /db_xref="taxon:3702" /clone="MPIZP772A226Q" /rname_type="whole plant" /dev_stage="adult plant, mixed stresses" /lab_host="E. coli TOP10" /clone_1fb="MPIZ-ADIS-027" /notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; cDNA library from Arabidopsis thaliana, accession Eifel-2; ten week old total plants grown under long-day conditions in soil, whole adult plants were treated for 24 hours with different stresses, (1) at 4M-0 C in the dark, (2), at 37 Grad C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding leaves with a foreceps, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 M-0C in the light/UV; equal quantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites SalI-NotI, Primer sites and orientation: T7-SalI-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-sp6; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection'. PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."	
ORIGIN		
Query Match	81.0%; Score 17;	DB 14; Length 606;
Best Local Similarity	100.0%; Pred. No. 1.6e+03;	
Matches	17; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Oy	5 CACTGCCAACTGGACA 21	
Db	115 CACCTCGCAACTGGAGA 131	
RESULT 4		
AG225492/c	AG225492	313 bp DNA linear GSS 19-JUN-2003
LOCUS	Lotus corniculatus var. japonicus DNA, clone:ljBj2h04_T1 genomic	
DEFINITION		

survey sequence.

ACCESSION AG225492  
 VERSION AG225492.1 GI:26536116  
 KEYWORDS GSS.  
 SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)  
 ORGANISM Lotus corniculatus var. japonicus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteeae;  
 Lotus.

REFERENCE 1  
 AUTHORS Sato, S., Nakamura, Y. and Tabata, S.  
 TITLE Lotus japonicus BAC End sequences  
 JOURNAL Published Only in Database (2002)  
 REFERENCE 2 (bases 1 to 313)  
 AUTHORS Sato, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,  
 The First Laboratory for Plant Gene Research; 2-6-7  
 Kazusa-kamatori, Kisarazu, Chiba 292-0818, Japan  
 (E-mail: sato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,  
 Tel: 81-438-52-3935 (ex. 2336), Fax: 81-438-52-3934)  
 Location/Qualifiers

FEATURES  
 source  
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 /organism="Lotus corniculatus var. japonicus"  
 /mol\_type="genomic DNA"  
 /strain="Miyakojima MG-20"  
 /variety="japonicus"  
 /db\_xref="taxon:34305"  
 /clone="LjB12H04.F"  
 /clone\_lib="genomic BAC library"  
 /note="VECTOR: pBelobAC11-synonym: Lotus japonicus"

ORIGIN  
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 Best Local Similarity 90.0%; Pred. No. 1.6e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAG 20  
 |||||  
 Db 234 CTACACCTCGCACTGGAG 215

RESULT 5  
 BE070797 362 bp mRNA linear EST 09-JUN-2000  
 LOCUS RC3-BT0502-251199-011-b12 BT0502 Homo sapiens CDNA, mRNA sequence.  
 DEFINITION BE070797  
 VERSION BE070797.1 GI:8415443  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 362)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Birones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.

REFERENCE 1  
 AUTHORS Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SF,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=et2=RC3-BT0502-251  
 199-011-b12&t3=1999-11-25&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 28  
 Location/Qualifiers

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 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="BT0502"  
 /note="Organ: breast; Vector: puc18; Site\_1: SmaI, Site\_2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No.  
 196,716 - Ludwig Institute for Cancer Research) profiles  
 into the puc 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."

ORIGIN  
 Query Match 80.0%; Score 16.8; DB 10; Length 362;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTACACCTCGCACTGGAG 20  
 |||||  
 Db 39 CTACCTCTCGCACTGGAG 58

RESULT 6  
 A0681735 458 bp DNA linear GSS 28-JUN-1999  
 LOCUS HS\_2142\_A2 E04 MR CIT Approved Human Genomic Sperm Library D Homo  
 DEFINITION sapiens genomic clone Plate=2142 Col=8 Row=I, genomic survey  
 sequence.  
 ACCESSION A0681735  
 VERSION A0681735.1 GI:5257718  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 458)  
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,  
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and  
 Hood, L.  
 Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 MEDLINE 99380589  
 PUBMED 10449764  
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones may be purchased from Research Genetics (info@resgen.com).  
 BAC end Web Server: http://www.htsc.washington.edu  
 Plate: 2142 row: I column: 8  
 Seq primer: M13 Reverse  
 Class: BAC ends  
 High quality sequence stop: 458.  
 Location/Qualifiers

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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

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/clone="Plate=2142 Col=8 Row=1"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
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Best Local Similarity 90.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
1 CTAACACCTCGCACTGGAG 20
|||||
439 CTAACACCTCGCACTGTAG 458

RESULT 7
A2191211      552 bp  DNA  linear  GSS 30-AUG-2000
LOCUS
DEFINITION
SP 1019_A1 A04 SP6E Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plate=1019 Col=7 Row=A, genomic survey sequence.
ACCESSION
A2191211
VERSION
A2191211.1 GI:8374390
KEYWORDS
GSS.
SOURCE
Strongylocentrotus purpuratus
ORGANISM
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoidea;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 552)
Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T.,
Wray,G.A., Ertensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H.
and Hood,L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
20402566
PUBMED
10920195
COMMENT
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 1019 Row: A Column: 7
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 552.
Location/Qualifiers
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/mol_xref="taxon:7668"
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/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli
DH10B"

ORIGIN
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Best Local Similarity 85.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
1 CTAACACCTCGCACTGGAGA 21
|||||
407 CTAACACCTCGCATCTGGAGA 427

RESULT 8

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AL955976
LOCUS
DEFINITION
AL955976 XGC-gastrula Silurana tropicalis cDNA clone Tga6124m04 5',
mRNA sequence.
ACCESSION
AL955976
VERSION
AL955976.1 GI:25779571
KEYWORDS
EST.
SOURCE
Silurana tropicalis (western clawed frog)
ORGANISM
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 586)
Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
CONTACT: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: Tga6124m04.plcSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
1. 586
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="Tga6124m04"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Xscherichia coli XL1-blue"
/clone_lib="XGC-gastrula"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

ORIGIN
Query Match      80.0%; Score 16.8; DB 9; Length 586;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
1 CTAACACCTCGCACTGGAG 20
|||||
551 CCAACACCTTGCACTGGAG 570

RESULT 9
BM440563      610 bp  mRNA  linear  EST 01-FEB-2002
LOCUS
DEFINITION
pgryn.pK003.h4 Normalized Chicken Reproductive Tract cDNA Library
(pgryn) Gallus gallus cDNA clone pgryn.pK003.h4 5' similar to no
significant hits (plog(P) 4), mRNA sequence.
ACCESSION
BM440563
VERSION
BM440563.1 GI:16471338
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 610)
Cogburn,L.A. and Nys,Y.
ESTs from Normalized Chicken Reproductive Tract cDNA library-
University of Delaware and INRA, Tours-Poultry Unit Project
Unpublished (2002)
CONTACT: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335

```



Fax: 302-831-2822  
Email: cogburn@udel.edu, www.chickest.udel.edu.  
Location/Qualifiers

# FEATURES

source

1. 610  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Commercial broiler and layer"  
/db\_xref="taxon:9031"  
/clone="pgrin.pk003.h4"  
/sex="Male and Female"  
/tissue\_type="testis, ovary and oviduct"  
/dev\_stage="Various stages; embryonic, post-hatch, immature and sexually-mature"  
/lab\_host="E. coli EMDH10B"  
/clone\_lib="Normalized Chicken Reproductive Tract cDNA library (pgrin)"  
/note="Vector: PCMVSPORT6; library made from three total RNA pools from each tissue (testis 25%, ovary 25%, and oviduct 50% of final RNA pool); single pass sequencing from 5'-end"

## ORIGIN

Query Match 80.0%; Score 16.8; DB 12; Length 610;  
Best Local Similarity 90.0%; Pred. No. 2e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAACACCTCGCACTGAGA 21  
|||||  
550 TAAGACCTCGCAATGAGA 569

Db

RESULT 10  
CG294089 639 bp DNA linear GSS 25-AUG-2003  
LOCUS CG1B182TH ZM 0.7.1.5 KB Zea mays genomic clone ZMMBMa0723N19,  
DEFINITION genomic survey sequence.  
ACCESSION CG294089  
VERSION CG294089.1 GI:34208303  
KEYWORDS GSS.  
SOURCE  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 639)  
White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, V.A., Rohlfing, T.,  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OG1B182TV  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.

## FEATURES

source

1. 639  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBMa0723N19"  
/clone\_lib="ZM\_0.7.1.5\_KB"  
/note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

## ORIGIN

source

Query Match 80.0%; Score 16.8; DB 29; Length 639;  
Best Local Similarity 90.0%; Pred. No. 2e+03;

## ORIGIN

Query Match 80.0%; Score 16.8; DB 29; Length 639;  
Best Local Similarity 90.0%; Pred. No. 2e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAACACCTCGCACTGAGA 21  
|||||  
Db 435 TAACACCGCACTGAGA 454

## RESULT 11

BU407567 646 bp mRNA linear EST 27-NOV-2002  
LOCUS 604140848F1 CSEQCHN59 Gallus gallus cDNA clone CHEST973012 5', mRNA  
DEFINITION sequence.  
ACCESSION BU407567  
VERSION BU407567.1 GI:25776623  
KEYWORDS EST.  
SOURCE  
ORGANISM Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 646)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
2235534  
MEDLINE  
PUBMED  
12445392

## COMMENT

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
12445392  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 10D, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

1. 646  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="White Leghorn, Hisex"  
/db\_xref="taxon:9031"  
/clone="CHEST973012"  
/dev\_stage="36"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN59"  
/note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:  
EcoRI; Site 2: NotI; This normalized library was  
constructed from 1 million independent clones. cDNA  
synthesis was initiated using an oligo(dT) primer, using  
methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunt-ended, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., EMAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 80.0%; Score 16.8; DB 13; Length 646;  
Best Local Similarity 90.0%; Pred. No. 2e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAACACCTCGCACTGAGA 21  
|||||  
Db 286 TAAGACCTCGCAATGAGA 305

RESULT 12  
BU235239 668 bp mRNA linear EST 26-NOV-2002  
LOCUS BU235239

DEFINITION	60379930391 CSEOCHN24 Gallus gallus CDNA clone CHEST759n10 5', mRNA sequence.					
ACCESSION	BU235239					
VERSION	BU235239.1 GI:25480437					
KEYWORDS	EST					
SOURCE	Gallus gallus (chicken)					
ORGANISM	Gallus gallus					
REFERENCE	Archosauroidae; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 668) Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)					
JOURNAL MEDLINE	22335534					
PUBMED	12445392					
COMMENT	Contact: Simon Hubbard Department of Biomedical Sciences University of Manchester Institute of Science and Technology (UMIST) PO Box 88, Manchester, M60 1QD, UK Tel: 01612008930 Fax: 01612360409 Email: Simon.Hubbard@umist.ac.uk. Location/Qualifiers					
FEATURES	source					
	1..668					
	/organism="Gallus gallus"					
	/mol_type="mRNA"					
	/strain="White Leghorn, Hisex"					
	/db_xref="taxon:9031"					
	/clone="CHEST759n10"					
	/dev_stage="22"					
	/lab_host="DH10B"					
	/clone_lib="CSEOCHN24"					
	/note="Organ: heads; Vector: pBluescript II KS(+); Site_1: EcoRI, Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dt) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntend, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."					
ORIGIN						
	Query Match 80.0%; Score 16.8; DB 13; Length 668; Best Local Similarity 90.0%; Pred.No.2.le+03;					
	Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
OY	2 TAACACCTCGCACTGGAGA 21					
Db	633 TAGACTTCGCAGATGGAGA 652					
RESULT 13						
LOCUS	BU482142					
DEFINITION	679 bp mRNA linear EST 30-NOV-2002 603841434F1 CSERQRN22 Gallus gallus CDNA clone CHEST823d10 5', mRNA sequence.					
ACCESSION	BU482142					
VERSION	BU482142.1 GI:25975719					
KEYWORDS	EST					
SOURCE	Gallus gallus (chicken)					
ORGANISM	Gallus gallus					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauroidae; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.					

```

REFERENCE
1 (bases 1 to 679)
AUTHORS
Boardman,P.E., Sans-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE
A Comprehensive Collection of Chicken CDNA
JOURNAL
Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE
22335534
PubMed
12445392
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1OD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. 679
FEATURES
source
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="layer and broiler"
/db_xref="taxon:9031"
/clone="CHST823d10"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate
cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1fb="CSEORBN22"
/notes="Vector: pBluescript II KS(+); Site 1: EcoRI;
Site 2: NotI; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunted, ligated to
NciI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."
ORIGIN
Query Match 80.0%; Score 16.8; DB 13; Length 679;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TAAACCTCGCAACTGGAGA 21
|||||
Db 571 TAAAGACCTCGCAATGGAGA 590
RESULT 14
BU311672 784 bp mRNA linear EST 28-NOV-2002
LOCUS BU311672
DEFINITION
603541288F1 CSEORHN61 Gallus gallus cDNA clone CHEST510p21 5', mRNA
sequence.
ACCESSION BU311672
VERSION BU311672
KEYWORDS BU311672.1 GI:25819673
SOURCE
EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaenidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 784)
AUTHORS
Boardman,P.E., Sans-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE
A Comprehensive Collection of Chicken CDNA
JOURNAL
Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE
22335534
PubMed
12445392

```

## COMMENT

Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

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1..784
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST510p21"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="CSEQCHN61"
/note="Organ: heart; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
```

## ORIGIN

Query Match 80.0%; Score 16.8; DB 13; Length 784;  
Best Local Similarity 90.0%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAACACCTCGCAACTGGAGA 21  
||| ||||| ||||| |||||  
DB 717 TAAGACCTCGCAATGGAGA 736

## RESULT 15

B0330991

LOCUS

DEFINITION 603870435F1 CSEQCHN65 Gallus gallus cDNA clone CHEST9669 5', mRNA

ACCESSION

B0330991

KEYWORDS

SOURCE

ORGANISM

EST.  
Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

REFERENCE

AUTHORS

1 (bases 1 to 811)  
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.,  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

FEATURES

Location/Qualifiers

source

```
1..811
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST9669"
/tissue_type="whole embryo"
/dev_stage="10"
/lab_host="DH10B"
/clone_1lb="CSEQCHN65"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site_1: EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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## ORIGIN

Query Match 80.0%; Score 16.8; DB 13; Length 811;  
Best Local Similarity 90.0%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAACACCTCGCAACTGGAGA 21  
||| ||||| ||||| |||||  
DB 55 TAAGACCTCGCAATGGAGA 74

Search completed: October 1, 2004, 08:01:59  
Job time : 302.333 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 ; Search time 146.608 Seconds  
(without alignments)  
5321.503 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18  
Sequence: 1 tctcagtcgctgcgcgc 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank1: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sgs: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vt: \*  
15: gb\_vt: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sgs: \*  
28: em\_un: \*  
29: em\_vt: \*  
30: em\_hcg\_hum: \*  
31: em\_hcg\_inv: \*  
32: em\_hcg\_other: \*  
33: em\_hcg\_mus: \*  
34: em\_hcg\_pln: \*  
35: em\_hcg\_rtd: \*  
36: em\_hcg\_mam: \*  
37: em\_hcg\_vtc: \*  
38: em\_sy: \*  
39: em\_hcgo\_hum: \*  
40: em\_hcgo\_mus: \*  
41: em\_hcgo\_other: \*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	AR206443	AR206443 Sequence
2	18	100.0	18	BD083634	BD083634 Nucleic a
3	16.4	91.1	310	AR206401	AR206401 Sequence
4	16.4	91.1	310	BD083592	BD083592 Nucleic a
5	16.4	91.1	310	AF117922	AF117922 Gibberella
6	16.4	91.1	351	AF162903	AF162903 Fusarium
7	16.4	91.1	392	AF502843	AF502843 Leaf lilt
8	16.4	91.1	393	AF502789	AF502789 Leaf lilt
9	16.4	91.1	402	AF502677	AF502677 Leaf lilt
10	16.4	91.1	418	AF502716	AF502716 Leaf lilt
11	16.4	91.1	419	AF111060	AF111060 Fusarium
12	16.4	91.1	421	AF430128	AF430128 Fusarium
13	16.4	91.1	421	AF430129	AF430129 Fusarium
14	16.4	91.1	427	AF502877	AF502877 Leaf lilt
15	16.4	91.1	434	AY243055	AY243055 Ascomycet
16	16.4	91.1	451	AF502788	AF502788 Leaf lilt
17	16.4	91.1	452	AF502714	AF502714 Leaf lilt
18	16.4	91.1	457	AF261745	AF261745 Cyindroc
19	16.4	91.1	457	AF502641	AF502641 Leaf lilt
20	16.4	91.1	458	AF008562	AF008562 Fusarium
21	16.4	91.1	458	AF502805	AF502805 Leaf lilt
22	16.4	91.1	462	AF502875	AF502875 Leaf lilt
23	16.4	91.1	463	AF493963	AF493963 Calonectr
24	16.4	91.1	463	AF493964	AF493964 Calonectr
25	16.4	91.1	463	AF493965	AF493965 Cyindroc
26	16.4	91.1	464	AF261740	AF261740 Calonectr
27	16.4	91.1	466	NGA228662	NGA228662 Nectria g
28	16.4	91.1	466	NGA228663	NGA228663 Nectria g
29	16.4	91.1	466	NGA228664	NGA228664 Nectria g
30	16.4	91.1	466	NGA228665	NGA228665 Nectria g
31	16.4	91.1	466	NGA228666	NGA228666 Nectria g
32	16.4	91.1	466	NGA228667	NGA228667 Nectria g
33	16.4	91.1	466	NGA228668	NGA228668 Nectria g
34	16.4	91.1	466	NGA228669	NGA228669 Nectria g
35	16.4	91.1	466	NGA228670	NGA228670 Nectria g
36	16.4	91.1	466	NGA228671	NGA228671 Nectria g
37	16.4	91.1	466	NGA228672	NGA228672 Nectria g
38	16.4	91.1	466	NGA228673	NGA228673 Nectria g
39	16.4	91.1	466	NGA228674	NGA228674 Nectria g
40	16.4	91.1	466	NGA228675	NGA228675 Nectria g
41	16.4	91.1	466	NGA228676	NGA228676 Nectria g
42	16.4	91.1	466	NGA228677	NGA228677 Nectria g
43	16.4	91.1	466	NGA228678	NGA228678 Nectria g
44	16.4	91.1	466	NGA228679	NGA228679 Nectria g
45	16.4	91.1	466	NGA228680	NGA228680 Nectria g

## ALIGNMENTS

RESULT 1  
LOCUS AR206443 18 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 49 from patent US 6372430.  
ACCESSION AR206443  
VERSION AR206443.1 GI:21505046  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
Morrison,C.O., Reles,E., Alderevich,L. and Choi,J.Soo.  
TITLE Nucleic acids for detecting Aspergillus species and other  
filamentous fungi  
JOURNAL Patent: US 6372430-A 49 16-APR-2002;

FEATURES  
source  
Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  
1 TCTAGTACGGCTCTCGCT 18  
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1 TCTAGTACGGCTCTCGCT 18

Db  
1 TCTAGTACGGCTCTCGCT 18

RESULT 2  
BD083634  
LOCUS  
DEFINITION  
Nucleic acids for detecting Aspergillus species and other filamentous fungi.  
ACCESSION  
BD083634.1 GI:22629244  
VERSION  
UP 2001525665-A/49.  
KEYWORDS  
Gibberella fujikuroi  
SOURCE  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.  
1 (bases 1 to 18)  
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.  
Nucleic acids for detecting Aspergillus species and other filamentous fungi  
Patent: JP 2001525665-A 49 11-DEC-2001;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE  
OS Fusarium moniliforme  
PN JP 2001525665-A/49  
PD 11-DEC-2001  
PF 01-MAY-1998 JP 1998548275  
PR 02-MAY-1997 US 60/045400  
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO  
PC C1201/68  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.

FEATURES  
source  
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Location/Qualifiers  
/organism="Gibberella fujikuroi"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:5127"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  
1 TCTAGTACGGCTCTCGCT 18  
|||||  
1 TCTAGTACGGCTCTCGCT 18

Db  
1 TCTAGTACGGCTCTCGCT 18

RESULT 3  
AR206401  
LOCUS  
DEFINITION  
Sequence 7 from patent US 6372430.  
ACCESSION  
AR206401  
VERSION  
AR206401.1 GI:21504992  
KEYWORDS  
SOURCE  
Unknown.

ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 310)  
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.Soo.  
Nucleic acids for detecting Aspergillus species and other filamentous fungi  
Patent: US 6372430-A 7 16-APR-2002;  
JOURNAL  
Location/Qualifiers  
source  
1..310  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 6; Length 310;  
Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  
1 TCTAGTACGGCTCTCGCT 18  
|||||  
174 TCTAGTACGGCTCTCGCT 191

Db  
174 TCTAGTACGGCTCTCGCT 191

RESULT 4  
BD083592  
LOCUS  
DEFINITION  
Nucleic acids for detecting Aspergillus species and other filamentous fungi.  
ACCESSION  
BD083592.1 GI:22629202  
VERSION  
JP 2001525665-A/7.  
KEYWORDS  
Gibberella fujikuroi  
SOURCE  
ORGANISM  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.  
1 (bases 1 to 310)  
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.  
Nucleic acids for detecting Aspergillus species and other filamentous fungi  
Patent: JP 2001525665-A 7 11-DEC-2001;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE  
OS Fusarium moniliforme  
PN JP 2001525665-A/7  
PD 11-DEC-2001  
PF 01-MAY-1998 JP 1998548275  
PR 02-MAY-1997 US 60/045400  
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO  
PC C1201/68  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.

FEATURES  
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1..310  
Location/Qualifiers  
/organism="Gibberella fujikuroi"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:5127"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 6; Length 310;  
Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  
1 TCTAGTACGGCTCTCGCT 18  
|||||  
174 TCTAGTACGGCTCTCGCT 191

Db  
174 TCTAGTACGGCTCTCGCT 191

RESULT 5

AF117922 310 bp DNA linear PLN 17-JUN-2000  
 LOCUS AF117922  
 DEFINITION *Gibberella fujikuroi* ATCC 38519 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
 ACCESSION AF117922  
 VERSION AF117922.1 GI:8570108  
 KEYWORDS  
 SOURCE  
 ORGANISM *Gibberella fujikuroi*  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; Nectriaceae; *Gibberella*; *Gibberella fujikuroi* complex.  
 REFERENCE 1 (bases 1 to 310)  
 Choi, J.S., Westerman, J.M. and Morrison, C.J.  
 Rapid differentiation of filamentous fungi using species-specific DNA probes  
 JOURNAL Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)  
 REFERENCE 2 (bases 1 to 310)  
 Choi, J.S., Westerman, J.M. and Morrison, C.J.  
 Direct Submission  
 Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA 30333, USA  
 FEATURES  
 source  
 1..310  
 /organism="Gibberella fujikuroi"  
 /mol\_type="genomic DNA"  
 /strain="ATCC 38519"  
 /db\_xref="ATCC:38519"  
 /db\_xref="taxon:5127"  
 <1..159  
 /product="5.8S ribosomal RNA"  
 159..272  
 /product="internal transcribed spacer 2"  
 /note="ITS2"  
 273..310  
 /product="28S ribosomal RNA"  
 rRNA  
 ORIGIN  
 Query Match 91.1%; Score 16.4; DB 8; Length 310;  
 Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Cy 1 TCTAGTACCGCTCGCT 18  
 |||||  
 Db 174 TCTAGTGGCGTCTCGCT 191  
 |||||  
 RESULT 6  
 LOCUS AF162903 351 bp DNA linear PLN 04-AUG-1999  
 DEFINITION *Fusarium proliferatum* 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
 ACCESSION AF162903  
 VERSION AF162903.1 GI:5690392  
 KEYWORDS  
 SOURCE  
 ORGANISM *Fusarium proliferatum*  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; Nectriaceae; *Gibberella*; *Gibberella fujikuroi* complex.  
 REFERENCE 1 (bases 1 to 351)  
 Min, B.R.  
 Direct Submission  
 Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea  
 TITLE location/Qualifiers  
 1..351  
 /organism="Fusarium proliferatum"  
 /mol\_type="genomic DNA"  
 /strain="6787"  
 /db\_xref="taxon:42674"

rRNA  
 misc\_RNA  
 rRNA  
 ORIGIN  
 Query Match 91.1%; Score 16.4; DB 8; Length 351;  
 Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Cy 1 TCTAGTACCGCTCGCT 18  
 |||||  
 Db 195 TCTAGTGGCGTCTCGCT 212  
 |||||  
 RESULT 7  
 LOCUS AF502843/c 392 bp DNA linear PLN 13-MAY-2002  
 DEFINITION *Leaf litter ascomycete strain its332 isolate 1000096451* internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
 ACCESSION AF502843  
 VERSION AF502843.1 GI:20531650  
 KEYWORDS  
 SOURCE  
 ORGANISM *Leaf litter ascomycete strain its332*  
 Leaf litter ascomycete strain its332  
 Eukaryota; Fungi; Ascomycota.  
 REFERENCE 1 (bases 1 to 392)  
 Gilbert, G.S., Garbelotto, M., Chapela, I., Moeller, C. and Dreyfuss, M.M.  
 Biogeography of leaf litter fungi  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 392)  
 Gilbert, G.S., Garbelotto, M., Chapela, I., Moeller, C. and Dreyfuss, M.M.  
 Direct Submission  
 Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA  
 TITLE location/Qualifiers  
 1..392  
 /organism="leaf litter ascomycete strain its332"  
 /mol\_type="genomic DNA"  
 /strain="its332"  
 /isolate="1000096451"  
 /specific\_host="Prestoea montana"  
 /db\_xref="taxon:194115"  
 /country="Puerto Rico"  
 <1..3592  
 /note="contains internal transcribed spacer 1, 5.8S ribosomal RNA and internal transcribed spacer 2"  
 misc\_RNA  
 ORIGIN  
 Query Match 91.1%; Score 16.4; DB 8; Length 392;  
 Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Cy 1 TCTAGTACCGCTCGCT 18  
 |||||  
 Db 51 TCTAGTGGCGTCTCGCT 34  
 |||||  
 RESULT 8  
 LOCUS AF502789 393 bp DNA linear PLN 13-MAY-2002  
 DEFINITION *Leaf litter ascomycete strain its265 isolate 1000143643* internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
 ACCESSION AF502789  
 VERSION AF502789.1 GI:20531596

KEYWORDS  
SOURCE leaf litter ascomycete strain its265  
ORGANISM leaf litter ascomycete strain its265  
REFERENCE Eukaryota; Fungi; Ascomycota.  
AUTHORS 1 (bases 1 to 393)  
Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
TITLE Biogeography of leaf litter fungi  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 393)  
AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA  
FEATURES  
source 1..393  
/organism="leaf litter ascomycete strain its265"  
/mol\_type="genomic DNA"  
/strain="its265"  
/isolate="1000143643"  
/specific\_host="Prestoea montana"  
/db\_xref="taxon:194061"  
/country="Puerto Rico"  
misc\_RNA <1..149  
/product="internal transcribed spacer 1"  
rRNA 150..304  
/product="5.8S ribosomal RNA"  
misc\_RNA 305..>393  
/product="internal transcribed spacer 2"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 8; Length 393;  
Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 TCTAGTACGCTCTCGCT 18  
|||||  
Db 366 TCTAGTACGCTCTCGCT 383

RESULT 9  
AF502667  
LOCUS 402 bp DNA linear PLN 13-MAY-2002  
DEFINITION leaf litter ascomycete strain its086 isolate 1000589588 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
ACCESSION AF502667  
VERSION AF502667.1 GI:20531474  
KEYWORDS  
SOURCE leaf litter ascomycete strain its086  
ORGANISM leaf litter ascomycete strain its086  
AUTHORS Eukaryota; Fungi; Ascomycota.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
TITLE Biogeography of leaf litter fungi  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 402)  
AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA  
FEATURES  
source 1..402  
/organism="leaf litter ascomycete strain its086"  
/mol\_type="genomic DNA"  
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/isolate="1000589588"  
/specific\_host="Brosimum alicastrum"  
/db\_xref="taxon:193939"

misc\_RNA /country="Panama"  
rRNA <1..120  
/product="internal transcribed spacer 1"  
misc\_RNA 121..275  
/product="5.8S ribosomal RNA"  
276..>402  
/product="internal transcribed spacer 2"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 8; Length 402;  
Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 TCTAGTACGCTCTCGCT 18  
|||||  
Db 342 TCTAGTACGCTCTCGCT 359

RESULT 10  
AF502716  
LOCUS 418 bp DNA linear PLN 13-MAY-2002  
DEFINITION leaf litter ascomycete strain its182 isolate 1000011379 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.  
ACCESSION AF502716  
VERSION AF502716.1 GI:20531523  
KEYWORDS  
SOURCE leaf litter ascomycete strain its182  
ORGANISM leaf litter ascomycete strain its182  
AUTHORS Eukaryota; Fungi; Ascomycota.  
REFERENCE 1 (bases 1 to 418)  
AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
TITLE Biogeography of leaf litter fungi  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 418)  
AUTHORS Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and Dreyfuss,M.M.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2002) Environmental Studies, University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA  
FEATURES  
source 1..418  
/organism="leaf litter ascomycete strain its182"  
/mol\_type="genomic DNA"  
/strain="its182"  
/isolate="1000011379"  
/specific\_host="Cousasapoa panamensis"  
/db\_xref="taxon:193988"  
/country="Panama"  
misc\_RNA <1..137  
/product="internal transcribed spacer 1"  
rRNA 138..292  
/product="5.8S ribosomal RNA"  
misc\_RNA 293..>418  
/product="internal transcribed spacer 2"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 8; Length 418;  
Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 TCTAGTACGCTCTCGCT 18  
|||||  
Db 353 TCTAGTACGCTCTCGCT 370

RESULT 11  
AF111060  
LOCUS 419 bp DNA linear PLN 20-JAN-1999  
DEFINITION Fusarium subglutnatum var. subglutnatum strain BBA62431 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,



complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION AF11060  
VERSION AF11060.1 GI:4160484  
KEYWORDS  
SOURCE Fusarium subglutinatum var. subglutinatum  
ORGANISM Fusarium subglutinatum var. subglutinatum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE  
AUTHORS Bulat,S.A., Yli-Mattila,T. and Alekhina,I.A.  
TITLE Molecular taxonomy of Fusarium strains by means of ribotyping, rDNA sequencing and UP-PCR analysis. A case study of Sporotrichiella section

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 419)  
AUTHORS Bulat,S.A. and Alekhina,I.A.  
TITLE Direct Submission  
JOURNAL Submitted (03-DEC-1998) Department of Molecular and Radiation Biophysics, Petersburg Nuclear Physics Institute RAS, Gatchina, Leningrad Region 188350, Russia

FEATURES  
source Location/Qualifiers  
1..419  
/organism="Fusarium subglutinatum var. subglutinatum"  
/mol\_type="genomic DNA"  
/strain="BBA62431"  
/variety="subglutinatum"  
/db\_xref="taxon:86548"  
<1..136  
/product="internal transcribed spacer 1"  
/note="ITS1"  
137..294  
/product="5.8S ribosomal RNA"  
295..>419  
/product="internal transcribed spacer 2"  
/note="ITS2"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 8; Length 419;  
Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  
1 TCTAGTGACGCTCGCT 18  
|||||  
Db 365 TCTAGTGACGCTCGCT 382  
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RESULT 12  
AF430128 421 bp DNA linear PLN 06-NOV-2002  
LOCUS  
DEFINITION Fusarium mangiferae strain MRC3477 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION AF430128  
VERSION AF430128.1 GI:24637153  
KEYWORDS  
SOURCE Fusarium mangiferae  
ORGANISM Fusarium mangiferae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE  
AUTHORS Britz,H., Coutinho,T.A., Wingfield,B.D., Marasas,W.F.O. and Wingfield,M.J.  
TITLE Vegetative compatibility and distribution of two Fusarium species associated with mango malformation in South Africa  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 421)  
AUTHORS Britz,H., Coutinho,T.A., Wingfield,B.D., Marasas,W.F.O. and Wingfield,M.J.  
TITLE Direct Submission  
JOURNAL Submitted (09-OCT-2001) Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Lunnonstreet, Pretoria, Gauteng 0002, South Africa

Gauteng 0002, South Africa

FEATURES  
source Location/Qualifiers  
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/organism="Fusarium mangiferae"  
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/db\_xref="taxon:192010"  
/note="section 1iseola"  
<1..24  
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25..161  
/product="internal transcribed spacer 1"  
162..320  
/product="5.8S ribosomal RNA"  
321..>421  
/product="internal transcribed spacer 2"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 8; Length 421;  
Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  
1 TCTAGTGACGCTCGCT 18  
|||||  
Db 387 TCTAGTGACGCTCGCT 404  
|||||

RESULT 13  
AF430129 421 bp DNA linear PLN 06-NOV-2002  
LOCUS  
DEFINITION Fusarium mangiferae strain MRC7035 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

ACCESSION AF430129  
VERSION AF430129.1 GI:24637154  
KEYWORDS  
SOURCE Fusarium mangiferae  
ORGANISM Fusarium mangiferae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE  
AUTHORS Britz,H., Coutinho,T.A., Wingfield,B.D., Marasas,W.F.O. and Wingfield,M.J.  
TITLE Vegetative compatibility and distribution of two Fusarium species associated with mango malformation in South Africa  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 421)  
AUTHORS Britz,H., Coutinho,T.A., Wingfield,B.D., Marasas,W.F.O. and Wingfield,M.J.  
TITLE Direct Submission  
JOURNAL Submitted (09-OCT-2001) Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Lunnonstreet, Pretoria, Gauteng 0002, South Africa

FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:192010"  
/note="section 1iseola"  
<1..24  
/product="18S ribosomal RNA"  
25..161  
/product="internal transcribed spacer 1"  
162..320  
/product="5.8S ribosomal RNA"  
321..>421  
/product="internal transcribed spacer 2"

ORIGIN  
Query Match 91.1%; Score 16.4; DB 8; Length 421;  
Best Local Similarity 94.4%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTGACGGCTCTCGCT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 387 TCTAGTGACGGCTCTCGCT 404

RESULT 14  
AF502877  
LOCUS  
DEFINITION  
AF502877 427 bp DNA linear PLN 13-MAY-2002  
Leaf litter ascomycete strain its389 isolate 1000096987 internal  
transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,  
complete sequence; and internal transcribed spacer 2, partial  
sequence.  
AF502877.1 GI:20531684

ACCESSION  
VERSION  
KEYWORDS  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1 leaf litter ascomycete strain its389  
leaf litter ascomycete strain its389  
Eukaryota; Fungi; Ascomycota.  
1 (bases 1 to 427)  
Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and  
Dreyfuss,M.M.  
Biogeography of leaf litter fungi  
Unpublished  
2 (bases 1 to 427)  
Gilbert,G.S., Garbelotto,M., Chapela,I., Moeller,C. and  
Dreyfuss,M.M.  
Direct Submission  
Submitted (12-APR-2002) Environmental Studies, University of  
California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064, USA  
Location/Qualifiers  
1..427  
/organism="leaf litter ascomycete strain its389"  
/mol\_type="genomic DNA"  
/strain="its389"  
/isolate="1000096987"  
/specific\_host="Prestoea montana"  
/db\_xref="taxon:194149"  
/country="Puerto Rico"  
<1..164  
/product="internal transcribed spacer 1"  
165..319  
/product="5.8S ribosomal RNA"  
320..>427  
/product="internal transcribed spacer 2"

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 427;  
Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTGACGGCTCTCGCT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 380 TCTAGTGACGGCTCTCGCT 397

RESULT 15  
AY243055  
LOCUS  
DEFINITION  
AY243055 434 bp DNA linear PLN 14-APR-2003  
Ascomycete sp. A77 internal transcribed spacer 1, partial sequence;  
5.8S ribosomal RNA gene, complete sequence; and internal  
transcribed spacer 2, partial sequence.  
AY243055  
AY243055.1 GI:29826150

ACCESSION  
VERSION  
KEYWORDS  
ORGANISM  
SOURCE  
REFERENCE  
AUTHORS  
TITLE

ascomycete sp. A77  
ascomycete sp. A77  
Eukaryota; Fungi; Ascomycota.  
1 (bases 1 to 434)  
Beckstead,J. and Parker,I.M.  
Invasiveness of *Ammophila arenaria*: Release from soil-borne  
pathogens?

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 434)  
AUTHORS Gambletta,G., Gilbert,G.S. and Parker,I.M.  
TITLE Direct Submission  
JOURNAL Submitted (23-FEB-2003) Ecology and Evolutionary Biology,  
University of California, Santa Cruz, 1156 High St., EMS, Santa  
Cruz, CA 95064, USA

FEATURES  
source  
1..434  
/organism="ascomycete sp. A77"  
/mol\_type="genomic DNA"  
/strain="A77"  
/isolation\_source="plants grown in greenhouse in  
unsterilized soil collected from Sunset State Beach,  
California"  
/specific\_host="Ammophila arenaria"  
/db\_xref="taxon:227269"  
<1..98  
/product="internal transcribed spacer 1"  
99..247  
/product="5.8S ribosomal RNA"  
248..>434  
/product="internal transcribed spacer 2"

ORIGIN

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Best Local Similarity 94.4%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTGACGGCTCTCGCT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 323 TCTAGTGACGGCTCTCGCT 340

Search completed: October 1, 2004, 05:17:01  
Job time : 149.108 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 23:11:57 ; Search time 31.9347 Seconds  
(without alignment)  
2394.501 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18  
Sequence: 1 tctagtcgacgctcgcct 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

- 1: geneeqn1980s:\*
- 2: geneeqn1990s:\*
- 3: geneeqn2000s:\*
- 4: geneeqn2001as:\*
- 5: geneeqn2001bs:\*
- 6: geneeqn2002s:\*
- 7: geneeqn2003as:\*
- 8: geneeqn2003bs:\*
- 9: geneeqn2003cs:\*
- 10: geneeqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AAV83696	AAV83696 Species-s
2	16.4	91.1	310	AAV70851	AAV70851 Internal
3	16.4	91.1	502	AA61893	AA61893 Fusarium
4	16.4	91.1	534	ACC50001	ACC50001 Internal
5	16.4	91.1	647	ABV78700	ABV78700 C. crassi
6	16.4	91.1	2293	AA616211	AA616211 Fungus ge
7	15.4	85.6	744	AA642796	AA642796 Arabidops
8	15	83.3	386	ACH46296	ACH46296 Human inf
9	15	83.3	432	ADC30089	ADC30089 Human nov
10	15	83.3	449	ACH47075	ACH47075 Human inf
11	15	83.3	473	ACH13812	ACH13812 Human adu
12	15	83.3	1182	AA799142	AA799142 S-adenosy
13	15	83.3	1596	AA888320	AA888320 DNA encod
14	15	83.3	2139	ADC32008	ADC32008 Human nov
15	15	83.3	37160	ABR84372	ABR84372 Human CDN
16	14.8	82.2	403	ABV02791	ABV02791 Human pro
17	14.8	82.2	506	AA088445	AA088445 Human sec
18	14.8	82.2	1502	AA088412	AA088412 Human sec
19	14.8	82.2	198285	ABR84699	ABR84699 Human CDN
20	14.8	82.2	198285	ABN97319	ABN97319 Gene #381
21	14.4	80.0	51	AA174530	AA174530 Human s11
22	14.4	80.0	51	AA174531	AA174531 Human s11
23	14.4	80.0	945	AAH53958	AAH53958 S. epider

C	24	14.4	80.0	1146	4	AAH53831	AAH53831 S. epider
	25	14.4	80.0	2982	4	AAH54021	AAH54021 S. epider
	26	14.4	80.0	3116	4	AAH54884	AAH54884 S. epider
	27	14.4	80.0	46899	2	AAQ54386	AAQ54386 T. niveum
	28	14	77.8	479	4	AAI27255	AAI27255 Probe #17
	29	14	77.8	479	4	ABW75543	ABW75543 Human foe
	30	14	77.8	479	4	AAI56113	AAI56113 Probe #24
	31	14	77.8	479	4	ABA40157	ABA40157 Probe #18
	32	14	77.8	479	4	AAK50175	AAK50175 Human bon
	33	14	77.8	479	4	AAK24114	AAK24114 Human bra
	34	14	77.8	479	4	ABSA4906	ABSA4906 Human liv
	35	14	77.8	479	6	ABSA23648	ABSA23648 Human gen
C	36	14	77.8	489	4	ABA08494	ABA08494 Human FC-
	37	14	77.8	550	4	AAI18119	AAI18119 Probe #80
	38	14	77.8	550	4	ABA63091	ABA63091 Human foe
	39	14	77.8	550	4	AAI43123	AAI43123 Probe #11
	40	14	77.8	550	4	ABA30343	ABA30343 Probe #88
	41	14	77.8	550	4	AAK37292	AAK37292 Human bra
	42	14	77.8	550	4	AAK11513	AAK11513 Human liv
	43	14	77.8	550	4	ABSA6962	ABSA6962 Human liv
	44	14	77.8	550	6	ABSI1282	ABSI1282 Human gen
C	45	14	77.8	615	2	AAQ62632	AAQ62632 Porphyrin

ALIGNMENTS

RESULT 1	AAV83696	AAV83696 standard; DNA; 18 BP.
ID	AAV83696	AAV83696 standard; DNA; 18 BP.
AC	AAV83696;	
XX		
DT	26-FEB-1999	(first entry)
DE	Species-specific probe targeted to the internal transcribed spacer 2.	
XX		
XX	Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus; M. circinalioides; F. circinalioides; Rhizopus oryzae; R. microsporus; R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera; Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum; Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.	
OS	Synthetic.	
OS	Gibberella fujikuroi.	
XX		
XX		
FT	Key	Location/Qualifiers
FT	modified_base	1
XX		/*tag= a
XX		/note= "labelled with digoxigenin"
XX	W09850584-A2.	
PD	12-NOV-1998.	
XX		
XX	01-MAY-1998;	98WO-USO08926.
PF		
XX	02-MAY-1997;	97US-0045400P.
PR		
XX		
XX	(USSH ) US DEPT HEALTH & HUMAN SERVICES.	
PA		
XX	Morrison CJ, Reiss E, Aidorevich L, Choi JS;	
XX	WPI, 1999-034737/03.	
DR		
XX		
XX	New nucleic acid probes for filamentous fungi - for detecting e.g.	
PT	Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia.	
PT	Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix	
PT	species.	
XX		
XX		
PS	Example 1; Page 22; 45pp; English.	

XX Probes AAV83677-708 are derived from the internal transcribed spacer 2 (ITS2) region of various filamentous fungi (see AAV70845-73). The probes are species-specific, and can be used for identifying a species selected from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*, *M. circinelloides* f. *circinelloides*, *Rhizopus oryzae*, *R. microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix schenckii*. The probes can be used for differentiating filamentous fungal species from each other and from other medically important fungi

SQ Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGTACGGTCTCGCT 18  
Db 1 TCTAGTACGGTCTCGCT 18

RESULT 2  
AAV70851  
ID AAV70851 standard; DNA; 310 BP.  
XX AAV70851;  
AC AAV70851;  
XX 17-OCT-2003 (revised)  
DT 26-FEB-1999 (first entry)  
XX Internal transcribed spacer 2 (ITS2) and adjacent regions.

DE Internal transcribed spacer 2 (ITS2) and adjacent regions.

XX Internal transcribed spacer 2; ITS2; probe; *Aspergillus flavus*; *A. niger*; *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*; *Mucor rouxii*; *M. racemosus*; *M. plumbeus*; *M. indicus*; *A. fumigatus*;  
KM *M. circinelloides* f. *circinelloides*; *Rhizopus oryzae*; *R. microsporus*;  
KM *R. circinans*; *R. stolonifer*; *Rhizomucor pusillus*; *Abidia corymbifera*;  
KM *Cunninghamella elegans*; *Pseudallescheria boydii*; *Scedosporium apiospermum*;  
KM *Penicillium notatum*; *Sporothrix schenckii*; filamentous fungus; ss.

XX *Gibberella fujikuroi*.  
OS WO9850584-A2.  
XX  
PN 12-NOV-1998.  
XX  
PD 01-MAY-1998; 98WO-US008926.  
XX  
PF 02-MAY-1997; 97US-0045400P.  
XX  
PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PA Morrison CJ, Reiss E, Aldorevich L, Choi JS;  
XX WPI; 1999-034737/03.  
XX  
DR New nucleic acid probes for filamentous fungi - for detecting e.g.  
XX *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Abidia*,  
PT *Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix*  
PT species.  
XX  
PS Claim 1; Page 12; 45pp; English.  
XX  
CC The present sequence represents an internal transcribed spacer 2 (ITS2)  
CC and adjacent regions. Probes can be derived from the present sequence  
CC which are species-specific. The specification also describes ITS2  
CC sequence-derived probes for identifying a species selected from  
CC *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,  
CC *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,  
CC *M. indicus*, *M. circinelloides* f. *circinelloides*, *Rhizopus oryzae*, *R.*

CC *microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia*  
CC *corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph  
CC of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix*  
CC *schenckii*. The probes can be used for differentiating filamentous fungal  
CC species from each other and from other medically important fungi.  
XX (Updated on 17-OCT-2003 to standardise OS field)

SQ Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 2; Length 310;  
Best Local Similarity 94.4%; Pred. No. 41;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGGTCTCGCT 18  
Db 174 TCTAGTACGGTCTCGCT 191

RESULT 3  
AAA61893  
ID AAA61893 standard; DNA; 502 BP.  
XX AAA61893;  
AC AAA61893;  
XX 15-SEP-2003 (revised)  
DT 14-NOV-2000 (first entry)  
XX *Fusarium* sp. MF6381 rDNA internal transcribed spacer (ITS) region.

DE *Fusarium* sp. MF6381 rDNA internal transcribed spacer (ITS) region.

XX Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469;  
KM HIV integrase inhibitor; steroid compound; human immunodeficiency virus;  
KM acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;  
KM symptomatic infection; asymptomatic infection; potential HIV exposure;  
KM combination therapy; ds.

XX *Fusarium* sp; MF6381.  
OS WO200036132-A1.  
XX  
PN 22-JUN-2000.  
XX  
PD 09-DEC-1999; 99WO-US029356.  
XX  
PF 14-DEC-1998; 98US-0112168P.  
XX  
PR (MERI ) MERCK & CO INC.  
XX  
PA Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;  
XX Dombrowski AW;  
XX WPI; 2000-431606/37.  
XX  
DR New steroid compounds are HIV integrase inhibitors used for treating HIV  
PT infection and AIDS.  
PT  
XX Disclosure; Page 14; 113pp; English.

XX The invention relates to novel steroid compounds derived from the African  
CC soil fungus *Fusarium* sp. MF6381 (ATCC 74469) which act as inhibitors of  
CC HIV integrase. The invention encompasses cultures of *Fusarium* sp. MF6381.  
CC The invention also relates to a composition comprising a compound of the  
CC invention in combination with an AIDS antiviral agent, an immunomodulator  
CC and an anti-infective agent. The compounds of the invention may be used in  
CC the inhibition of HIV integrase and in the prevention and treatment of  
CC HIV infection. A wide range of state of HIV infection may be treated;  
CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex);  
CC both symptomatic and asymptomatic HIV infection; and actual or potential  
CC exposure to HIV. The compounds may be used to isolate HIV integrase  
CC mutants which are potentially useful as screening tools for antiviral  
CC compounds. The compounds may also be used to establish or determine the  
CC site at which other antivirals bind to HIV integrase (e.g., by  
CC competitive inhibition). The present sequence represents the ribosomal  
CC DNA (rDNA) internal transcribed spacer (ITS) region of *Fusarium* sp.

```

CC MF6381, which may be used to characterise MF6381. (Updated on 15-SEP-2003
CC to standardise OS field)
SQ Sequence 502 BP, 127 A; 144 C; 118 G; 113 T; 0 U; 0 Other;
Query Match          91.1%; Score 16.4; DB 3; Length 502;
Best Local Similarity 94.4%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCTAGTGACGGTCTCGCT 18
   ||||| ||||| |||||
Db 371 TCTAGTGCGCGTCTCGCT 388

RESULT 4
ACC50001
ID ACC50001 standard; DNA; 534 BP.
XX
AC ACC50001;
XX
DT 14-JUL-2003 (first entry)
XX
DE Internal transcribed spacer RNA encoding sequence #3.
XX
KM Mitochondria; fungal pathogen; ds.
XX
OS Paearium proliferatum.
XX
PN WO2003027635-A2.
XX
PD 03-APR-2003.
XX
PF 19-SEP-2002; 2002MO-US030311.
XX
PR 24-SEP-2001; 2001US-00961755.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Beck JI, Barnett CJ;
XX
DR WPI; 2003-363229/34.
XX
PT Detecting a fungal pathogen, useful for monitoring disease development,
PT comprises subcloning the DNA to PCR amplification using at least one
PT primer having sequence identity with at least 10 contiguous nucleotides
PT of Fusarium spp.
XX
PS Claim 5; Page 38-39; 44pp; English.
XX
CC This invention relates to the detection of a fungal pathogen comprising
CC isolating DNA from a plant leaf infected with a pathogen. The methods and
CC primers are useful for identifying fungal isolates of fungal pathogens
CC and monitoring of disease development in plant populations. The present
CC sequence represents an internal transcribed spacer RNA encoding sequence
XX
SQ Sequence 534 BP, 135 A; 149 C; 130 G; 120 T; 0 U; 0 Other;
Query Match          91.1%; Score 16.4; DB 7; Length 534;
Best Local Similarity 94.4%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCTAGTGACGGTCTCGCT 18
   ||||| ||||| |||||
Db 402 TCTAGTGCGCGTCTCGCT 419

RESULT 5
ABV78700
ID ABV78700 standard; RNA; 647 BP.
XX
AC ABV78700;
XX
DT 14-JAN-2003 (first entry)

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```

XX
DE C. crassisporea RNA sequence #2.
XX
KM Ribosome ribonucleic acid; RNA; Cordyceps crassisporea; classification;
KM Cordyceps sinensis; ss.
XX
OS Cordyceps crassisporea.
XX
PN JP2002204696-A.
XX
PD 23-JUL-2002.
XX
PF 12-JAN-2001; 2001JP-00004805.
XX
PR 12-JAN-2001; 2001JP-00004805.
XX
PA (HEAL-) HEALTHWAY KK.
XX (KANE//) KANESHIRO N.
XX
DR WPI; 2002-639075/69.
XX
PT Ribosome RNA gene base sequence of Cordyceps sinensis for classification
PT of seeds of Cordyceps sinensis.
XX
PS 2; Page 12; 33pp; Japanese.
XX
CC The invention relates to a novel base sequence which is part of a fully
CC defined ribosome ribonucleic acid (rRNA) gene of Cordyceps crassisporea.
CC The base sequences can be used for the classification of Cordyceps
CC sinensis. The sequence represents a C. crassisporea RNA sequence of the
CC invention
XX
SQ Sequence 647 BP, 166 A; 178 C; 160 G; 143 T; 0 U; 0 Other;
Query Match          91.1%; Score 16.4; DB 6; Length 647;
Best Local Similarity 94.4%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCTAGTGACGGTCTCGCT 18
   ||||| ||||| |||||
Db 418 TCTAGTGCGCGTCTCGCT 435

RESULT 6
AAS16211
ID AAS16211 standard; DNA; 2293 BP.
XX
AC AAS16211;
XX
DT 29-JAN-2002 (first entry)
XX
DE Fungus genomic DNA spanning 18S, 5.8S and 28S rRNA and ITS sequences.
XX
KM Gibberellin; 18S rRNA; internal transcribed spacer region; ITS1; ITS2;
KM 5.8S rRNA; LTR-1027; species differentiation; GA_4; GA_3; GA_7;
KM flowering; fruit cell elongation; apple; pear; grape; fruit;
KM russet control; fungus; ds.
XX
OS Gibberella fujiikuroi.
XX
FH Key
XX Location/Qualifiers
FT misc_feature 1..1774
FT /*tag= a
FT /note= "18S rRNA gene"
FT misc_feature 1775..1921
FT /*tag= b
FT /note= "ITS1 region"
FT misc_feature 1922..2078
FT /*tag= c
FT /note= "5.8S rRNA gene"
FT misc_feature 2079..2243
FT /*tag= d
FT /note= "ITS2 region"

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FT misc_feature 2244..2293
FT /*tag= e
FT /note= "28S rRNA gene"
XX
XX US6287800-B1.
XX
XX 11-SEP-2001.
XX
XX 23-AUG-2000; 2000US-00645073.
XX
XX 31-AUG-1999; 99US-0151770P.
XX
XX (GALL/) GALLIAZZO J L.
XX (LEEM/) LEE M D.
XX
XX Galliazzo JL, Lee MD;
XX WPI; 2001-662197/76.
XX
XX A new method for producing a mixture of gibberellins from Gibberella
PT fujiikuroi results in high titers of GA4 and GA7 useful to promote
PT flowering and fruit growth in the fruit growing industry.
XX
XX Example 4; Col 9-12; 7yp; English.
XX
XX This sequence represents a genomic DNA sequence containing the 18S rRNA
CC gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S
CC rRNA sequences from a mutant strain of Gibberella fujiikuroi (LTB-1027) of
CC the invention. This region of DNA is highly variable and can be used for
CC species and strain differentiation. The LTB-1027 mutant produces a
CC mixture of gibberellins which is at least 70 % GA 4 and GA 7.
CC Gibberellins GA 4 and GA 7 promote flowering and fruit cell elongation,
CC and are used by growers of apples, pears and grapes to produce larger
CC fruits and earlier harvests. The mixture of GA_3, GA 4 and GA 7 achieved
CC using the method of this invention should be particularly useful in the
CC apple industry where GA_4 has been found more effective in russet control
CC and in promoting fruit set. This method produces GA_4 and GA_7 in much
CC higher titers than prior art methods
XX
XX Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 U; 0 Other;
SQ
Query Match 91.1%; Score 16.4; DB 4; Length 2293;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTAGTACGGTCTCGCT 18
Db 2145 TCTAGTGGCGTCTCGCT 2162
RESULT 7
AAC42796
ID AAC42796 standard; DNA; 744 BP.
XX
XX AAC42796;
AC
XX
XX 17-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 36883.
DE
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-00301439.
PF
XX
XX 25-FEB-1999; 99US-0121825P.
PR
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PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 21-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135553P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 18-JUN-1999; 99US-0139454P.
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PR 18-JUN-1999; 99US-0139456P.
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PR 22-JUN-1999; 99US-0139899P.
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PR 28-JUN-1999; 99US-0140823P.
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PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142820P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR 14-JUL-1999; 99US-0143624P.  
 PR 15-JUL-1999; 99US-0144005P.  
 PR 16-JUL-1999; 99US-0144088P.  
 PR 16-JUL-1999; 99US-0144086P.  
 PR 19-JUL-1999; 99US-0144325P.  
 PR 19-JUL-1999; 99US-0144331P.  
 PR 19-JUL-1999; 99US-0144332P.  
 PR 19-JUL-1999; 99US-0144333P.  
 PR 19-JUL-1999; 99US-0144334P.  
 PR 19-JUL-1999; 99US-0144335P.  
 PR 20-JUL-1999; 99US-0144352P.  
 PR 20-JUL-1999; 99US-0144632P.  
 PR 21-JUL-1999; 99US-0144884P.  
 PR 21-JUL-1999; 99US-0145086P.  
 PR 21-JUL-1999; 99US-0145088P.  
 PR 22-JUL-1999; 99US-0145085P.  
 PR 22-JUL-1999; 99US-0145087P.  
 PR 22-JUL-1999; 99US-0145089P.  
 PR 23-JUL-1999; 99US-0145192P.  
 PR 23-JUL-1999; 99US-0145145P.  
 PR 23-JUL-1999; 99US-0145218P.  
 PR 23-JUL-1999; 99US-0145224P.  
 PR 26-JUL-1999; 99US-0145276P.  
 PR 27-JUL-1999; 99US-0145913P.  
 PR 27-JUL-1999; 99US-0145918P.  
 PR 27-JUL-1999; 99US-0145919P.  
 PR 28-JUL-1999; 99US-0145951P.  
 PR 02-AUG-1999; 99US-0146386P.  
 PR 02-AUG-1999; 99US-0146388P.  
 PR 03-AUG-1999; 99US-0146389P.  
 PR 04-AUG-1999; 99US-0147038P.  
 PR 04-AUG-1999; 99US-0147204P.  
 PR 04-AUG-1999; 99US-0147302P.  
 PR 05-AUG-1999; 99US-0147192P.  
 PR 05-AUG-1999; 99US-0147260P.  
 PR 06-AUG-1999; 99US-0147303P.  
 PR 06-AUG-1999; 99US-0147416P.  
 PR 09-AUG-1999; 99US-0147493P.  
 PR 09-AUG-1999; 99US-0147935P.  
 PR 10-AUG-1999; 99US-0148171P.  
 PR 11-AUG-1999; 99US-0148319P.  
 PR 12-AUG-1999; 99US-0148341P.  
 PR 13-AUG-1999; 99US-0148565P.  
 PR 13-AUG-1999; 99US-0148684P.  
 PR 16-AUG-1999; 99US-0149368P.  
 PR 17-AUG-1999; 99US-0149175P.  
 PR 18-AUG-1999; 99US-0149426P.  
 PR 20-AUG-1999; 99US-0149722P.  
 PR 20-AUG-1999; 99US-0149723P.  
 PR 20-AUG-1999; 99US-0149929P.  
 PR 23-AUG-1999; 99US-0149902P.  
 PR 23-AUG-1999; 99US-0149930P.  
 PR 25-AUG-1999; 99US-0150566P.  
 PR 26-AUG-1999; 99US-0150884P.  
 PR 27-AUG-1999; 99US-0151065P.  
 PR 27-AUG-1999; 99US-0151066P.  
 PR 27-AUG-1999; 99US-0151080P.  
 PR 30-AUG-1999; 99US-0151303P.  
 PR 31-AUG-1999; 99US-0151438P.  
 PR 01-SEP-1999; 99US-0151930P.  
 PR 07-SEP-1999; 99US-0152363P.  
 PR 10-SEP-1999; 99US-0153070P.  
 PR 13-SEP-1999; 99US-0153758P.  
 PR 15-SEP-1999; 99US-0154018P.  
 PR 16-SEP-1999; 99US-0154039P.  
 PR 20-SEP-1999; 99US-0154779P.  
 PR 22-SEP-1999; 99US-0155139P.  
 PR 23-SEP-1999; 99US-0155486P.  
 PR 24-SEP-1999; 99US-0156559P.  
 PR 28-SEP-1999; 99US-0156458P.  
 PR 29-SEP-1999; 99US-0156596P.  
 PR 04-OCT-1999; 99US-0157117P.

PR 05-OCT-1999; 99US-0157753P.  
 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
 PR 08-OCT-1999; 99US-0158232P.  
 PR 12-OCT-1999; 99US-0158359P.  
 PR 13-OCT-1999; 99US-0159293P.  
 PR 13-OCT-1999; 99US-0159294P.  
 PR 13-OCT-1999; 99US-0159295P.  
 PR 14-OCT-1999; 99US-0159329P.  
 PR 14-OCT-1999; 99US-0159330P.  
 PR 14-OCT-1999; 99US-0159331P.  
 PR 14-OCT-1999; 99US-0159637P.  
 PR 14-OCT-1999; 99US-0159638P.  
 PR 18-OCT-1999; 99US-0159584P.  
 PR 21-OCT-1999; 99US-0160741P.  
 PR 21-OCT-1999; 99US-0160767P.  
 PR 21-OCT-1999; 99US-0160768P.  
 PR 21-OCT-1999; 99US-0160770P.  
 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
 PR 22-OCT-1999; 99US-0160980P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0160982P.  
 PR 25-OCT-1999; 99US-0161404P.  
 PR 25-OCT-1999; 99US-0161405P.  
 PR 25-OCT-1999; 99US-0161406P.  
 PR 26-OCT-1999; 99US-0161359P.  
 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161992P.  
 PR 28-OCT-1999; 99US-0161993P.  
 PR 29-OCT-1999; 99US-0162124P.

Query Match 85.6%; Score 15.4; DB 3; Length 744;  
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CTAGTGACGCTTCGCT 18  
 Db 218 CTAGTGCCGCTTCGCT 234

RESULT 8  
 ACH46296/c  
 ID ACH46296 standard; cDNA; 386 BP.  
 AC ACH46296;  
 AC ACH46296;  
 DT 13-OCT-2003 (first entry)  
 XX  
 XX Human infant brain cDNA #359.  
 DE Human;  
 XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
 KW genome mapping; biodiversity; genetic disorder.  
 XX Homo sapiens.  
 OS  
 XX  
 PN US2003073623-A1.  
 XX  
 PD 17-Apr-2003.  
 XX  
 PF 30-JUL-2001; 2001US-00918995.  
 XX  
 PR 30-JUL-2001; 2001US-00918995.  
 XX  
 PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 XX  
 PI Dmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX  
DR WPI; 2003-615964/58.  
XX  
XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.  
XX  
PS Claim 1; SEQ ID NO 33508; 44pp; English.  
XX  
CC The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH2769-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docID=20030073623  
CC  
XX  
SQ Sequence 386 BP; 101 A; 105 C; 116 G; 64 T; 0 U; 0 Other;  
Query Match 83.3%; Score 15; DB 8; Length 386;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4 AGTGACGGTCTCGCT 18  
|||  
Db 208 AGTGACGGTCTCGCT 194  
|||  
RESULT 9  
ADCC0089/c  
ID ADC30089 standard; cDNA; 432 BP.  
XX  
AC ADC30089;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human novel cDNA sequence, SEQ ID NO:171.  
XX  
KW Human; diagnostic; drug screening; forensics; gene mapping;  
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;  
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;  
KW ulcers; osteoporosis; autoimmune disease; cancer;  
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;  
KW neuroprotective; antihaemetic; anticoagulant; thrombolytic; vulnery;  
KW antifiber; osteopathic; immunosuppressive; antiinflammatory; cytostatic;  
KW gene therapy; chromosome 6p21.3; Gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003029271-A2.  
XX  
PD 10-APR-2003.  
XX  
PF 24-SEP-2002; 2002WO-US030474.  
XX  
PR 24-SEP-2001; 2001US-0324631P.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehman T;  
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;  
PI Haley-Vicente D, Drmanac RT;

XX  
DR WPI; 2003-371981/35.  
DR P-PSDB; ADC31060.  
XX  
XX New polynucleotide and polypeptide useful for diagnosing, preventing or  
PT treating conditions such as neurodegenerative diseases, anemias, platelet  
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
PT cancer.  
XX  
PS Claim 1; SEQ ID NO 171; 1185pp; English.  
XX  
XX  
CC The invention relates to 971 novel human cDNA sequences (ADC29919-  
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The  
CC invention also relates to nucleic acid sequences over 99% identical with  
CC the novel human cDNAs. The invention additionally encompasses expression  
CC vectors and host cells comprising a nucleic acid of the invention; the  
CC recombinant production of a polypeptide of the invention; an antibody  
CC against a polypeptide of the invention; a method of detecting  
CC polynucleotides or polypeptides of the invention; and methods of  
CC identifying a compound which binds to a polypeptide of the invention. The  
CC invention further discloses methods of preventing, treating or  
CC ameliorating a medical condition; kits comprising polynucleotide probes  
CC and/or monoclonal antibodies for carrying out the methods of the  
CC invention; methods for the identification of compounds that modulate the  
CC expression or activity of the polynucleotide and/or polypeptide; and 767  
CC config sequences corresponding to the cDNA sequences of the invention  
CC (ADC31861-ADC32627) and the polypeptides encoded by the configs (ADC32628  
CC -ADC33394). The nucleic acids and polypeptides of the invention are  
CC useful in diagnostics, drug screening, forensics, gene mapping, in the  
CC identification of mutations responsible for genetic disorders or other  
CC traits, for assessing biodiversity, and in producing many other types of  
CC data and products dependent on DNA and amino acid sequences. They are  
CC also used for treating diseases such as Parkinson's disease, Alzheimer's  
CC disease and other neurodegenerative diseases, anaemia, platelet  
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
CC cancer. The nucleic acids may also be used as hybridisation probes or  
CC primers, and in the recombinant production of a protein. The polypeptides  
CC are also useful in generating antibodies, as molecular weight markers,  
CC and as food supplements. The present sequence represents a specifically  
CC claimed human cDNA sequence of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
XX  
SQ Sequence 432 BP; 118 A; 113 C; 123 G; 78 T; 0 U; 0 Other;  
Query Match 83.3%; Score 15; DB 9; Length 432;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4 AGTGACGGTCTCGCT 18  
|||  
Db 123 AGTGACGGTCTCGCT 109  
|||  
RESULT 10  
ACH47075/c  
ID ACH47075 standard; cDNA; 449 BP.  
XX  
AC ACH47075;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human infant brain cDNA #1138.  
XX  
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
KW genome mapping; biodiversity; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN US2003073623-A1.  
XX  
XX 17-APR-2003.



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XX 30-JUL-2001; 2001US-00918995.
PF
XX
XX 30-JUL-2001; 2001US-00918995.
PR
XX
XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
PI WPI; 2003-615964/58.
XX
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 34287; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 CDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030073623
XX
XX
XX Sequence 449 BP; 118 A; 124 C; 127 G; 77 T; 0 U; 3 Other;
SQ
XX
XX Query Match 83.3%; Score 15; DB 8; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AGTGACGCTCGCT 18
Db 253 AGTGACGCTCGCT 239
XX
XX RESULT 11
ACH13812/c
XX ID ACH13812 standard; cDNA; 473 BP.
XX
XX ACH13812;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human adult brain cDNA #1024.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
XX
XX OS
XX US2003073623-A1.
XX
XX 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX
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XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
PI WPI; 2003-615964/58.
XX
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 1024; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 CDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030073623
XX
XX
XX Sequence 473 BP; 126 A; 121 C; 145 G; 80 T; 0 U; 1 Other;
SQ
XX
XX Query Match 83.3%; Score 15; DB 8; Length 473;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AGTGACGCTCGCT 18
Db 230 AGTGACGCTCGCT 216
XX
XX RESULT 12
AAT99142/c
XX ID AAT99142 standard; cDNA to mRNA; 1182 BP.
XX
XX AAT99142;
XX
XX 26-MAR-1998 (first entry)
XX
XX S-adenosylmethionine synthase 2 gene.
XX
XX S-adenosylmethionine synthase 2 gene; barley; alkali resistant plant;
XX sam2; ss.
XX
XX Hordeum vulgare.
XX
XX OS
XX JP09313186-A.
XX
XX 09-DEC-1997.
XX
XX 28-MAY-1996; 96JP-00133406.
XX
XX 28-MAY-1996; 96JP-00133406.
XX
XX (NIOC ) NIPPON OIL CO LTD.
XX
XX WPI; 1998-080077/08.
XX
XX
```



CC identifying a compound which binds to a polypeptide of the invention. The  
CC invention further discloses methods of preventing, treating or  
CC ameliorating a medical condition; kits comprising polynucleotide probes  
CC and/or monoclonal antibodies for carrying out the methods of the  
CC invention; methods for the identification of compounds that modulate the  
CC expression or activity of the polynucleotide and/or polypeptide; and 767  
CC contig sequences corresponding to the cDNA sequences of the invention  
CC (ADCC31661-ADCC32627) and the polypeptides encoded by the contigs (ADCC32628  
CC -ADCC3394). The nucleic acids and polypeptides of the invention are  
CC useful in diagnostics, drug screening, forensics, gene mapping, in the  
CC identification of mutations responsible for genetic disorders or other  
CC traits, for assessing biodiversity, and in producing many other types of  
CC data and products dependent on DNA and amino acid sequences. They are  
CC also used for treating diseases such as Parkinson's disease, Alzheimer's  
CC disease and other neurodegenerative diseases, anaemia, platelet  
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
CC cancer. The nucleic acids may also be used as hybridisation probes or  
CC primers, and in the recombinant production of a protein. The polypeptides  
CC are also useful in generating antibodies, as molecular weight markers,  
CC and as food supplements. The present sequence represents a human contig  
CC sequence used in an example of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp://ipo.int/pub/published\_pct\_sequences.

XX Sequence 2139 BP; 524 A; 520 C; 567 G; 528 T; 0 U; 0 Other;

Query Match	83.3%	Score 15;	DB 9;	Length 2139;
Best Local Similarity	100.0%;	Pred. No. 2.9e+02;		
Matches 15; Conservative	0;	Mismatches 0;	Gaps 0;	

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QY      4 AGTGACGGTCTCGCT 18
      |||||
Db      123 AGTGACGGTCTCGCT 1937

```

RESULT 15  
ABK84372  
ID ABK84372 standard; cDNA; 37160 BP

AC	ABK84372;	
XX		
DT	14-AUG-2002	(first entry)

DE Human CDNA differentially expressed in granulocytic cells #943.

KM Human/ISS: granulocytic cell; DNA chip; bacterial infection;  
KM viral infection; parasitic infection; protozoal infection;  
KM fungal infection; sterile inflammatory disease; psoriasis;  
KM rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
KM cardiac reperfusion injury; renal reperfusion injury; ARDS;  
KM adult respiratory distress syndrome; inflammatory bowel disease;  
KM Crohn's disease; ulcerative colitis; periodontal disease;  
KM granulocyte activation; chronic inflammation; allergy.

**OS Homo sapiens.**

PN WO200228999-A2

PD 11-APR-2002

PF 03-OCT-2001; 2001WO-US030821.

PR 03-OCT-2000; 2000US-0237189P.

PA (GENE-) GENE LOGIC INC.

PI Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;

DR WPI; 2002-435328/46.

**PT** Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic

PT markers that is useful for monitoring disease states and drug toxicity  
XX  
PS Claim 1; SEQ ID NO 943; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GC; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, AIDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Wipo at <http://wipo.int/publ/publseq>

Sequence 37160 BP; 10453 A; 8097 C; 8175 G; 10435 T; 0 U; 0 Other;

Query Match	83.3%	Score 15;	DB 6;	Length 37160;
Best Local Similarity	100.0%	Pred. No. 3.8e+02;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 4 AGTGACGGTCTCGCT 18  
|||  
Db 11663 AGTGACGGTCTCGCT 11677

Search completed: October 1, 2004, 03:41:10  
Job time : 38.9347 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:09:43 ; Search time 5.93182 Seconds  
(without alignments)  
1683.989 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtcacgcttcgct 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq: \*  
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6: /cgn2\_6/ptodata/2/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	16.4	91.1	310	4	US-09-423-233-7
3	16.4	91.1	583	1	US-08-652-127C-8
4	16.4	91.1	594	1	US-08-652-127C-5
5	16.4	91.1	2293	3	US-09-645-073-1
6	14.8	82.2	531	1	US-08-652-127C-7
7	14.8	82.2	581	1	US-08-652-127C-6
8	14.4	80.0	1629	4	US-09-252-991A-2042
9	14.4	80.0	1908	4	US-09-252-991A-1914
10	14.4	80.0	4689	1	US-08-471-119A-1
11	14	77.8	636	2	US-08-737-129A-1
12	14	77.8	639	4	US-09-170-769A-1
13	14	77.8	645	4	US-09-170-769A-5
14	14	77.8	666	2	US-08-737-129A-5
15	14	77.8	717	5	PCT-US94-14106-58
16	14	77.8	735	5	PCT-US94-14106-50
17	14	77.8	735	5	PCT-US94-14106-54
18	14	77.8	777	2	US-08-860-882A-25
19	14	77.8	777	4	US-09-011-769A-20
20	14	77.8	798	1	US-08-133-011-99
21	14	77.8	798	1	US-08-322-730A-99
22	14	77.8	798	1	US-08-387-874-71
23	14	77.8	798	1	US-08-383-619-99
24	14	77.8	798	3	US-08-907-739-99
25	14	77.8	798	4	US-09-729-597-99
26	14	77.8	798	5	PCT-US93-08364-71
27	14	77.8	830	1	US-08-133-011-115

C 28	14	77.8	830	1	US-08-322-730A-115	Sequence 115, App
C 29	14	77.8	830	1	US-08-387-874-88	Sequence 88, Appl
C 30	14	77.8	830	3	US-08-383-619-115	Sequence 115, App
C 31	14	77.8	830	3	US-08-907-739-115	Sequence 115, App
C 32	14	77.8	830	4	US-09-729-597-115	Sequence 88, Appl
C 33	14	77.8	830	5	PCT-US93-08364-88	Sequence 1, Appl
C 34	14	77.8	923	5	PCT-US94-07659-1	Sequence 1514, Ap
C 35	14	77.8	1077	4	US-09-489-039A-1514	Patent No. 5455030
C 36	14	77.8	1347	6	5455030-2	Sequence 19, Appl
C 37	14	77.8	1443	3	US-08-403-853-19	Sequence 130, App
C 38	14	77.8	1446	2	US-09-171-945-130	Sequence 23, Appl
C 39	14	77.8	1572	1	US-08-353-400-23	Sequence 8, Appl
C 40	14	77.8	1632	2	US-08-792-824-8	Sequence 5, Appl
C 41	14	77.8	1641	2	US-08-792-824-5	Sequence 2, Appl
C 42	14	77.8	1672	2	US-08-792-824-2	Sequence 17, Appl
C 43	14	77.8	1797	1	US-08-442-542-17	Sequence 17, Appl
C 44	14	77.8	1797	3	US-08-765-469-17	Sequence 6, Appl
C 45	14	77.8	1800	2	US-08-579-940-6	

#### ALIGNMENTS

```
RESULT 1
US-09-423-233-49
Sequence 49, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 49
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-09-423-233-49

Query Match      100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1  TCTAGTACGCTTCGCT 18
Db      1  TCTAGTACGCTTCGCT 18

RESULT 2
US-09-423-233-7
Sequence 7, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 310
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-09-423-233-7

Query Match      91.1%; Score 16.4; DB 4; Length 310;
Best Local Similarity 94.4%; Pred. No. 6.3;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 TCTAGTACGGTCTCGCT 18  
|||||  
Db 174 TCTAGTACGGTCTCGCT 191

## RESULT 3

US-08-652-127C-8  
; Sequence 8, Application US/08652127C  
; Patent No. 5792611  
; GENERAL INFORMATION:  
; APPLICANT: Richard C. Hamelin  
; TITLE OF INVENTION: DETECTION OF PLANT  
; TITLE OF INVENTION: PATHOGEN FUNGI  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: George A. Seaby  
; ADDRESSEE: Seaby & Maclean  
; STREET: 880 Wellington Street, Suite 708  
; CITY: Ottawa  
; COUNTRY: Canada  
; ZIP: K1R 6K7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,127C  
; FILING DATE: May 23, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: George A. Seaby  
; REGISTRATION NUMBER: 24,034  
; REFERENCE/DOCKET NUMBER: 1898  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (613) 232-5815  
; TELEFAX: (613) 232-5831  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 583  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-652-127C-8

Query Match 91.1%; Score 16.4; DB 1; Length 583;  
Best Local Similarity 94.4%; Pred. No. 6.6;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGGTCTCGCT 18  
|||||  
Db 429 TCTAGTACGGTCTCGCT 446

## RESULT 4

US-08-652-127C-5  
; Sequence 5, Application US/08652127C  
; Patent No. 5792611  
; GENERAL INFORMATION:  
; APPLICANT: Richard C. Hamelin  
; TITLE OF INVENTION: DETECTION OF PLANT  
; TITLE OF INVENTION: PATHOGEN FUNGI  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: George A. Seaby  
; ADDRESSEE: Seaby & Maclean  
; STREET: 880 Wellington Street, Suite 708  
; CITY: Ottawa  
; COUNTRY: Canada  
; ZIP: K1R 6K7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,127C  
; FILING DATE: May 23, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: George A. Seaby  
; REGISTRATION NUMBER: 24,034  
; REFERENCE/DOCKET NUMBER: 1898  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (613) 232-5815  
; TELEFAX: (613) 232-5831  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 594  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-08-652-127C-5

Query Match 91.1%; Score 16.4; DB 1; Length 594;  
Best Local Similarity 94.4%; Pred. No. 6.6;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGGTCTCGCT 18  
|||||  
Db 439 TCTAGTACGGTCTCGCT 456

## RESULT 5

US-09-645-073-1  
; Sequence 1, Application US/09645073  
; Patent No. 6287800  
; GENERAL INFORMATION:  
; APPLICANT: Lee, May  
; APPLICANT: Galazzo, Jorge  
; TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7  
; FILE REFERENCE: L02-01NP  
; CURRENT APPLICATION NUMBER: US/09/645,073  
; CURRENT FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,770  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 2293  
; TYPE: DNA  
; ORGANISM: Gibberella fujikuroi  
; US-09-645-073-1

Query Match 91.1%; Score 16.4; DB 3; Length 2293;  
Best Local Similarity 94.4%; Pred. No. 7.5;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTACGGTCTCGCT 18  
|||||  
Db 2145 TCTAGTACGGTCTCGCT 2162

## RESULT 6

US-08-652-127C-7  
; Sequence 7, Application US/08652127C  
; Patent No. 5792611  
; GENERAL INFORMATION:  
; APPLICANT: Richard C. Hamelin  
; TITLE OF INVENTION: DETECTION OF PLANT  
; TITLE OF INVENTION: PATHOGEN FUNGI  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: George A. Seaby  
; ADDRESSEE: Seaby & Maclean

STREET: 880 Wellington Street, Suite 708  
CITY: Ottawa  
COUNTRY: Canada  
ZIP: K1R 6K7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,127C  
FILING DATE: May 23, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George A. Seaby  
REGISTRATION NUMBER: 24,034  
REFERENCE/DOCKET NUMBER: 1898  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (613) 232-5815  
TELEFAX: (613) 232-5831  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 531  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-652-127C-7

Query Match 82.2%; Score 14.8; DB 1; Length 531;  
Best Local Similarity 88.9%; Pred. No. 49;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTAGTACGGTCTCGCT 18  
|||  
Db 377 TATAGTGGCGGTCTCGCT 394

RESULT 7  
US-08-652-127C-6  
Sequence 6, Application US/08652127C  
Patent No. 5792611  
GENERAL INFORMATION:  
APPLICANT: Richard C. Hamelin  
TITLE OF INVENTION: DETECTION OF PLANT  
TITLE OF INVENTION: PATHOGEN FUNGI  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: George A. Seaby  
ADDRESS: Seaby & Maclean  
STREET: 880 Wellington Street, Suite 708  
CITY: Ottawa  
COUNTRY: Canada  
ZIP: K1R 6K7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,127C  
FILING DATE: May 23, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George A. Seaby  
REGISTRATION NUMBER: 24,034  
REFERENCE/DOCKET NUMBER: 1898  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (613) 232-5815  
TELEFAX: (613) 232-5831  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 581  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-652-127C-6

Query Match 82.2%; Score 14.8; DB 1; Length 581;  
Best Local Similarity 88.9%; Pred. No. 49;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTAGTACGGTCTCGCT 18  
|||  
Db 427 TATAGTGGCGGTCTCGCT 444

RESULT 8  
US-09-252-991A-2042  
Sequence 2042, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 2042  
LENGTH: 1629  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-2042

Query Match 80.0%; Score 14.4; DB 4; Length 1629;  
Best Local Similarity 93.8%; Pred. No. 89;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TAGTGACGGTCTCGCT 18  
|||  
Db 440 TACTGACGGTCTCGCT 455

RESULT 9  
US-09-252-991A-1914/c  
Sequence 1914, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 1914  
LENGTH: 1908  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-1914

Query Match 80.0%; Score 14.4; DB 4; Length 1908;  
Best Local Similarity 93.8%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TAGTGACGGTCTCGCT 18  
|||  
Db 1286 TACTGACGGTCTCGCT 1271

```
RESULT 10
US-08-471-119A-1
; Sequence 1, Application US/08471119A
; Patent No. 5827706
; GENERAL INFORMATION:
; APPLICANT: Letner, Ernst
; APPLICANT: Schneider, Elisabeth
; APPLICANT: Schoerendorfer, Kurt
; APPLICANT: Weber, Gerhard
; TITLE OF INVENTION: Cyclosporin Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827706artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,119A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kasenoff, Melvyn
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 503 8474
; TELEFAX: 201 503 8807
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46899 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tolypocladium niveum
; STRAIN: ATCC 34921
; US-08-471-119A-1

Query Match      80.0%; Score 14.4; DB 1; Length 46899;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTAGTACGGTCTCGC 17
Db      15595 CTGCTACGGTCTCGC 15610

RESULT 11
US-08-737-129A-1/c
; Sequence 1, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
```

```
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 588516ember 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TEXT:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-737-129A-1
```

```
Query Match      77.8%; Score 14; DB 2; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GTGACGGTCTCGCT 18
Db      566 GTGACGGTCTCGCT 553
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```
RESULT 12
US-09-170-769A-1/c
; Sequence 1, Application US/09170769A
; Patent No. 6444206
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier
; APPLICANT: MORIATRY, Ann
; APPLICANT: ULEVITCH, Richard
; APPLICANT: TOBIAS, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
; FILE REFERENCE: SCRIP1140-3
; CURRENT APPLICATION NUMBER: US/09/170,769A
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/070,160
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(639)
; US-09-170-769A-1
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```
Query Match      77.8%; Score 14; DB 4; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GTGACGGTCTCGCT 18
|||||
```



Db 590 GTGACGGTCTCGCT 577

RESULT 13

US-09-170-769A-5/c  
Sequence 5, Application US/09170769A  
Patent No. 6444206  
GENERAL INFORMATION:  
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
APPLICANT: LETURCO, Didier  
APPLICANT: MORIATRY, Ann  
APPLICANT: ULAVITCH, Richard  
APPLICANT: TOBIAS, Peter  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA  
FILE REFERENCE: SCRIPT140-3  
CURRENT APPLICATION NUMBER: US/09/170,769A  
CURRENT FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: US 08/070,160  
PRIOR FILING DATE: 1993-05-28  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 645  
TYPE: DNA  
ORGANISM: Murine  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(645)  
OTHER INFORMATION: CDR1=Nucleic acids 85-99; CDR2=Nucleic acids 142-189; CDR3=Nuclei  
US-09-170-769A-5

Query Match 77.8%; Score 14; DB 4; Length 645;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTGACGGTCTCGCT 18  
Db 596 GTGACGGTCTCGCT 583

RESULT 14  
US-08-737-129A-5/c  
Sequence 5, Application US/08737129A  
Patent No. 5885816  
GENERAL INFORMATION:  
APPLICANT: IKUO FUJII et al.  
TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY  
TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/737,129A  
FILING DATE: No. 5885816ember 15, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 666 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-737-129A-5

Query Match 77.8%; Score 14; DB 2; Length 666;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTGACGGTCTCGCT 18  
Db 596 GTGACGGTCTCGCT 583

RESULT 15  
PCT-US94-14106-58/c  
Sequence 58, Application PC/TUS9414106  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Process for Generating Specific Antibodies  
NUMBER OF SEQUENCES: 61  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/14106  
FILING DATE:  
CLASSIFICATION:  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 717 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 67..717  
PCT-US94-14106-58

Query Match 77.8%; Score 14; DB 5; Length 717;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTGACGGTCTCGCT 18  
Db 653 GTGACGGTCTCGCT 640

Search completed: October 1, 2004, 08:05:42  
Job time : 7.93182 secs

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:20:11 ; Search time 73.304 Seconds  
(without alignments)  
1244.847 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtcagcgtctgcgt 18

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
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11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
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17: /cgn2\_6/ptodata/1/pubpna/US10C\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	15	US-10-046-955-49
2	16.4	91.1	310	15	US-10-046-955-7
3	16.4	91.1	534	10	US-09-961-755A-7
4	15	83.3	386	10	US-09-918-995-33508
5	15	83.3	449	10	US-09-918-995-34287
6	15	83.3	473	10	US-09-918-995-1024
7	14.8	82.2	388	13	US-10-424-599-44516
8	14.8	82.2	558	17	US-10-437-963-74582
9	14.8	82.2	599	13	US-10-027-632-215234
10	14.8	82.2	599	13	US-10-027-632-215235
11	14.8	82.2	599	16	US-10-027-632-215234
12	14.8	82.2	599	16	US-10-027-632-215235
13	14.8	82.2	675	17	US-10-767-701-8208
14	14.8	82.2	3461	17	US-10-437-963-82331

15	14.8	82.2	28573	17	US-10-741-601-5769	Sequence 5769, Ap
16	14.8	82.2	60500	13	US-10-087-192-1024	Sequence 1024, Ap
17	14.8	82.2	75839	13	US-10-087-192-166	Sequence 166, Ap
18	14.8	82.2	198285	9	US-09-880-107-3814	Sequence 3814, Ap
19	14.8	82.2	198285	17	US-10-775-169-338	Sequence 338, App
20	14	77.8	479	9	US-09-864-761-25477	Sequence 25477, A
21	14	77.8	489	13	US-10-276-774-270	Sequence 270, App
22	14	77.8	550	9	US-09-864-761-8809	Sequence 8809, Ap
23	14	77.8	613	17	US-10-767-701-24494	Sequence 24494, A
24	14	77.8	666	17	US-10-679-620-81	Sequence 81, Appl
25	14	77.8	672	16	US-10-410-907A-35	Sequence 35, Appl
26	14	77.8	736	14	US-10-006-773-12	Sequence 12, Appl
27	14	77.8	741	16	US-10-251-215-48	Sequence 48, Appl
28	14	77.8	798	16	US-10-273-973-99	Sequence 99, Appl
29	14	77.8	830	16	US-10-273-973-115	Sequence 115, App
30	14	77.8	1056	17	US-10-134-188-30	Sequence 30, Appl
31	14	77.8	1314	9	US-09-903-327A-5	Sequence 5, Appl1
32	14	77.8	1353	17	US-10-679-620-77	Sequence 77, Appl
33	14	77.8	1371	17	US-10-719-642-82	Sequence 82, Appl
34	14	77.8	1383	17	US-10-719-642-95	Sequence 95, Appl
35	14	77.8	1383	17	US-10-719-642-96	Sequence 96, Appl
36	14	77.8	1386	15	US-10-281-479A-21	Sequence 21, Appl
37	14	77.8	1386	15	US-10-286-132A-21	Sequence 21, Appl
38	14	77.8	1398	15	US-10-275-180A-21	Sequence 21, Appl
39	14	77.8	1445	17	US-10-679-620-71	Sequence 71, Appl
40	14	77.8	1446	9	US-09-910-059-130	Sequence 130, App
41	14	77.8	1516	9	US-09-903-327A-1	Sequence 1, Appl1
42	14	77.8	1636	17	US-10-767-701-13810	Sequence 13810, A
43	14	77.8	1671	17	US-10-679-620-85	Sequence 85, Appl
44	14	77.8	1701	9	US-09-815-837-62	Sequence 62, Appl
45	14	77.8	1707	9	US-09-815-837-64	Sequence 64, Appl

#### ALIGNMENTS

RESULT 1  
US-10-046-955-49  
Sequence 49, Application US/10046955  
Publication No. US20030129600A1  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America, as Represented by the  
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease  
APPLICANT: Control and Prevention  
APPLICANT: Morrison, Christine J.  
APPLICANT: Reiss, Errol  
APPLICANT: Aidorevich, Lilianna  
APPLICANT: Choi, Jong Soo  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
TITLE OF INVENTION: Other Filamentous Fungi  
FILE REFERENCE: 6395-62064  
CURRENT APPLICATION NUMBER: US/10/046,955  
CURRENT FILING DATE: 2002-06-04  
PRIOR APPLICATION NUMBER: US 09/423,233  
PRIOR FILING DATE: 2000-06-27  
PRIOR APPLICATION NUMBER: PCT/US98/08926  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: US 60/045,400  
PRIOR FILING DATE: 1997-05-02  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 49  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Fusarium moniliforme  
US-10-046-955-49  
Query Match 100.0%; Score 18; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.4; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0;  
1 TCTAGTCAGCCTCGCT 18  
|||||

Db 1 TCTAGTGACGGTCTCGCT 18

## RESULT 2

US-10-046-955-7  
; Sequence 7, Application US/10046955  
; Publication No. US20030128600A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as Represented by the  
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis  
; APPLICANT: Control and Prevention  
; APPLICANT: Morrison, Christine J.  
; APPLICANT: Reiss, Errol  
; APPLICANT: Aldorevich, Liliانا  
; APPLICANT: Choi, Jong Soo  
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
; TITLE OF INVENTION: Other Filamentous Fungi  
; FILE REFERENCE: 6395-62064  
; CURRENT APPLICATION NUMBER: US/10/046,955  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 09/423,233  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: PCT/US98/08926  
; PRIOR FILING DATE: 1998-05-01  
; PRIOR APPLICATION NUMBER: US 60/045,400  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 310  
; TYPE: DNA  
; ORGANISM: Fusarium moniliforme  
US-10-046-955-7

Query Match 91.1%; Score 16.4; DB 15; Length 310;  
Best Local Similarity 94.4%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTGACGGTCTCGCT 18  
|||||  
Db 174 TCTAGTGACGGTCTCGCT 191

## RESULT 3

US-09-961-755A-7  
; Sequence 7, Application US/09961755A  
; Publication No. US20030113722A1  
; GENERAL INFORMATION:  
; APPLICANT: Beck, Jim  
; APPLICANT: Barnett, Jason  
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; FILE REFERENCE: 60055  
; CURRENT APPLICATION NUMBER: US/09/961,755A  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 534  
; TYPE: DNA  
; ORGANISM: Fusarium proliferatum  
US-09-961-755A-7

Query Match 91.1%; Score 16.4; DB 10; Length 534;  
Best Local Similarity 94.4%; Pred. No. 55;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCTAGTGACGGTCTCGCT 18  
|||||  
Db 402 TCTAGTGACGGTCTCGCT 419

## RESULT 4

US-09-918-995-33508/C  
; Sequence 33508, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33508  
; LENGTH: 386  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-33508

Query Match 83.3%; Score 15; DB 10; Length 386;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTGACGGTCTCGCT 18  
|||||  
Db 208 AGTGACGGTCTCGCT 194

## RESULT 5

US-09-918-995-34287/C  
; Sequence 34287, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 34287  
; LENGTH: 449  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(449)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-34287

Query Match 83.3%; Score 15; DB 10; Length 449;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTGACGGTCTCGCT 18  
|||||  
Db 253 AGTGACGGTCTCGCT 239

## RESULT 6

US-09-918-995-1024/C  
; Sequence 1024, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995

;; CURRENT FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: US/09/235,076  
;; PRIOR FILING DATE: 1999-01-20  
;; NUMBER OF SEQ ID NOS: 38054  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 1024  
;; LENGTH: 473  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(473)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-1024

Query Match 83.3%; Score 15; DB 10; Length 473;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AGTGACGGCTCTCGCT 18  
DB 230 AGTGACGGCTCTCGCT 216

RESULT 7  
US-10-424-599-44516  
;; Sequence 44516, Application US/10424599  
;; Publication No. US20040031072A1  
;; GENERAL INFORMATION:  
;; APPLICANT: La Rosa Thomas J  
;; APPLICANT: Kovalic David K  
;; APPLICANT: Zhou Yihua  
;; APPLICANT: Cao Yongwei  
;; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
;; FILE REFERENCE: 38-21(53223)B  
;; CURRENT APPLICATION NUMBER: US/10/424,599  
;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 285684  
;; SEQ ID NO 44516  
;; LENGTH: 388  
;; TYPE: DNA  
;; ORGANISM: Glycine max  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_140197C.1  
US-10-424-599-44516

Query Match 82.2%; Score 14.8; DB 13; Length 388;  
Best Local Similarity 88.9%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TCTAGTACGGCTCTCGCT 18  
DB 319 TTTACTGACGGCTCTCGCT 336

RESULT 8  
US-10-437-963-74582/C  
;; Sequence 74582, Application US/10437963  
;; Publication No. US20040123343A1  
;; GENERAL INFORMATION:  
;; APPLICANT: La Rosa, Thomas J.  
;; APPLICANT: Kovalic, David K.  
;; APPLICANT: Zhou, Yihua  
;; APPLICANT: Cao, Yongwei  
;; APPLICANT: Wu, Wei  
;; APPLICANT: Boukharov, Andrey A.  
;; APPLICANT: Barbazuk, Brad  
;; APPLICANT: Li, Ping  
;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
;; FILE REFERENCE: 38-21(53221)B  
;; CURRENT APPLICATION NUMBER: US/10/437,963

;; CURRENT FILING DATE: 2003-05-14  
;; NUMBER OF SEQ ID NOS: 204966  
;; SEQ ID NO 74582  
;; LENGTH: 558  
;; TYPE: DNA  
;; ORGANISM: Oryza sativa  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_74754C.1  
US-10-437-963-74582

Query Match 82.2%; Score 14.8; DB 17; Length 558;  
Best Local Similarity 88.9%; Pred. No. 3.9e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TCTAGTACGGCTCTCGCT 18  
DB 504 TCTAGACGGCTCTCGCT 487

RESULT 9  
US-10-027-632-215234  
;; Sequence 215234, Application US/10027632  
;; Publication No. US20020198371A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
;; TITLE OF INVENTION: Polymorphisms in the Human Genome  
;; FILE REFERENCE: 108827.129  
;; CURRENT APPLICATION NUMBER: US/10/027,632  
;; CURRENT FILING DATE: 2002-04-30  
;; PRIOR APPLICATION NUMBER: US 60/218,006  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: US 60/198,676  
;; PRIOR FILING DATE: 2000-04-20  
;; PRIOR APPLICATION NUMBER: US 60/193,483  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 215234  
;; LENGTH: 599  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-215234

Query Match 82.2%; Score 14.8; DB 13; Length 599;  
Best Local Similarity 88.9%; Pred. No. 3.9e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TCTAGTACGGCTCTCGCT 18  
DB 206 TCTAGACGGCTCTCGCT 223

RESULT 10  
US-10-027-632-215235  
;; Sequence 215235, Application US/10027632  
;; Publication No. US20020198371A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
;; TITLE OF INVENTION: Polymorphisms in the Human Genome  
;; FILE REFERENCE: 108827.129  
;; CURRENT APPLICATION NUMBER: US/10/027,632  
;; CURRENT FILING DATE: 2002-04-30  
;; PRIOR APPLICATION NUMBER: US 60/218,006

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; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215235
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215235
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Query Match      82.2%; Score 14.8; DB 13; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 TCTAGTACGCGTCTCGCT 18
      ||||| ||||| ||||| |||||
Db      206 TCTAGAGACGCTGTGGCT 223
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RESULT 11
US-10-027-632-215234
; Sequence 215234, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215234
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215234
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Query Match      82.2%; Score 14.8; DB 16; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 TCTAGTACGCGTCTCGCT 18
      ||||| ||||| ||||| |||||
Db      206 TCTAGAGACGCTGTGGCT 223
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RESULT 12

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US-10-027-632-215235
; Sequence 215235, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215235
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215235
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Query Match      82.2%; Score 14.8; DB 16; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 TCTAGTACGCGTCTCGCT 18
      ||||| ||||| ||||| |||||
Db      206 TCTAGAGACGCTGTGGCT 223
```

```

RESULT 13
US-10-767-701-8208
; Sequence 8208, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; PRIOR FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 8208
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS29720_1
US-10-767-701-8208
```

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Query Match      82.2%; Score 14.8; DB 17; Length 675;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 TCTAGTACGCGTCTCGCT 18
      ||||| ||||| ||||| |||||
Db      361 TCTGTGACGCGTCTACT 378
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RESULT 14

```

US-10-437-963-82321
; Sequence 82321, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 82321
; LENGTH: 3461
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81762C.1
US-10-437-963-82321

```

```

Query Match      82.2%; Score 14.8; DB 17; Length 3461;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

Oy      1 TCTAGTGACGGTCTCGCT 18
          |||||
Db      2359 TCTAGTGATGCTCTTGCT 2376

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RESULT 15
US-10-741-601-5769
; Sequence 5769, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: C0001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5769
; LENGTH: 28573
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-5769

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Query Match      82.2%; Score 14.8; DB 17; Length 28573;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy      1 TCTAGTGACGGTCTCGCT 18
          |||||
Db      27720 TCTGAGACGGTCTCGCT 27737

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Search completed: October 1, 2004, 08:53:45
Job time : 75.304 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 ; Search time 252 Seconds

(without alignments)  
2133.013 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtcagcgtcgcgt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estov:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hrc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hrc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrt1:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	621	14	CF947869
2	16.4	91.1	855	29	CG856355
3	16.4	91.1	870	29	CG856546
4	16.4	91.1	936	29	CNS03M43

Result No.	Score	Query Match	Length	ID	Description
5	16	88.9	714	29	CC623601
6	16	88.9	784	29	CG416849
7	16	88.9	817	29	CC623607
8	16	88.9	955	28	B2819718
9	16	88.9	986	28	B2819712
10	15.4	85.6	464	14	CA991730
11	15.4	85.6	481	28	BH625357
12	15.4	85.6	486	10	BE784335
13	15.4	85.6	571	14	CD317267
14	15.4	85.6	626	12	BJ130132
15	15.4	85.6	629	12	BJ147480
16	15.4	85.6	665	29	CG740356
17	15.4	85.6	670	29	CG807448
18	15.4	85.6	680	29	CC640679
19	15.4	85.6	703	5	AU004847
20	15.4	85.6	710	29	CC640688
21	15.4	85.6	718	9	AV398645
22	15.4	85.6	738	29	CC623422
23	15.4	85.6	809	29	CG231200
24	15.4	85.6	811	14	CK240384
25	15.4	85.6	821	28	B2647230
26	15.4	85.6	858	29	CG35667
27	15.4	85.6	868	29	CC621659
28	15.4	85.6	882	28	B2706123
29	15.4	85.6	883	28	CC348570
30	15.4	85.6	930	29	CG186978
31	15.4	85.6	1005	12	BG760845
32	15.4	85.6	1311	12	BG757034
33	15	83.3	112	9	AV940706
34	15	83.3	168	9	AV922948
35	15	83.3	241	9	AA324668
36	15	83.3	256	9	AA367189
37	15	83.3	276	9	AA339193
38	15	83.3	292	12	BM709519
39	15	83.3	329	10	AW351943
40	15	83.3	360	9	AJ464008
41	15	83.3	360	9	AJ464010
42	15	83.3	360	9	AJ467366
43	15	83.3	360	9	AJ468366
44	15	83.3	360	29	TA301806P
45	15	83.3	362	14	N49663

## ALIGNMENTS

RESULT 1  
LOCUS CF947869/c  
DEFINITION UI-D-GC1-aag-p-10-0-UI.81 UI-D-GC1 Alexandrium tamarense cDNA clone  
ACCESSION CF947869  
VERSION CF947869.1 GI:38452687  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

CF947869 621 bp mRNA linear EST 19-NOV-2003  
UI-D-GC1-aag-p-10-0-UI.81 UI-D-GC1 Alexandrium tamarense cDNA clone  
CF947869  
CF947869.1 GI:38452687  
EST.  
Alexandrium tamarense  
Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Gonyaulacaceae;  
Alexandrium.  
1 (bases 1 to 621)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Provasoli-Guillard National Center for Culture



RESULT 4  
CNS03M43  
LOCUS  
DEFINITION  
936 bp DNA linear GSS 01-SEP-2000  
Tetrarodon nigroviridis genome survey sequence T7 end of clone  
037103 of library G from Tetrarodon nigroviridis, genomic survey  
sequence.

ACCESSION  
AL250284.1 GI:7971296  
VERSION  
GSS; genome survey sequence.  
KEYWORDS  
Tetrarodon nigroviridis  
SOURCE  
Tetrarodon nigroviridis  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE  
1  
Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fitzames,C., Wincker,P., Brotier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence  
Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL  
MEDLINE  
20296633  
PUBMED  
10835645

REFERENCE  
2  
Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Costaz,C.,  
Fitzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,  
Saurin,W., Bernot,A. and Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Genome Res. 10 (7), 939-949 (2000)

JOURNAL  
MEDLINE  
20359837  
PUBMED  
10899143

REFERENCE  
3 (bases 1 to 936)  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr  
This sequence is a single read and was generated as part of a large  
scale clone-and-sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/tetraodon.

COMMENT  
Location/Qualifiers  
1..936  
/organism="Tetrarodon nigroviridis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:99883"  
/clone="037103"  
/clone\_11b="G"  
/note="Genoscope sequence ID : COBG037AE02LP1-end : T7"

FEATURES  
source

ORIGIN  
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Best Local Similarity 94.4%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  
1 TCTAGTGACGCTCGCT 18  
|||  
168 TCCAGTACGCTCTCGCT 185

Db

RESULT 5  
CC623601  
LOCUS  
DEFINITION  
714 bp DNA linear GSS 19-JUN-2003  
OGVAZ30TH ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMMBMA0493E12,  
genomic survey sequence.  
ACCESSION  
CC623601  
VERSION  
CC623601.1 GI:31990367  
KEYWORDS  
GSS.  
SOURCE  
Zea mays

ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 714)  
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGVAZ30TV  
Contact: Cathy Whitelaw  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.

FEATURES  
source  
Location/Qualifiers  
1..714  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
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/clone\_11b="ZM\_0.7\_1.5\_KB"  
/note="Vector: pBCKR-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN  
Query Match 88.9%; Score 16; DB 29; Length 714;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  
3 TAGTGACGCTCGCT 18  
|||  
447 TAGTGACGCTCGCT 462

Db

RESULT 6  
CG416849  
LOCUS  
DEFINITION  
784 bp DNA linear GSS 22-SEP-2003  
ZMMBMA0026J18f ZMMBc (EcORI) Zea mays subsp. mays genomic clone  
ZMMBc0026J18 5', genomic survey sequence.  
ACCESSION  
CG416849  
VERSION  
CG416849.1 GI:34561694  
KEYWORDS  
GSS.  
ORGANISM  
Zea mays subsp. mays (maize)  
Zea mays subsp. mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 784)  
Bharti,A.K., Young,S., Kavchok,S., Keiser,G., Bronzino,A.C.,  
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.  
Sequencing of the maize genome at PCR (2003c)  
Unpublished (2003)  
Contact: Bharti,A.K.  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: T7  
Class: BAC ends  
High quality sequence start: 407.  
Location/Qualifiers  
1..784  
/organism="Zea mays subsp. mays"  
/mol\_type="genomic DNA"

FEATURES  
source

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ORIGIN
Query Match      88.9%; Score 16; DB 29; Length 784;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TAGTACGGTCTCGCT 18
      |||||
      586 TAGTACGGTCTCGCT 601

RESULT 7
CC623607/c      817 bp      DNA      linear      GSS 19-JUN-2003
LOCUS           CC623607
DEFINITION      OGVAZ30TV_ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0493E12,
ACCESSION       CC623607
VERSION         CC623607.1
KEYWORDS        GSS.
SOURCE          Zea mays
ORGANISM        Zea mays
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                clade; Panicoidae; Andropogoneae; Zea.
                1 (bases 1 to 817)
                Whiteaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
                Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Konliff,T.,
                Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.
                Consortium for Maize Genomics
                Unpublished (2002)
                Other GSSs: OGVAZ30TH
                Contact: Cathy Whiteaw
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA
                Tel: 301-838-5843
                Fax: 301-838-0208
                Email: whiteaw@tigr.org
                Seq primer: TR
                Class: sheared ends.
                Location/Qualifiers
                1. 817
                /organism="Zea mays"
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                /strain="B73"
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FEATURES
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VERSION      BZ819718.1      GI:29034540
KEYWORDS     GSS.
SOURCE       Zea mays
ORGANISM     Zea mays
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                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                clade; Panicoidae; Andropogoneae; Zea.
                1 (bases 1 to 955)
                Whiteaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
                Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                Bennettzen,J.
                Maize Genomics Consortium
                Unpublished (2003)
                Other GSSs: PUGCC66TB
                Contact: Cathy Whiteaw
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA
                Tel: 301-838-5843
                Fax: 301-838-0208
                Email: whiteaw@tigr.org
                Seq primer: TR
                Class: sheared ends.
                Location/Qualifiers
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                /mol_type="genomic DNA"
                /strain="B73"
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                /clone="ZMMBma334L11"
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                cot selected genomic DNA library"

ORIGIN
Query Match      88.9%; Score 16; DB 28; Length 955;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TAGTACGGTCTCGCT 18
      |||||
      658 TAGTACGGTCTCGCT 673

RESULT 9
BZ819712/c      986 bp      DNA      linear      GSS 19-MAR-2003
LOCUS           BZ819712
DEFINITION      PUGCC66TB_ZM_0.6_1.0_KB Zea mays genomic clone ZMMBma334L11,
ACCESSION       BZ819712
VERSION         BZ819712.1
KEYWORDS        GSS.
SOURCE          Zea mays
ORGANISM        Zea mays
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                clade; Panicoidae; Andropogoneae; Zea.
                1 (bases 1 to 986)
                Whiteaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
                Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                Bennettzen,J.
                Maize Genomics Consortium
                Unpublished (2003)
                Other GSSs: PUGCC66TB
                Contact: Cathy Whiteaw
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA
                Tel: 301-838-5843
                Fax: 301-838-0208
                Email: whiteaw@tigr.org
                Seq primer: TR
                Class: sheared ends.
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                /note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
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FEATURES
    source

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/organism="Zea mays"  
 /mol\_type="genomic DNA"  
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 /clone\_1db="ZM0334111"  
 /clone\_1lb="ZM 0.6-1.0 KB"  
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 cot selected genomic DNA library"

## ORIGIN

Query Match 88.9%; Score 16; DB 28; Length 986;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TAGTACGGCTCTCGCT 18  
 |||||  
 Db 349 TAGTACGGCTCTCGCT 334

RESULT 10  
 LOCUS CA991730 464 bp mRNA linear EST 10-OCT-2003  
 DEFINITION HC0455 GIBCOBRL CAT. NO. 19643-014 Brassica rapa subsp. pekinensis  
 cDNA, mRNA sequence.  
 ACCESSION CA991730  
 VERSION CA991730.1 GI:37621025  
 KEYWORDS EST.  
 SOURCE Brassica rapa subsp. pekinensis  
 ORGANISM Brassica rapa subsp. pekinensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 464)  
 Gao, R.J., Dai, D.P. and Ma, R.C.  
 AUTHORS Expressed sequence tags of heading leaf during the heading process  
 TITLE Unpublished (2003)  
 JOURNAL Contact: Rongcai Ma  
 COMMENT Plant Functional Genomics  
 Beijing Agrobiotechnology Research Center  
 Haiidian District, Ban-Jing Rd., Beijing 100089, China  
 Tel: 86 10 5150 3831  
 Fax: 86 10 5150 3980  
 Email: rcma@yahoo.com  
 Seq primer: 17  
 High quality sequence stop: 464  
 POLYA=No.

## FEATURES

## SOURCE

Location/Qualifiers  
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 /db\_xref="taxon:51351"  
 /tissue\_type="heading leaf"  
 /dev\_stage="folding stage"  
 /lab\_host="E.coli DH10B(ZIP)"  
 /clone\_1lb="GIBCOBRL CAT. NO. 19643-014"  
 /note="Vector: pZL1; Site 1: NotI; Site 2: SalI; cDNA  
 library was constructed by SUPERScriptTM lambda system for  
 cDNA synthesis and cloning (GIBCOBRL, CAT. NO. 19643-014)."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 464;  
 Best Local Similarity 94.1%; Pred. No. 4.1e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CTAGTACGGCTCTCGCT 18  
 |||||  
 Db 140 CTAGTACGGCTCTCGCT 124

RESULT 11  
 BH625357/c

LOCUS BH625357 481 bp DNA linear GSS 30-JAN-2002  
 DEFINITION 1007106H02.y1.1007 - Rescuemu Grid H Zea mays genomic, genomic  
 survey sequence.  
 ACCESSION BH625357  
 VERSION BH625357.1 GI:18438608  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 481)  
 Walbot, V.  
 Maize genomic sequences found using engineered Rescuemu transposon  
 Unpublished (2001)  
 CONTACT: Walbot, V.  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2237  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 1007106 column: 29  
 Class: transposon-tagged.

## FEATURES

## SOURCE

Location/Qualifiers  
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 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
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 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_1lb="1007 - Rescuemu Grid H"  
 /note="Organ: leaf; Vector: Rescuemu (engineered from  
 pBlueScript backbone); Site 1: BamHI; Site 2: BglII;  
 Rescuemu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on Rescuemu, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'Rescuemu.' Grid H was grown at Berkeley in 2001. DNA  
 was extracted from leaf punches, double digested using  
 BamHI and BglII, and ligated to form circular plasmids.  
 DH10B cells were transformed and then screened on DB  
 plates with ampicillin."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 28; Length 481;  
 Best Local Similarity 94.1%; Pred. No. 4.2e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CTAGTACGGCTCTCGCT 18  
 |||||  
 Db 410 CTAGTACGGCTCTCGCT 394

RESULT 12  
 LOCUS BE784335/c 486 bp mRNA linear EST 20-OCT-2000  
 DEFINITION 601473488F1 NIH\_MGC\_68 Homo sapiens cDNA clone IMAGE:3876726 5',  
 mRNA sequence.

ACCESSION BE784335  
 VERSION BE784335.1 GI:10205533  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 486)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@biomail.nih.gov Tissue Procurement: DCTD/DTP/gazdar cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.lnl.gov">http://image.lnl.gov</a>
FEATURES	High quality sequence stop: 160.
SOURCE	Location/Qualifiers 1..486 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3876716" /tissue_type="large cell carcinoma" /lab_host="DH10B (phage-resistant)" /clone_id="NH_MCC_68" /note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."
ORIGIN	
Query Match	85.6%; Score 15.4; DB 10; Length 486;
Best Local Similarity	94.1%; Pred. No. 4.2e+03;
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	2 CTAGGACGGTCTGCCT 18
Dn	 232 CAAGTAGCGGTCTGCCT 216
RESULT 13	
LOCUS	CDJ17267/c
DEFINITION	StrPu621.001629 Sea urchin unfertilised egg cDNA library MPWGp621
ACCESSION	Strongylocentrotus purpuratus cDNA clone
VERSION	MPWGp621G2116;MPI_621_16G21 5', mRNA sequence.
KEYWORDS	CDJ17267
SOURCE	CDJ17267.1 GI:34789328
ORGANISM	EST.
REFERENCE	Strongylocentrotus purpuratus
AUTHORS	Strongylocentrotus purpuratus
TITLE	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae; Strongylocentrotus.
JOURNAL	1 (bases 1 to 511)
COMMENT	Pousterka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A., Reinhardt,R., Herwig,R., Panopoulou,G. and Jernach,H. Generation, annotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters Genome Res. 13 (12), 2736-2746 (2003) Contact: Pousterka AU Laboratory 145, dept. Jernach Max-Planck-Institut fuer Molekulare Genetik Innesstr.63-73, D-14195 Berlin, Germany Tel: +49 30 8413 1235 Fax: +49 30 8413 1128 Email: pousterka@olgen.mpg.de The library was characterised by oligonucleotide fingerprinting (ONF) to reduce sequencing redundancy. According to the ONF procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONF cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the other clones assigned to the same ONF cluster as the clone from which the above EST is generated is available at the sea urchin project web site at: <a href="http://www.molgen.mpg.de/ag_seaurchin/">http://www.molgen.mpg.de/ag_seaurchin/</a> . cDNA clones and filters are distributed via the Resource Center/Primary

```

Database of the German Human Genome Project (http://www.rzpd.de)
PCR primers
FORWARD: 5' CCCAGCGCTTACACTTTATGCTCCGGCTGC 3' (M18SP) 5'-seq
BACKWARD: 5' GCTATTACGCCCACTGACCAGAAAGGGAGATGTG 3' (M18FP) 3'-seq
Seq primer: 5'-CCGGTCGGGAATTCCTCCGGGT-3' pSPORT3/86
High quality sequence stop: 571.
Location/Qualifiers
1..571
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="MPMGp621G2116/WPI 621 16G21"
/tissue_type="whole unfertilised eggs"
/dev_stage="embryonic ohr"
/lab_host="B.coli, XL1 blue"
/clone_id="Sea urchin unfertilised egg cDNA library MPMGP621"
name="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Random
primed and directionally cloned in pSPORT1 vector using a
NotI (5'-TGACTGATTCATGATCGCAGCGGCC (T115-3') and a
SalI (5'-TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"

FEATURES
source
ORIGIN
Query Match      85.6%; Score 15.4; DB 14; Length 571;
Best Local Similarity 94.1%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 TCTAGTAGCGGTCTGCG 17
        ||| ||||| ||||| |||
Db       507 TCTGTGACGGTCTGCG 491

RESULT 14
BU130132          626 bp      mRNA      linear    EST 23-JAN-2002
LOCUS             BU130132
DEFINITION        Caenorhabditis elegans cDNA clone YK1039d08 3', mRNA sequence.
ACCESSION         BU130132
VERSION           BU130132.1 GI:18290289
KEYWORDS          EST.
SOURCE            Caenorhabditis elegans
ORGANISM          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                  Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE         1 (bases 1 to 626)
AUTHORS           Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
                  and Sugano,S.
TITLE             A complementary view of the C.elegans genome
JOURNAL           Unpublished (2002)
COMMENT          Contact: Tadasu Shin-i
                  Center For Genetic Resource Information
                  National Institute of Genetics
                  111 Yata, Mishima, Shizuoka 411-8540, Japan
                  Tel: 81-559-81-6856
                  Fax: 81-559-81-6855
                  Email: tshini@genes.nig.ac.jp.
FEATURES
source
ORIGIN
Query Match      85.6%; Score 15.4; DB 12; Length 626;
Best Local Similarity 88.9%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Oy 1 TCTAGTACGGCTCGCT 18  
 |||||  
 Db 455 TCNAGTACGGGCTCGCT 472

## RESULT 15

Bj147480

LOCUS

Bj147480 unpublished oligo-capped cDNA library, C. elegans L1 stage

Caenorhabditis elegans cDNA clone yk1251f07 3', mRNA sequence.

ACCESSION

Bj147480.1 GI:18315465

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 629

/organism="Caenorhabditis elegans"

/mol\_type="mRNA"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1251f07"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/clone\_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"

Location/Qualifiers

1. 629

/organism="Caenorhabditis elegans"

/mol\_type="mRNA"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1251f07"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/clone\_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"

Location/Qualifiers

1. 629

/organism="Caenorhabditis elegans"

/mol\_type="mRNA"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1251f07"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/clone\_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"

Location/Qualifiers

1. 629

/organism="Caenorhabditis elegans"

/mol\_type="mRNA"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1251f07"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/clone\_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"

Location/Qualifiers

1. 629

/organism="Caenorhabditis elegans"

/mol\_type="mRNA"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk1251f07"

/sex="hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L1"

/clone\_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"

Location/Qualifiers

1. 629

Search completed: October 1, 2004, 08:01:43  
 Job time : 259.333 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 23:11:57 ; Search time 31.9347 Seconds  
(without alignments)  
2394.501 Million cell updates/sec

Title: US-10-046-955-59

Perfect score: 18  
Sequence: 1 cccactctcgaatgctg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*

1: Geneseqn1980s:\*\n2: Geneseqn1990s:\*\n3: Geneseqn2000s:\*\n4: Geneseqn2001as:\*\n5: Geneseqn2001bs:\*\n6: Geneseqn2002s:\*\n7: Geneseqn2003as:\*\n8: Geneseqn2003bs:\*\n9: Geneseqn2003cs:\*\n10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	2	AAV83706 Species-s
2	18	100.0	310	2	AAV70851 Internal
3	18	100.0	319	2	AAV70850 Internal
4	18	100.0	502	3	AAAG1893 Fusarium
5	18	100.0	503	2	AAT05401 Internal
6	18	100.0	503	2	AAV62592 Fusarium
7	18	100.0	503	2	AAV59029 F. gramine
8	18	100.0	504	2	AAV62591 Fusarium
9	18	100.0	504	2	AAV62591 Fusarium
10	18	100.0	504	4	AAV59028 F. culmox
11	18	100.0	504	4	AAV59028 F. culmox
12	18	100.0	521	7	ACC50000 Internal
13	18	100.0	522	7	ACC49999 Internal
14	18	100.0	522	7	ACC49999 Internal
15	18	100.0	534	7	ACC50002 Internal
16	18	100.0	545	2	AAV62593 Fusarium
17	18	100.0	545	2	AAV59030 F. monili
18	18	100.0	546	2	AAV62596 Fusarium
19	18	100.0	546	2	AAV59007 F. poae i
20	18	100.0	561	2	AAV59009 F. avenac
21	18	100.0	659	6	ABV78724 C. sinens
22	18	100.0	2293	4	AAV16211 Fungus ge
23	17	94.4	1258	2	AAQ32259 Catfeoyl-

24	16.4	91.1	593	6	ABN60159
25	16.4	91.1	13444	4	AAI37295
26	16.4	91.1	13444	7	ABX60283
27	16	88.9	110000	3	AAF22305_01
28	15.4	85.6	536	4	AAI12562
29	15.4	85.6	578	3	AAI37760
30	15.4	85.6	610	2	AAI90111
31	15.4	85.6	616	4	AAI21435
32	15.4	85.6	1470	5	AAI84251
33	15.4	85.6	1599	7	AAI84250 DNA encod
34	15.4	85.6	2679	5	AAI84250 DNA encod
35	15.4	85.6	6914	5	AAI79198
36	15.4	85.6	6914	5	AAI79198
37	15.4	85.6	24935	4	AB103390
38	15.4	85.6	49999	2	AAI23899
39	15.4	85.6	55155	6	ABN87364
40	15.4	85.6	90091	9	ADIC85509
41	15.4	85.6	90100	8	ADA03029
42	15.4	85.6	90100	9	ADB72767
43	15	83.3	251	2	AAI10662
44	15	83.3	278	2	AAH87528
45	15	83.3	918	3	AAI52096

## ALIGNMENTS

RESULT 1	AAV83706	standard; DNA, 18 BP.
ID	AAV83706	
AC	AAV83706;	
DT	26-FEB-1999	(first entry)
DE	Species-specific probe targeted to the internal transcribed spacer 2.	
XX	Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus; A. niger;	
KM	A. terreus; A. nidulans; Fusarium solani; F. moniliforme; Mucor rouxii;	
KM	M. racemosus; M. plumbeus; M. indicus; A. fumigatus;	
KM	M. circinilloides f. circinelloides; Rhizopus oryzae; R. microsporus;	
KM	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;	
KM	Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;	
KM	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.	
XX	Synthetic.	
OS	Fusarium sp.	
XX		
FT	modified_base	Location/Qualifiers
FT		/*tag= a
FT		/note= "labelled with digoxigenin"
XX	W09850584-A2.	
PN	12-NOV-1998.	
XX	01-MAY-1998;	98WO-US008926.
XX	02-MAY-1997;	97US-0045400P.
PR	(USSS ) US DEPT HEALTH & HUMAN SERVICES.	
PA	Morrison CJ, Reiss B, Aidorevich L, Choi JS;	
XX	WPI; 1999-034737/03.	
DR	New nucleic acid probes for filamentous fungi - for detecting e.g.	
PT	Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,	
PT	Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix	
XX	species.	
PS	Claim 47; Page 23; 45pp; English.	

XX Probes AAV83677-708 are derived from the internal transcribed spacer 2  
 CC (ITS2) region of various filamentous fungi (see AAV70845-73). The probes  
 CC are species-specific, and can be used for identifying a species selected  
 CC from *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,  
 CC *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,  
 CC *M. indicus*, *M. circinilloides* f. *circinelloides*, *Rhizopus oryzae*, *R.*  
 CC *microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia corymbifera*,  
 CC *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph  
 CC *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix*  
 CC *schenkii*. The probes can be used for differentiating filamentous fungal  
 CC species from each other and from other medically important fungi  
 XX  
 XX Sequence 18 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCAAGTTCTGAATGTTG 18  
 DB 1 CCCAAGTTCTGAATGTTG 18  
 RESULT 2  
 AAV70851  
 ID AAV70851 standard; DNA; 310 BP.  
 XX  
 AC AAV70851;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 26-FEB-1999 (first entry)  
 XX  
 DE Internal transcribed spacer 2 (ITS2) and adjacent regions.  
 XX  
 KW Internal transcribed spacer 2; ITS2; probe; *Aspergillus flavus*; *A. niger*;  
 KW *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*; *Mucor rouxii*;  
 KW *M. racemosus*; *M. plumbeus*; *M. indicus*; *A. fumigatus*;  
 KW *M. circinilloides* f. *circinelloides*; *Rhizopus oryzae*; *R. microsporus*;  
 KW *R. circinans*; *R. stolonifer*; *Rhizomucor pusillus*; *Abidia corymbifera*;  
 KW *Cunninghamella elegans*; *Pseudallescheria boydii*; *Scedosporium apiospermum*;  
 KW *Penicillium notatum*; *Sporothrix schenkii*; filamentous fungus; ss.  
 XX  
 OS *Gibberella fujikuroi*.  
 XX  
 PN WO9850584-A2.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PP 01-MAY-1998; 98WO-US008926.  
 XX  
 PR 02-MAY-1997; 97US-0045400P.  
 XX  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Morrison CJ, Reiss E, Aidorevich L, Choi JS;  
 XX  
 DR WPI; 1999-034737/03.  
 XX  
 PT New nucleic acid probes for filamentous fungi - for detecting e.g.  
 PT *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Abidia*,  
 PT *Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix*  
 PT species.  
 XX  
 PS Claim 1; Page 12; 45pp; English.  
 XX  
 CC The present sequence represents an internal transcribed spacer 2 (ITS2)  
 CC and adjacent regions. Probes can be derived from the present sequence  
 CC which are species-specific. The specification also describes ITS2  
 CC sequence-derived probes for identifying a species selected from  
 CC *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,  
 CC *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,  
 CC *M. indicus*, *M. circinilloides* f. *circinelloides*, *Rhizopus oryzae*, *R.*

CC *microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia*  
 CC *corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph  
 CC of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix*  
 CC *schenkii*. The probes can be used for differentiating filamentous fungal  
 CC species from each other and from other medically important fungi.  
 CC (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 XX Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 2; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCAAGTTCTGAATGTTG 18  
 DB 258 CCCAAGTTCTGAATGTTG 275  
 RESULT 3  
 AAV70850  
 ID AAV70850 standard; DNA; 319 BP.  
 XX  
 AC AAV70850;  
 XX  
 DT 26-FEB-1999 (first entry)  
 DT  
 XX  
 DE Internal transcribed spacer 2 (ITS2) and adjacent regions.  
 XX  
 KW Internal transcribed spacer 2; ITS2; probe; *Aspergillus flavus*; *A. niger*;  
 KW *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*; *Mucor rouxii*;  
 KW *M. racemosus*; *M. plumbeus*; *M. indicus*; *A. fumigatus*;  
 KW *M. circinilloides* f. *circinelloides*; *Rhizopus oryzae*; *R. microsporus*;  
 KW *R. circinans*; *R. stolonifer*; *Rhizomucor pusillus*; *Abidia corymbifera*;  
 KW *Cunninghamella elegans*; *Pseudallescheria boydii*; *Scedosporium apiospermum*;  
 KW *Penicillium notatum*; *Sporothrix schenkii*; filamentous fungus; ss.  
 XX  
 OS *Fusarium solani*.  
 XX  
 PN WO9850584-A2.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PP 01-MAY-1998; 98WO-US008926.  
 XX  
 PR 02-MAY-1997; 97US-0045400P.  
 XX  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Morrison CJ, Reiss E, Aidorevich L, Choi JS;  
 XX  
 DR WPI; 1999-034737/03.  
 XX  
 PT New nucleic acid probes for filamentous fungi - for detecting e.g.  
 PT *Aspergillus*, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Abidia*,  
 PT *Cunninghamella*, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix*  
 PT species.  
 XX  
 PS Claim 1; Page 12; 45pp; English.  
 XX  
 CC The present sequence represents an internal transcribed spacer 2 (ITS2)  
 CC and adjacent regions. Probes can be derived from the present sequence  
 CC which are species-specific. The specification also describes ITS2  
 CC sequence-derived probes for identifying a species selected from  
 CC *Aspergillus flavus*, *A. fumigatus*, *A. niger*, *A. terreus*, *A. nidulans*,  
 CC *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*,  
 CC *M. indicus*, *M. circinilloides* f. *circinelloides*, *Rhizopus oryzae*, *R.*  
 CC *microsporus*, *R. circinans*, *R. stolonifer*, *Rhizomucor pusillus*, *Abidia*  
 CC *corymbifera*, *Cunninghamella elegans*, *Pseudallescheria boydii* (teleomorph  
 CC of *Scedosporium apiospermum*), *Penicillium notatum*, or *Sporothrix*  
 CC *schenkii*. The probes can be used for differentiating filamentous fungal  
 CC species from each other and from other medically important fungi  
 XX  
 XX Sequence 319 BP; 77 A; 96 C; 84 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18  
 |||||  
 Db 267 CCCAACTTCTGAATGTTG 284

RESULT 4  
 ID AAA61893 standard; DNA; 502 BP.  
 XX  
 AC AAA61893;

DT 15-SEP-2003 (revised)  
 DT 14-NOV-2000 (first entry)

DE Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.

KM Ribosomal DNA, rDNA ITS region; internal transcribed spacer; ATCC 74469;  
 KM HIV integrase inhibitor; steroid compound; human immunodeficiency virus;  
 KM acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;  
 KM symptomatic infection; asymptomatic infection; potential HIV exposure;  
 KM combination therapy; de.

OS Fusarium sp; MF6381.

PN WO200036132-A1.

PD 22-JUN-2000.

PF 09-DEC-1999; 99WO-US029356.

PR 14-DEC-1998; 98US-0112168P.

PA (MERI ) MERCK & CO INC.

PI Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;  
 PI Dombrowski AW;

DR WPI; 2000-431606/37.

PT New steroid compounds are HIV integrase inhibitors used for treating HIV  
 PT infection and AIDS.

PS Disclosure; Page 14; 113pp; English.

XX The invention relates to novel steroid compounds derived from the African  
 CC soil fungus *Fusarium* sp. MF6381 (ATCC 74469) which act as inhibitors of  
 CC HIV integrase. The invention encompasses cultures of *Fusarium* sp. MF6381.  
 CC The invention also relates to a composition comprising a compound of the  
 CC invention in combination with an AIDS antiviral agent, an immunomodulator  
 CC and an antineoplastic agent. The compounds of the invention may be used in  
 CC the inhibition of HIV integrase and in the prevention and treatment of  
 CC HIV infection. A wide range of state of HIV infection may be treated;  
 CC AIDS (acquired immunodeficiency syndrome); ARC (AIDS-related complex);  
 CC both symptomatic and asymptomatic HIV infection; and actual or potential  
 CC exposure to HIV. The compounds may be used to isolate HIV integrase  
 CC mutants which are potentially useful as screening tools for antiviral  
 CC compounds. The compounds may also be used to establish or determine the  
 CC site at which other antiviral bind to HIV integrase (e.g., by  
 CC competitive inhibition). The present sequence represents the ribosomal  
 CC DNA (rDNA) internal transcribed spacer (ITS) region of *Fusarium* sp.  
 CC MF6381, which may be used to characterise MF6381. (Updated on 15-SEP-2003  
 CC to standardise OS field)

SO Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 502;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18  
 |||||  
 Db 455 CCCAACTTCTGAATGTTG 472

RESULT 5  
 ID AAT05401 standard; DNA; 503 BP.  
 XX  
 AC AAT05401;

DT 16-OCT-2003 (revised)  
 DT 04-JUN-1996 (first entry)

DE *Fusarium* graminearum internal transcribed spacer sequence.

KM Plant pathogen; fungus; *Septoria nodorum*; *Septoria tritici*; *Fusarium*;  
 KM *Pseudocercospora* *hepwortrichoides*; *Mycosphaerella* *fijiensis*; PCR;  
 KM *Mycosphaerella* *musicola*; amplification; primer; ribosomal RNA gene;  
 KM internal transcribed region; strain; capture; colourimetric assay;  
 KM isolate; development; population; random amplified polymorphic DNA; ss.  
 OS *Gibberella* *zeae*.

PN WO9529260-A2.

PD 02-NOV-1995.

PF 19-APR-1995; 95WO-US004712.

PR 25-APR-1994; 94US-00233608.

PA (CIBA ) CIBA GEIGY AG.

PI Ligon JM, Beck JF;

DR WPI; 1995-383005/49.

PT DNA encoding intervening transcribed sequence - used for detection of  
 PT plant fungal pathogens.

PS Claim 1; Page 55; 65pp; English.

XX A novel method for the detection of plant pathogenic strains of fungi  
 CC e.g. *Septoria nodorum*, *S. tritici*, *Pseudocercospora* *hepwortrichoides*,  
 CC *Mycosphaerella* *fijiensis*, *M. musicola* or *Fusarium* spp. involves the PCR  
 CC amplification of sequences found in the internal transcribed region (ITS)  
 CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AA094359-93  
 CC and AAT05357-72. These primers are derived from the ITS sequences of  
 CC these fungi (AAT05394-705404 and AA094398) and are strain specific. The  
 CC amplification products of the reactions using these primers can be used  
 CC with the capture primers AAT05378-93 in colourimetric assays. The primers  
 CC and ITS DNAs can be used for the detection of specific fungal pathogen  
 CC isolates and in monitoring disease development in plant populations.  
 CC (Updated on 16-OCT-2003 to standardise OS field)

SO Sequence 503 BP; 131 A; 127 C; 108 G; 116 T; 0 U; 21 Other;

Query Match 100.0%; Score 18; DB 2; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18  
 |||||  
 Db 451 CCCAACTTCTGAATGTTG 468

RESULT 6  
 ID AAV62592 standard; DNA; 503 BP.  
 XX  
 AC AAV62592;

```

XX 17-OCT-2003 (revised)
DT 17-DEC-1998 (first entry)
XX
DE Fusarium graminearum PCR amplified ITS region consensus DNA sequence.
XX
XX Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
XX Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
XX Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
XX PCR; nucleic acid detection; ss.
XX
OS Gibberella zeae.
XX
FH Key Location/Qualifiers
FT misc_feature 1..9
FT /tag= a
FT /note= "3' end of small subunit rRNA gene"
FT misc_feature 10..155
FT /tag= b
FT /note= "ITS 1"
FT misc_feature 156..312
FT /tag= c
FT /note= "5.8S rRNA gene"
FT misc_feature 313..466
FT /tag= d
FT /note= "ITS 2"
FT misc_feature 467..503
FT /tag= e
FT /note= "5' end of large subunit rRNA gene"
XX
XX US5814453-A.
XX
XX 29-SEP-1998.
XX
XX 02-JUL-1997; 97US-00887480.
XX
XX 19-APR-1995; 95WO-US004712.
XX 15-OCT-1996; 96US-00722187.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JI;
XX
XX WPI; 1998-541745/46.
XX
XX DNA isolated from fungal RNA, and its internal transcribed spacer
XX sequence - used for detecting fungal pathogens in plant tissue.
XX
XX Claim 2; Fig 3; 56pp; English.
XX
XX This represents the consensus DNA sequence of the internal transcribed
XX spacer (ITS) region that was PCR amplified from Fusarium graminearum
XX isolates, R-8417, R-8422 and R-8546. The invention provides a DNA
XX molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal
XX pathogen, where the DNA molecule consists of an ITS sequence selected
XX from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
XX moniliforme, Septoria avenae or Microdochium nivale. A method for
XX detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.
XX avenaceum and M. nivale isolates is also provided. The method comprises
XX isolating DNA from a plant leaf infected with at least one of the above
XX pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
XX PCR using specific primers from within these sequences. The pathogen(s)
XX are detected by visualising the amplified part of the ITS sequence.
XX (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 503 BP; 131 A; 127 C; 108 G; 116 T; 0 U; 21 Other;
Query Match 100.0%; Score 18; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCACTTCTGAATGTTG 18
|||||

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```

DB 451 CCCACTTCTGAATGTTG 468
RESULT 7
AAVS9029
ID AAVS9029 standard; DNA; 503 BP.
XX
XX AAVS9029;
XX
XX 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE F. graminearum internal transcribed spacer.
XX
XX Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
XX fungal pathogen identification; infection identification; ss.
XX
XX Gibberella zeae.
XX
FH Key Location/Qualifiers
FT misc_feature 10..155
FT /tag= a
FT /note= "ITS1"
FT misc_feature 313..466
FT /tag= b
FT /note= "ITS2"
XX
XX US5827695-A.
XX
XX 27-OCT-1998.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JI;
XX
XX WPI; 1998-593995/50.
XX
XX DR
XX
XX wheat pathogen internal transcribed spacer sequences - used as a basis
XX for primers for the species-specific polymerase chain reaction detection
XX of the pathogens.
XX
XX Disclosure; Col 23-24; 20pp; English.
XX
XX This sequence represents an internal transcribed spacer (ITS) sequence of
XX the invention. The primer pairs, based on the ITS sequences, are used for
XX the PCR amplification detection of wheat Microdochium and Fusarium fungal
XX pathogens, especially M. nivale, F. graminearum, F. culmorum, F.
XX avenaceum, F. poae, F. moniliforme or F. roseum. The two different
XX strains of fungi show different symptoms during infection, which may or
XX may not be due to infection. Early identification of the strain causing
XX the infection allows early, and more specific fungicidal treatment.
XX (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
XX correct PR field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 503 BP; 131 A; 127 C; 108 G; 116 T; 0 U; 21 Other;
Query Match 100.0%; Score 18; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCACTTCTGAATGTTG 18
|||||
DB 451 CCCACTTCTGAATGTTG 468
RESULT 8
AAVS400
ID AAVS400 standard; DNA; 504 BP.

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```

XX AC AAT05400;
XX XX
XX 04-JUN-1996 (first entry)
XX DE Fusarium culmorum internal transcribed spacer sequence.
XX XX
XX Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
XX KM Pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PCR;
XX KM Mycosphaerella musicola; amplification; primer; ribosomal RNA gene;
XX KM internal transcribed region; strain; capture; colourimetric assay;
XX KM isolate; development; population; random amplified polymorphic DNA; ss.
XX OS Fusarium culmorum.
XX PN MO9529260-A2.
XX XX
XX 02-NOV-1995.
XX PD
XX PF 19-APR-1995; 95MO-US004712.
XX XX
XX PR 25-APR-1994; 94US-00233608.
XX XX
XX PA (CIBA ) CIBA GEIGY AG.
XX XX
XX PI Ligon JM, Beck JI;
XX DR WPI; 1995-383005/49.
XX XX
XX PT DNA encoding intervening transcribed sequence - used for detection of
XX PT plant fungal pathogens.
XX PS
XX BS Claim 1; Page 54-55; 65pp; English.
XX XX
XX CC A novel method for the detection of plant pathogenic strains of fungi
XX CC e.g. Septoria nodorum, S. tritici, Pseudocercospora herpotrichoides,
XX CC Mycosphaerella fijiensis, M. musicola or Fusarium spp. involves the PCR
XX CC amplification of sequences found in the internal transcribed region (ITS)
XX CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93
XX CC and AAU05357-72. These primers are derived from the ITS sequences of
XX CC these fungi (AAT05394-T05404 and AAQ94398) and are strain specific. The
XX CC amplification products of the reactions using these primers can be used
XX CC with the capture primers AAT05378-93 in colourimetric assays. The primers
XX CC and ITS DNAs can be used for the detection of specific fungal pathogen
XX CC isolates and in monitoring disease development in plant populations
XX CC
XX SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
XX
XX Query Match 100.0%; Score 18; DB 2; Length 504;
XX Best local Similarity 100.0%; Pred. No. 16;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCAACTTCTGAATGTTG 18
Db 457 CCCAACTTCTGAATGTTG 474

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XX XX
XX FH Key Location/Qualifiers
XX FT misc_feature 1..12
XX FT /tag= a
XX FT /note= "3' end of small subunit rRNA gene"
XX FT 13..161
XX FT /tag= b
XX FT /note= "ITS 1"
XX FT 162..318
XX FT /tag= c
XX FT /note= "5.8S rRNA gene"
XX FT 319..472
XX FT /tag= d
XX FT /note= "ITS 2"
XX FT 473..504
XX FT /tag= e
XX FT /note= "5' end of large subunit rRNA gene"
XX PN US5814453-A.
XX XX
XX PD 29-SEP-1998.
XX XX
XX PF 02-JUL-1997; 97US-00887480.
XX XX
XX PR 19-APR-1995; 95MO-US004712.
XX PR 15-OCT-1996; 96US-00722187.
XX XX
XX PA (NOVUS ) NOVARTIS FINANCE CORP.
XX XX
XX PI Beck JI;
XX DR WPI; 1998-541745/46.
XX XX
XX PT DNA isolated from fungal RNA, and its internal transcribed spacer
XX PT sequence - used for detecting fungal pathogens in plant tissue.
XX PS
XX BS Claim 2; Fig 3; 56pp; English.
XX XX
XX CC This represents the consensus DNA sequence of the internal transcribed
XX CC spacer (ITS) region that was PCR amplified from Fusarium culmorum
XX CC isolates, R-5106, R-5126 and R-5146. The invention provides a DNA
XX CC molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal
XX CC pathogen, where the DNA molecule consists of an ITS sequence selected
XX CC from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
XX CC moniliforme, Septoria avenae or Microdochium nivale. A method for
XX CC detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.
XX CC avenaceum and M. nivale isolates is also provided. The method comprises
XX CC isolating DNA from a plant leaf infected with at least one of the above
XX CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
XX CC PCR using specific primers from within these sequences. The pathogen(s)
XX CC are detected by visualising the amplified part of the ITS sequence
XX CC
XX SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
XX
XX Query Match 100.0%; Score 18; DB 2; Length 504;
XX Best local Similarity 100.0%; Pred. No. 16;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCAACTTCTGAATGTTG 18
Db 457 CCCAACTTCTGAATGTTG 474

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RESULT 9
ID AAV62591 standard; DNA; 504 BP.
XX AC AAV62591;
XX XX
XX 17-DEC-1998 (first entry)
XX DE Fusarium culmorum PCR amplified ITS region consensus DNA sequence.
XX XX
XX Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
XX KM Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
XX KM Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
XX KM PCR; nucleic acid detection; ss.
XX OS Fusarium culmorum.

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RESULT 10
ID AAV59028 standard; DNA; 504 BP.
XX AC AAV59028;
XX XX
XX 25-MAR-2003 (revised)
XX KM Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
XX KM PCR; nucleic acid detection; ss.
XX OS Fusarium culmorum.

```

```
XX Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
KM fungal pathogen identification; infection identification; ss.
XX
OS Fusarium culmorum.
FH Key Location/Qualifiers
FT misc_feature 13..161
FT /*tag= a
FT /note= "ITS1"
FT 319..472
FT /*tag= b
FT /note= "ITS2"
XX
XX US5827695-A.
XX
XX 27-OCT-1998.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX 04-AUG-1997; 97US-00905314.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JJ;
XX
XX WPI; 1998-593995/50.
XX
XX Wheat pathogen internal transcribed spacer sequences - used as a basis
PT for primers for the species-specific polymerase chain reaction detection
PT of the pathogens.
XX
XX Disclosure; Col 21-22; 20pp; English.
XX
XX This sequence represents an internal transcribed spacer (ITS) sequence of
CC the invention. The primer pairs, based on the ITS sequences, are used for
CC the PCR amplification detection of wheat Microdochium and Fusarium fungal
CC pathogens, especially M. nivale, F. graminearum, F. culmorum, F.
CC avenaceum, F. poae, F. moniliforme or F. roseum. The two different
CC strains of fungi show different symptoms during infection, which may or
CC may not be due to infection. Early identification of the strain causing
CC the infection allows early, and more specific fungicidal treatment.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
XX Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 0 U; 4 Other;
XX
XX Query Match 100.0%; Score 18; DB 2; Length 504;
XX Best Local Similarity 100.0%; Pred. No. 16;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCAACTTCTGAATGTTG 18
DB 457 CCCAACTTCTGAATGTTG 474
RESULT 11
AAS08426
ID AAS08426 standard; DNA; 504 BP.
XX
XX AAS08426;
XX
XX 26-SEP-2001 (first entry)
XX
XX Internal transcribed spacer, ITS, region #16.
XX
XX Internal transcribed spacer; ITS; fungal pathogen; ss; wheat disease;
KM Sharp eyespot; fungal pathotype identification; isolate 62215.
XX
XX Fusarium culmorum.
XX
XX WO200151653-A1.
XX
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PD 19-JUL-2001.
XX
XX 09-JAN-2001; 2001WO-EP000172.
XX
XX 11-JAN-2000; 2000US-00481293.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Beck JJ, Barnett CJ;
XX
XX WPI; 2001-442154/47.
XX
XX New internal transcribed spacer DNA sequences, useful for identifying
PT fungal pathogen, particularly Rhizoctonia cerealis, and for monitoring
PT disease development in plant population.
XX
XX Disclosure; Page 31; 35pp; English.
XX
XX The sequence is an internal transcribed spacer (ITS) region from Fusarium
CC culmorum, isolate 62215. The ITS DNA sequences are useful for detecting
CC Rhizoctonia cerealis, a fungal pathogen of wheat causing Sharp eyespot.
CC for monitoring disease development in plant population, and for providing
CC detailed information on the development and spread of specific pathogen
CC races over extended geographical areas. The DNA sequences are
CC specifically used as primers in PCR-based analysis for the identification
CC of fungal pathotypes
XX
XX Sequence 504 BP; 132 A; 133 C; 114 G; 123 T; 0 U; 2 Other;
XX
XX Query Match 100.0%; Score 18; DB 4; Length 504;
XX Best Local Similarity 100.0%; Pred. No. 16;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCAACTTCTGAATGTTG 18
DB 459 CCCAACTTCTGAATGTTG 476
RESULT 12
ACC50000
ID ACC50000 standard; DNA; 521 BP.
XX
XX ACC50000;
XX
XX 14-JUL-2003 (first entry)
XX
XX Internal transcribed spacer RNA encoding sequence #2.
XX
XX Mitochondria; fungal pathogen; ds.
XX
XX Gibberella zeae.
XX
XX WO2003027635-A2.
XX
XX 03-APR-2003.
XX
XX 19-SEP-2002; 2002WO-US030311.
XX
XX 24-SEP-2001; 2001US-00961755.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Beck JJ, Barnett CJ;
XX
XX WPI; 2003-363229/34.
XX
XX Detecting a fungal pathogen, useful for monitoring disease development,
PT comprises subjecting the DNA to PCR amplification using at least one
PT primer having sequence identity with at least 10 contiguous nucleotides
PT of Fusarium spp.
XX
XX Claim 5; Page 38; 44pp; English.
XX
```

CC This invention relates to the detection of a fungal pathogen comprising  
CC isolating DNA from a plant leaf infected with a pathogen. The methods and  
CC primers are useful for identifying fungal isolates of fungal pathogens  
CC and monitoring of disease development in plant populations. The present  
CC sequence represents an internal transcribed spacer RNA encoding sequence  
SQ Sequence 521 BP; 138 A; 140 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 521;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18  
|||  
DB 473 CCCAACTTCTGAATGTTG 490

RESULT 13  
ACC49999  
ID ACC49999 standard; DNA; 522 BP.  
XX  
AC ACC49999;

XX 14-JUL-2003 (first entry)

DE Internal transcribed spacer RNA encoding sequence.

KM Mitochondria; fungal pathogen; ds.

OS Fusarium subglutinans.

PN WO2003027635-A2.

XX 03-APR-2003.

PF 19-SEP-2002; 2002WO-US030311.

PR 24-SEP-2001; 2001US-00961755.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

PI Beck JI, Barnett CJ;

DR WPI; 2003-363229/34.

PT Detecting a fungal pathogen, useful for monitoring disease development,  
PT comprises subjecting the DNA to PCR amplification using at least one  
PT primer having sequence identity with at least 10 contiguous nucleotides  
of Fusarium spp.

PS Claim 5; Page 38; 44pp; English.

CC This invention relates to the detection of a fungal pathogen comprising  
CC isolating DNA from a plant leaf infected with a pathogen. The methods and  
CC primers are useful for identifying fungal isolates of fungal pathogens  
CC and monitoring of disease development in plant populations. The present  
CC sequence represents an internal transcribed spacer RNA encoding sequence  
SQ Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 522;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18  
|||  
DB 474 CCCAACTTCTGAATGTTG 491

RESULT 14  
ACC50002  
ID ACC50002 standard; DNA; 522 BP.  
XX

AC ACC50002;

XX 27-OCT-2003 (revised)

DT 14-JUL-2003 (first entry)

DE Internal transcribed spacer RNA encoding sequence #4.

KM Mitochondria; fungal pathogen; ds.

OS Gibberella moniliformis.

PN WO2003027635-A2.

XX 03-APR-2003.

PF 19-SEP-2002; 2002WO-US030311.

PR 24-SEP-2001; 2001US-00961755.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

PI Beck JI, Barnett CJ;

DR WPI; 2003-363229/34.

PT Detecting a fungal pathogen, useful for monitoring disease development,  
PT comprises subjecting the DNA to PCR amplification using at least one  
PT primer having sequence identity with at least 10 contiguous nucleotides  
of Fusarium spp.

PS Claim 5; Page 39; 44pp; English.

CC This invention relates to the detection of a fungal pathogen comprising  
CC isolating DNA from a plant leaf infected with a pathogen. The methods and  
CC primers are useful for identifying fungal isolates of fungal pathogens  
CC and monitoring of disease development in plant populations. The present  
CC sequence represents an internal transcribed spacer RNA encoding sequence.  
(Updated on 27-OCT-2003 to standardise OS field)

SQ Sequence 522 BP; 138 A; 141 C; 119 G; 124 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 522;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18  
|||  
DB 474 CCCAACTTCTGAATGTTG 491

RESULT 15  
ACC50001  
ID ACC50001 standard; DNA; 534 BP.  
XX  
AC ACC50001;

DT 14-JUL-2003 (first entry)

DE Internal transcribed spacer RNA encoding sequence #3.

KM Mitochondria; fungal pathogen; ds.

OS Fusarium proliferatum.

PN WO2003027635-A2.

XX 03-APR-2003.

PF 19-SEP-2002; 2002WO-US030311.

PR 24-SEP-2001; 2001US-00961755.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Beck JJ, Barnett CJ;  
PI  
XX WPI; 2003-363229/34.  
DR  
XX  
XX Detecting a fungal pathogen, useful for monitoring disease development,  
PT comprises subjecting the DNA to PCR amplification using at least one  
PT primer having sequence identity with at least 10 contiguous nucleotides  
PT of *Fusarium* spp.  
XX  
XX  
PS Claim 5; Page 38-39; 44pp; English.  
XX  
XX This invention relates to the detection of a fungal pathogen comprising  
CC isolating DNA from a plant leaf infected with a pathogen. The methods and  
CC primers are useful for identifying fungal isolates of fungal pathogens  
CC and monitoring of disease development in plant populations. The present  
CC sequence represents an internal transcribed spacer RNA encoding sequence  
XX  
SQ Sequence 534 BP; 135 A; 149 C; 130 G; 120 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 534;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCCACTTCTGAATGTTG 18  
|||||  
Db 486 CCCCACTTCTGAATGTTG 503

Search completed: October 1, 2004, 03:41:25  
Job time : 35.9347 secs



GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 00:59:07 : Search time 146.608 Seconds  
(without alignments)  
5321.503 Million cell updates/sec

Title: US-10-046-955-59

Perfect score: 18

Sequence: 1 cccacatctcgatgctg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vt: \*  
15: em\_da: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vt: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_mus: \*  
34: em\_htg\_pln: \*  
35: em\_htg\_rod: \*  
36: em\_htg\_mam: \*  
37: em\_htg\_vrt: \*  
38: em\_sy: \*  
39: em\_hngo\_hum: \*  
40: em\_hngo\_mus: \*  
41: em\_hngo\_other: \*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6 AR206453	AR206453 Sequence
2	18	100.0	18	6 BD083644	BD083644 Nucleic a
3	18	100.0	298	8 AY226096	AY226096 Nectria h
4	18	100.0	310	6 AR206401	AR206401 Sequence
5	18	100.0	310	6 BD083592	BD083592 Nucleic a
6	18	100.0	310	8 AF117922	AF117922 Gibberella
7	18	100.0	319	6 AR206400	AR206400 Sequence
8	18	100.0	319	6 BD083591	BD083591 Nucleic a
9	18	100.0	319	8 AF117921	AF117921 Nectria h
10	18	100.0	332	8 AF162901	AF162901 Fusarium
11	18	100.0	334	8 AF162902	AF162902 Fusarium
12	18	100.0	335	8 AF162898	AF162898 Fusarium
13	18	100.0	335	8 AF162899	AF162899 Fusarium
14	18	100.0	336	8 AF162900	AF162900 Fusarium
15	18	100.0	338	8 AF339418	AF339418 Fusarium
16	18	100.0	338	8 AY074751	AY074751 Theobroma
17	18	100.0	338	8 AY074752	AY074752 Theobroma
18	18	100.0	338	8 AY074753	AY074753 Theobroma
19	18	100.0	349	8 AF162897	AF162897 Fusarium
20	18	100.0	351	8 AF162903	AF162903 Fusarium
21	18	100.0	432	8 AY273305	AY273305 Unculture
22	18	100.0	434	8 AY243055	AY243055 Ascomycet
23	18	100.0	447	8 AY387701	AY387701 Fusarium
24	18	100.0	449	8 AY143084	AY143084 Fusarium
25	18	100.0	451	8 AF502788	AF502788 Leaf lict
26	18	100.0	471	8 AF161222	AF161222 Fusarium
27	18	100.0	472	8 AY210325	AY210325 Fusarium
28	18	100.0	473	8 AY210328	AY210328 Fusarium
29	18	100.0	473	8 AY210333	AY210333 Fusarium
30	18	100.0	475	8 SCAJ2875	AY002875 Fungal is
31	18	100.0	477	8 AY210330	AY210330 Fusarium
32	18	100.0	480	8 AY210331	AY210331 Fusarium
33	18	100.0	480	8 AY210332	AY210332 Fusarium
34	18	100.0	481	8 AY210327	AY210327 Nectria s
35	18	100.0	482	8 AF111057	AF111057 Fusarium
36	18	100.0	483	8 AY043477	AY043477 Nectria h
37	18	100.0	483	8 AY273333	AY273333 Unculture
38	18	100.0	486	8 SCAJ2876	AY002876 Fungal is
39	18	100.0	487	8 AF165875	AF165875 Fusarium
40	18	100.0	489	8 AF502862	AF502862 Leaf lict
41	18	100.0	489	8 AY160207	AY160207 Fusarium
42	18	100.0	489	8 AY160209	AY160209 Fusarium
43	18	100.0	490	8 AF502792	AF502792 Leaf lict
44	18	100.0	492	8 AF111053	AF111053 Fusarium
45	18	100.0	492	8 AF111059	AF111059 Fusarium

## ALIGNMENTS

RESULT 1  
AR206453  
LOCUS AR206453 18 bp DNA  
DEFINITION Sequence 59 from patent US 6372430.  
ACCESSION AR206453  
VERSION AR206453.1 GI:21505059  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.Soo.  
Nucleic acids for detecting Aspergillus species and other  
filamentous fungi  
Patent: US 6372430-A 59 16-APR-2002;

Pred. No. is the number of results predicted by chance to have a

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Best Local Similarity	100.0%; Pred. No. 42;	
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DB	1	CCCACTTCTGATGTTG 18
RESULT 2		
BD083644		18 bp DNA linear PAT 27-AUG-2002
LOCUS		
DEFINITION	BD083644	Nucleic acids for detecting Aspergillus species and other filamentous fungi.
ACCESSION	BD083644	
VERSION	BD083644.1	GI:22629254
KEYWORDS	JP 2001525665-A/59.	
SOURCE		Rhizopus microsporus
ORGANISM		Rhizopus microsporus
		Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae; Rhizopus.
REFERENCE		1 (baes 1 to 18)
AUTHORS		Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.
TITLE		Nucleic acids for detecting Aspergillus species and other filamentous fungi
JOURNAL		Patent: JP 2001525665-A 59 11-DEC-2001;
		THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE
COMMENT		PN JP 2001525665-A/59
	PD	11-DEC-2001
	PF	01-MAY-1998 JP 1998548275
	PR	02-MAY-1997 US 60/045400
	PI	CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO
	PI	CHOI
	PC	CI2Q1/68
	CC	Strandedness: Single;
	CC	Topology: linear;
FEATURES		
source	FH	key Location/Qualifiers.
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		/mol_type="genomic DNA"
		/db_xref="taxon:58291"
ORIGIN		
Query Match	100.0%; Score 18; DB 6; Length 18;	
Best Local Similarity	100.0%; Pred. No. 42;	
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1	CCCACTTCTGATGTTG 18
DB	1	CCCACTTCTGATGTTG 18
RESULT 3		
AY226096		298 bp DNA linear PLN 27-MAR-2003
LOCUS		
DEFINITION	AY226096	Nectria haematococca 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION	AY226096	
VERSION	AY226096.1	GI:29293692
KEYWORDS		Nectria haematococca
SOURCE		

ORGANISM	Nectria haematococca
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
AUTHORS	1 (bases 1 to 298)
TITLE	Millar,B.C., Xu,J. and Moore,J.E.
JOURNAL	Direct Submission
FEATURES	Submitted (28-JUN-2003) Department of Bacteriology, Northern Ireland Public Health Laboratory, Belfast City Hospital, Lisburn Road, Belfast, Co. Antrim BT9 7AD, Northern Ireland, UK
SOURCE	Location/Qualifiers 1..298 /organism="Nectria haematococca" /mol_type="genomic DNA" /strain="260499/24" /db_xref="taxon:140110" <1..132 /product="5.8S ribosomal RNA" 133..245 /product="internal transcribed spacer 2" 246..>298 /product="28S ribosomal RNA"
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Query Match	100.0%; Score 18; DB 8; Length 298;
Best Local Similarity	100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 CCCAACTTCGAATGTTG 18       Db 240 CCCAATTCTGAATGTTG 257
RESULT 4	
LOCUS	AR206401 310 bp DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 7 from patent US 6372430.
ACCESSION	AR206401
VERSION	AR206401.1 GI:21504992
KEYWORDS	.
SOURCE	Unknown. Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 310)
AUTHORS	Morrison,C.V., Reis,E., Aidorevich,L. and Choi,V.Soo.
TITLE	Nucleic acids for detecting Aspergillus species and other filamentous fungi
JOURNAL	Patent: US 6372430-A 7 16-APR-2002;
FEATURES	Location/Qualifiers 1..310 /organism="unknown" /mol_type="unassigned DNA"
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 CCCAACTTCGAATGTTG 18       Db 258 CCCAATTCTGAATGTTG 275
RESULT 5	
LOCUS	BD083592 310 bp DNA linear PAT 27-AUG-2002
DEFINITION	Nucleic acids for detecting Aspergillus species and other filamentous fungi.
ACCESSION	BD083592
VERSION	BD083592.1 GI:22629202
KEYWORDS	JP 2001525665-A/7.
SOURCE	Gibberella fujikuroi Gibberella fujikuroi Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujiikuroi complex.  
1 (bases 1 to 310)  
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.  
Nucleic acids for detecting Aspergillus species and other filamentous fungi.  
Patent: JP 2001525665-A 7 11-DEC-2001;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE  
OS Fusarium moniliforme  
PN JP 2001525665-A/7  
PD 11-DEC-2001  
PF 01-MAY-1998 JP 1998548275  
PR 02-MAY-1997 US 60/045400  
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO  
PC C1201/68  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18  
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258 CCCAACTTCTGAATGTTG 275

Db 258 CCCAACTTCTGAATGTTG 275

RESULT 6  
AF117922 310 bp DNA linear PLN 17-JUN-2000  
LOCUS Gibberella fujiikuroi ATCC 38519 5.8S ribosomal RNA gene, partial  
DEFINITION sequence: internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
AF117922 AF117922.1 GI:8570108

ACCESSION  
VERSION AF117922.1  
KEYWORDS  
SOURCE  
ORGANISM Gibberella fujiikuroi  
Gibberella fujiikuroi  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella; Gibberella fujiikuroi complex.  
1 (bases 1 to 310)  
Choi,J.S., Westerman,J.M. and Morrison,C.J.  
Rapid differentiation of filamentous fungi using species-specific DNA probes  
Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)  
2 (bases 1 to 310)  
Choi,J.S., Westerman,J.M. and Morrison,C.J.  
Direct Submission  
Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA 30333, USA  
Location/Qualifiers  
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/organism="Gibberella fujiikuroi"  
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159..272  
misc\_RNA

/product="internal transcribed spacer 2"  
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273..310  
/product="28S ribosomal RNA"

ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 310;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18  
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258 CCCAACTTCTGAATGTTG 275

Db 258 CCCAACTTCTGAATGTTG 275

RESULT 7  
AR206400 319 bp DNA linear PAT 20-JUN-2002  
LOCUS AR206400  
DEFINITION Sequence 6 from patent US 6372430.  
AR206400  
VERSION AR206400.1 GI:21504990

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 319)  
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.Soo.  
Nucleic acids for detecting Aspergillus species and other filamentous fungi  
Patent: US 6372430-A 6 16-APR-2002;  
Location/Qualifiers  
1..319  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 319;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18  
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267 CCCAACTTCTGAATGTTG 284

Db 267 CCCAACTTCTGAATGTTG 284

RESULT 8  
BD083591 319 bp DNA linear PAT 27-AUG-2002  
LOCUS BD083591  
DEFINITION Nucleic acids for detecting Aspergillus species and other filamentous fungi.  
BD083591  
VERSION BD083591.1 GI:22629201  
KEYWORDS JP 2001525665-A/6.  
SOURCE Fusarium solani  
ORGANISM Fusarium solani  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
1 (bases 1 to 319)  
Morrison,C.J., Reiss,E., Aidorevich,L. and Choi,J.S.  
Nucleic acids for detecting Aspergillus species and other filamentous fungi  
Patent: JP 2001525665-A 6 11-DEC-2001;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES C/O CENTERS FOR JAPAN FORAGE SEED ASSOCIATION DISEASE CONTROL AND PREVENTION TECHNOLOGY TRANSFER OFFICE  
OS Fusarium solani  
PN JP 2001525665-A/6  
PD 11-DEC-2001  
PF 01-MAY-1998 JP 1998548275  
PR 02-MAY-1997 US 60/045400  
PI CHRISTINE J MORRISON,ERROL REISS,LILIANA AIDOREVICH,JONG SOO

FEATURES	source	PI	CHOI
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		CC	Strandedness: Single;
		CC	Topology: Linear;
	FH	Key	Location/Qualifiers.
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			/note="Fusarium solani"
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Best Local Similarity	100.0%; Pred. NO. 44;		
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 CCCAACTTCTGAATGTTG 18		
Db	267 CCCAATTCTGAATGTTG 284		
RESULT 9			
LOCUS	AF117921	319 bp	DNA linear
DEFINITION	Nectria haematococca 5.8S ribosomal RNA gene, partial sequence, internal transcribed spacer 2, complete sequence, and 26S ribosomal RNA gene, partial sequence.		
ACCESSION	AF117921		
VERSION	AF117921.1	GI:8570107	
KEYWORDS			
SOURCE			
ORGANISM	Fusarium solani		
	Fusarium solani		
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.		
REFERENCE	1 (bases 1 to 319)		
AUTHORS	Choi,J.S., Westerman,J.M. and Morrison,C.J.		
TITLE	Rapid differentiation of filamentous fungi using species-specific DNA probes		
JOURNAL	Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)		
REFERENCE	2 (bases 1 to 319)		
AUTHORS	Choi,J.S., Westerman,J.M. and Morrison,C.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA 30333, USA		
FEATURES	Location/Qualifiers		
source	1. .319		
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	/db_xref="taxon:169388"		
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misc_RNA	160. .272		
	/product="internal transcribed spacer 2"		
rRNA	/note="ITS2"		
	273. .>319		
	/product="28S ribosomal RNA"		
ORIGIN			
Query Match	100.0%; Score 18; DB 8; Length 319;		
Best Local Similarity	100.0%; Pred. NO. 44;		
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 CCCAACTTCTGAATGTTG 18		
Db	267 CCCAATTCTGAATGTTG 284		
RESULT 10			
LOCUS	AF162901	332 bp	DNA linear
DEFINITION	Fusarium equiseti 5.8S ribosomal RNA gene, partial sequence, internal transcribed spacer 2, complete sequence, and 26S ribosomal		

ACCESSION	RNA gene, partial sequence.					
VERSION	AF162901					
KEYWORDS	AF162901.1 GI:5690390					
SOURCE						
ORGANISM	Fusarium equiseti					
REFERENCE	Submitted (28-JUN-1999) Biology, SangWYung University, 7 Hong Ji					
AUTHORS	Min,B.R.					
TITLE	Direct Submission					
JOURNAL	Submitted (28-JUN-1999) Biology, SangWYung University, 7 Hong Ji					
FEATURES	Hypocremyces; Hypocreales; mitosporic Hypocreales; Fusarium.					
SOURCE	1 (bases 1 to 332)					
	Location/Qualifiers					
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	/strain="MAFF 236724"					
	/db_xref="taxon:61235"					
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	/product="5.8S ribosomal RNA"					
misc_RNA	129..274					
	/product="internal transcribed spacer 2"					
rRNA	275..>332					
	/product="28S ribosomal RNA"					
ORIGIN						
Query Match	100.0%; Score 18; DB 8; Length 332;					
Best Local Similarity	100.0%; Pred. No. 44;					
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1 CCCAACTTCGAATGTTG 18					
Db	260 CCCAACTTCGAATGTTG 277					
RESULT 11						
LOCUS	AF162902 334 bp DNA linear PLN 04-AUG-1999					
DEFINITION	Fusarium pallidoreum 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.					
ACCESSION	AF162902					
VERSION	AF162902.1 GI:5690391					
KEYWORDS	Fusarium pallidoreum					
SOURCE	Fusarium pallidoreum					
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocremyces; Hypocreales; mitosporic Hypocreales; Fusarium.					
REFERENCE	1 (bases 1 to 334)					
AUTHORS	Min,B.R.					
TITLE	Direct Submission					
JOURNAL	Submitted (28-JUN-1999) Biology, SangWYung University, 7 Hong Ji					
FEATURES	Dong, Chong Ro-Gu, Seoul 110-743, Korea					
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rRNA	277..>334					
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Best Local Similarity	100.0%; Pred. No. 44;					
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1 CCCAACTTCGAATGTTG 18					

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Db      262  CCNACTTCGATGTTG 279
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RESULT 12
AF162898      335 bp  DNA  linear  PLN 15-NOV-2001
LOCUS      AF162898
DEFINITION  Fusarium oxysporum f. sp. conglutinans 5.8S ribosomal RNA gene,
partial sequence; internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence.
ACCESSION  AF162898.1 GI:5690387
VERSION    AF162898
KEYWORDS
SOURCE
ORGANISM  Fusarium oxysporum f. sp. conglutinans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 335)
REFERENCE  Min,B.R.
AUTHORS   Direct Submission
TITLE     Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
JOURNAL   Dong, Chong Ro-Gu, Seoul 110-743, Korea
FEATURES
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/strain="MAF 744001"
/db_xref="taxon:100902"
/note="forma specialis: conglutinans"
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129..277
/product="internal transcribed spacer 2"
278..335
/product="28S ribosomal RNA"

ORIGIN
Query Match      100.0%; Score 18; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCCAACTTCGATGTTG 18
|||||
Db      263  CCNACTTCGATGTTG 280
|||||

RESULT 13
AF162899      335 bp  DNA  linear  PLN 04-AUG-1999
LOCUS      AF162899
DEFINITION  Fusarium oxysporum f. sp. fragariae 5.8S ribosomal RNA gene,
partial sequence; internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence.
ACCESSION  AF162899.1 GI:5690388
VERSION    AF162899
KEYWORDS
SOURCE
ORGANISM  Fusarium oxysporum f. sp. fragariae
Fusarium oxysporum f. sp. fragariae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 335)
REFERENCE  Min,B.R.
AUTHORS   Direct Submission
TITLE     Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
JOURNAL   Dong, Chong Ro-Gu, Seoul 110-743, Korea
FEATURES
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129..277
/product="internal transcribed spacer 2"
278..335
/product="28S ribosomal RNA"

ORIGIN
Query Match      100.0%; Score 18; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCCACTTCGATGTTG 18
|||||
Db      263  CCNACTTCGATGTTG 280
|||||

RESULT 14
AF162900      336 bp  DNA  linear  PLN 04-AUG-1999
LOCUS      AF162900
DEFINITION  Fusarium oxysporum f. sp. raphani 5.8S ribosomal RNA gene, partial
sequence; internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION  AF162900.1 GI:5690389
VERSION    AF162900
KEYWORDS
SOURCE
ORGANISM  Fusarium oxysporum f. sp. raphani
Fusarium oxysporum f. sp. raphani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
1 (bases 1 to 336)
REFERENCE  Min,B.R.
AUTHORS   Direct Submission
TITLE     Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
JOURNAL   Dong, Chong Ro-Gu, Seoul 110-743, Korea
FEATURES
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/db_xref="taxon:96318"
/note="forma specialis: raphani"
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129..274
/product="internal transcribed spacer 2"
275..336
/product="28S ribosomal RNA"

ORIGIN
Query Match      100.0%; Score 18; DB 8; Length 336;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCCACTTCGATGTTG 18
|||||
Db      264  CCNACTTCGATGTTG 281
|||||

RESULT 15
AF339418      338 bp  DNA  linear  PLN 25-OCT-2002
LOCUS      AF339418
DEFINITION  Fusarium oxysporum strain FS-1 5.8S ribosomal RNA gene, partial
sequence; internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION  AF339418.1 GI:24369714
VERSION    AF339418
KEYWORDS
SOURCE
ORGANISM  Fusarium oxysporum
Fusarium oxysporum


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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;  
Fusarium oxysporum complex.

REFERENCE  
AUTHORS  
TITLE  
1 (bases 1 to 338)  
Toohey, P.W., Hatziloukas, E., Scott, D.L. Jr. and Carras, M.M.  
Use of ligase chain reaction for detection of Phytophthora  
infestans in potatoes

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 338)  
Toohey, P.W., Hatziloukas, E., Scott, D.L. Jr. and Carras, M.M.  
Direct Submission  
Submitted (22-JAN-2001) Agricultural Research Service, U.S.  
Department of Agriculture, 1301 Ditto Ave., Ft. Detrick, MD  
21702-5023, USA

FEATURES  
source  
Location/Qualifiers  
1..338  
/organism="Fusarium oxysporum"  
/mol\_type="genomic DNA"  
/strain="PS-1"  
/db\_xref="taxon:5507"  
<1..>338  
/note="contains 5.8S ribosomal RNA, internal transcribed  
spacer 2, and 28S ribosomal RNA"

ORIGIN  
Query Match 100.0%; Score 18; DB 8; Length 338;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAAGTTGGAATGTTG 18  
|||  
Db 265 CCCAAGTTGGAATGTTG 282

Search completed: October 1, 2004, 05:17:04  
Job time : 148.108 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:09:43 ; Search time 5.93182 Seconds  
(without alignments)  
1683.989 Million cell updates/sec

Title: US-10-046-955-59

Perfect score: 18  
Sequence: 1 cccactctcgatgctg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfilest.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	4	US-09-423-233-59
2	18	100.0	310	4	US-09-423-233-7
3	18	100.0	319	4	US-09-423-233-6
4	18	100.0	503	1	US-08-887-480-83
5	18	100.0	503	1	US-08-905-314A-20
6	18	100.0	503	1	US-08-722-187-83
7	18	100.0	503	1	PCT-US95-04712-83
8	18	100.0	504	1	US-08-887-480-82
9	18	100.0	504	1	US-08-905-314A-19
10	18	100.0	504	2	US-08-722-187-82
11	18	100.0	504	4	US-09-481-293-32
12	18	100.0	504	5	PCT-US95-04712-82
13	18	100.0	545	1	US-08-887-480-84
14	18	100.0	545	1	US-08-905-314A-21
15	18	100.0	546	1	US-08-887-480-96
16	18	100.0	546	1	US-08-905-314A-22
17	18	100.0	561	1	US-08-905-314A-24
18	18	100.0	2293	3	US-09-645-073-1
19	18	100.0	1258	3	US-08-335-518-1
20	17	94.4	1258	3	US-08-988-054-1
21	15.4	85.6	583	1	US-08-652-127C-8
22	15.4	85.6	611	1	US-08-986-727-4
23	15	83.3	1309	2	US-08-933-750C-63
24	15	83.3	1309	3	US-09-234-613-63
25	15	83.3	1426	3	US-09-121-425-4
26	15	83.3	1426	4	US-09-634-493A-4
27	15	83.3	2513	4	US-09-016-434-1166

28	15	83.3	39982	4	US-09-820-924-3	Sequence 3, Appli
29	14.8	82.2	894	4	US-09-107-532A-1065	Sequence 1065, Ap
30	14.8	82.2	1536	4	US-09-489-039A-511	Sequence 511, App
31	14.8	82.2	4079	4	US-09-016-434-1219	Sequence 1219, Ap
32	14.8	82.2	4910	3	US-09-023-655-1125	Sequence 1125, Ap
33	14.8	82.2	11703	3	US-09-101-886B-3	Sequence 3, Appli
34	14.8	82.2	246240	2	US-08-724-394A-20	Sequence 20, Appl
35	14.8	82.2	246240	2	US-08-724-394A-21	Sequence 21, Appl
36	14.8	82.2	246240	2	US-08-724-394A-22	Sequence 22, Appl
37	14.4	80.0	163	3	US-08-986-727-13	Sequence 13, Appl
38	14.4	80.0	284	4	US-09-313-294A-1021	Sequence 1021, Ap
39	14.4	80.0	415	3	US-08-905-223-166	Sequence 166, App
40	14.4	80.0	1053	4	US-09-148-545-91	Sequence 91, Appl
41	14.4	80.0	1075	4	US-09-148-545-92	Sequence 92, Appl
42	14.4	80.0	1105	4	US-09-148-545-26	Sequence 26, Appl
43	14.4	80.0	1317	4	US-09-350-756-5	Sequence 5, Appli
44	14.4	80.0	2088	1	US-08-331-394-1	Sequence 1, Appli
45	14.4	80.0	2088	1	US-08-250-858-1	Sequence 1, Appli

## ALIGNMENTS

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RESULT 1
US-09-423-233-59
Sequence 59, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 59
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium sp.
US-09-423-233-59

Query Match      100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CCCAAGCTTGAATGTTG 18
Db      1 CCCAAGCTTGAATGTTG 18

RESULT 2
US-09-423-233-7
Sequence 7, Application US/09423233
Patent No. 6372430
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 03063-0341WP
CURRENT APPLICATION NUMBER: US/09/423,233
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 310
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-09-423-233-7

Query Match      100.0%; Score 18; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCCACTTCTGAATGTTG 18  
Db 258 CCCACTTCTGAATGTTG 275

## RESULT 3

US-09-423-233-6  
Sequence 6, Application US/09423233  
Patent No. 6372430  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America as  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
FILE REFERENCE: 03063-0341WP  
CURRENT FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 6  
LENGTH: 319  
TYPE: DNA  
ORGANISM: Fusarium solani  
US-09-423-233-6

Query Match 100.0%; Score 18; DB 4; Length 319;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18  
Db 267 CCCACTTCTGAATGTTG 284

## RESULT 4

US-08-887-480-83  
Sequence 83, Application US/08887480  
Patent No. 5814453  
GENERAL INFORMATION:  
APPLICANT: Beck, James J.  
TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
TITLE OF INVENTION: Polymerase Chain Reaction  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5814453artis Corporation  
STREET: 520 White Plains Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,480  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/722,187  
FILING DATE: 15-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 503 base pairs  
TYPE: nucleic acid

## STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Fusarium graminearum

INDIVIDUAL ISOLATE: R-8417, R-8422, and R-8546

INDIVIDUAL ISOLATE: (consensus sequence)

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..9 /note= "3' end of small subunit

OTHER INFORMATION: rRNA gene"

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 10..155 /note= "ITS 1"

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 156..312 /note= "5.8S rRNA gene"

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 313..466 /note= "ITS 2"

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 467..503 /note= "5' end of large subunit

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 504..503

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 504..503

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 504..503

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 504..503

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 504..503

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 504..503

OTHER INFORMATION:

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NAME/KEY: misc\_feature

LOCATION: 504..503

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 504..503

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 504..503

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 504..503

Query Match 100.0%; Score 18; DB 1; Length 503;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18  
Db 451 CCCACTTCTGAATGTTG 468

## RESULT 5

US-08-905-314A-20  
Sequence 20, Application US/08905314A  
Patent No. 5827695  
GENERAL INFORMATION:  
APPLICANT: Beck, James J.  
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5827695artis Corporation Patent Department  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 20779-2257  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,314A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1944  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 20:



```
SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium graminearum
INDIVIDUAL ISOLATE: R-8417, R-8422, and R-8546
INDIVIDUAL ISOLATE: (consensus sequence)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..9
OTHER INFORMATION: /note="3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10..155
OTHER INFORMATION: /note="ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 156..312
OTHER INFORMATION: /note="5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 313..466
OTHER INFORMATION: /note="ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 467..503
OTHER INFORMATION: /note="5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314A-20
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Query Match          100.0%; Score 18; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CCCAACTTCGAAGTTG 18
    |||||
Db 451 CCCAACTTCGAAGTTG 468
```

```
RESULT 6
US-08-722-187-83
Sequence 83, Application US/08722187
GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722.187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..503
OTHER INFORMATION: /note="DNA sequence for the
OTHER INFORMATION: internal transcribed spacer region of Fusarium graminearum"
OTHER INFORMATION: (fggram.con)"
US-08-722-187-83
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Query Match          100.0%; Score 18; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CCCAACTTCGAAGTTG 18
    |||||
Db 451 CCCAACTTCGAAGTTG 468
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```
RESULT 7
PCT-US95-04712-83
Sequence 83, Application PC/TUS9504712
GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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? HYPOTHEITICAL: NO
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 1..503
? OTHER INFORMATION: /note= "DNA sequence for the
? OTHER INFORMATION: internal transcribed spacer region of Fusarium graminearum
? OTHER INFORMATION: (Igram.com)"
? CCT-US95-04712-83

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Query Match	100.0%;	Score 18;	DB 5;	Length 503;
Best Local Similarity	100.0%;	Pred. No. 2;		
Matches	18;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAAGCTTCTGAATGTTG 18  
 Db 451 CCCAAGCTTCTGAATGTTG 468

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1 RESULT 8
2 US-08-887-480-82
3 ; Sequence 82, Application US/08887480
4 Patent No. 581453
5 GENERAL INFORMATION:
6 APPLICANT: Beck, James J
7 TITLE OF INVENTION: Detection of Fungal Pathogens Using the
8 TITLE OF INVENTION: Polymerase Chain Reaction
9 NUMBER OF SEQUENCES: 96
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: No. 581453artis Corporation
12 STREET: 520 White Plains Road
13 CITY: Tarrytown
14 STATE: NY
15 COUNTRY: USA
16 ZIP: 10591
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/887,480
24 FILING DATE:
25 CLASSIFICATION: 435
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 08/722,187
28 FILING DATE: 15-OCT-1996
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Weigs, J. Timothy
31 REGISTRATION NUMBER: 38,241
32 REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 919-541-8587
35 TELEFAX: 919-541-8689
36 INFORMATION FOR SEQ ID NO: 82:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 504 base pairs
39 TYPE: nucleic acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 MOLECULE TYPE: DNA (genomic)
43 ORIGINAL SOURCE:
44 ORGANISM: Fusarium culmorum
45 INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
46 INDIVIDUAL ISOLATE: (consensus sequence)
47 FEATURE:
48 NAME/KEY: misc_feature
49 LOCATION: 1..112
50 OTHER INFORMATION: /note= "3' end of small subunit"
51 OTHER INFORMATION: rRNA gene"
52 FEATURE:
53 NAME/KEY: misc_feature
54 LOCATION: 13..161
55 OTHER INFORMATION: /note= "ITS 1"
56

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? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 162..318
? OTHER INFORMATION: /note="5.8S rRNA gene"
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 319..472
? OTHER INFORMATION: /note="ITS 2"
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 473..504
? OTHER INFORMATION: /note="5' end of large subunit"
? OTHER INFORMATION: rRNA gene"
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US-08-887-480-82
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Query Match	100.0%	Score 18	DB 1	Length 504
Best Local Similarity	100.0%	Pred. No. 2		
Matches 18	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 CCCAACTTCTGAATGTTG 18  
Db 457 CCCAACTTCTGAATGTTG 474

RESULT 9  
 US-08-905-314A-19  
 Sequence 19, Application US/08905314A  
 Patent No. 5827695  
 GENERAL INFORMATION:  
 APPLICANT: Beck, James J.  
 TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
 TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: No. 5827695artis Corporation Patent Department  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: NC  
 COUNTRY: USA  
 ZIP: 20779-2257  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/905,314A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: CGC 1944  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 541-8587  
 TELEFAX: (919) 541-8689  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 504 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 ORGANISM: *Fusarium culmorum*  
 INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146  
 INDIVIDUAL ISOLATE: (consensus sequence)  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1..12  
 OTHER INFORMATION: /note="3" end of small subunit  
 OTHER INFORMATION: rRNA gene"

NAME/KEY: misc\_feature  
LOCATION: 13..161  
OTHER INFORMATION: /note="ITS 1"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 162..318  
OTHER INFORMATION: /note="5.8S rRNA gene"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 319..472  
OTHER INFORMATION: /note="ITS 2"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 473..504  
OTHER INFORMATION: /note="5' end of large subunit"  
OTHER INFORMATION: rRNA gene"  
US-08-905-314A-19

Query Match 100.0%; Score 18; DB 1; Length 504;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAAGTTCTGAATGTTG 18  
|||||  
DB 457 CCCAAGTTCTGAATGTTG 474

RESULT 10  
US-08-722-187-82  
Sequence 82, Application US/08722187  
Patent No. 5955274  
GENERAL INFORMATION:  
APPLICANT: Ligon, James M  
TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
TITLE OF INVENTION: Polymerase Chain Reaction  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ciba-Geigy Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/722.187  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/233,608  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Walsh, Andrea C.  
REGISTRATION NUMBER: 34,988  
REFERENCE/DOCKET NUMBER: CGC 1739  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8666  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: misc\_feature

LOCATION: 1..504  
OTHER INFORMATION: /note="DNA sequence for the  
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum  
OTHER INFORMATION: (fculm.con)"  
US-08-722-187-82

Query Match 100.0%; Score 18; DB 2; Length 504;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAAGTTCTGAATGTTG 18  
|||||  
DB 457 CCCAAGTTCTGAATGTTG 474

RESULT 11  
US-09-481-293-32  
Sequence 32, Application US/09481293  
Patent No. 6485907  
GENERAL INFORMATION:  
APPLICANT: Beck, James  
APPLICANT: Barnett, Jason  
TITLE OF INVENTION: PCR-Based Detection of Rhizoctonia cerealis  
FILE REFERENCE: PB/5-31135p1  
CURRENT APPLICATION NUMBER: US/09/481.293  
CURRENT FILING DATE: 2000-01-11  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 32  
LENGTH: 504  
TYPE: DNA  
ORGANISM: Fusarium culmorum  
US-09-481-293-32

Query Match 100.0%; Score 18; DB 4; Length 504;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAAGTTCTGAATGTTG 18  
|||||  
DB 459 CCCAAGTTCTGAATGTTG 476

RESULT 12  
PCT-US95-04712-82  
Sequence 82, Application PC/TUS9504712  
GENERAL INFORMATION:  
APPLICANT: Ligon, James M  
APPLICANT: Beck, James J  
TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
TITLE OF INVENTION: Polymerase Chain Reaction  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ciba-Geigy Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04712  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/233,608  
FILING DATE: 04-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Walsh, Andrea C.

REGISTRATION NUMBER: 34,988  
REFERENCE/DOCKET NUMBER: CGC 1739  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8666  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..504  
OTHER INFORMATION: /note= "DNA sequence for the  
OTHER INFORMATION: internal transcribed spacer region of Fusarium culmorum  
OTHER INFORMATION: (fcuim.con)"  
PCT-US95-04712-82

Query Match 100.0%; Score 18; DB 5; Length 504;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACTTCGATGTTG 18  
Db 457 CCCACTTCGATGTTG 474

RESULT 13  
US-08-887-480-84  
; Sequence 84, Application US/08887480  
; Patent No. 5814453  
; GENERAL INFORMATION:  
; APPLICANT: Beck, James J  
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 581453artis Corporation  
; STREET: 520 White Plains Road  
; CITY: Tarrytown  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,480  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/722,187  
; FILING DATE: 15-OCT-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 84:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 545 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:

ORGANISM: Fusarium moniliforme  
INDIVIDUAL ISOLATE: 4551  
IMMEDIATE SOURCE:  
CLONE: PCRMON1  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..30  
OTHER INFORMATION: /note= "3' end of small subunit  
OTHER INFORMATION: rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 31..178  
OTHER INFORMATION: /note= "ITS 1"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 179..335  
OTHER INFORMATION: /note= "5.8S rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 336..488  
OTHER INFORMATION: /note= "ITS 2"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 489..545  
OTHER INFORMATION: /note= "5' end of large subunit  
OTHER INFORMATION: rRNA gene"  
US-08-887-480-84

Query Match 100.0%; Score 18; DB 1; Length 545;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACTTCGATGTTG 18  
Db 473 CCCACTTCGATGTTG 490

RESULT 14  
US-08-905-314A-21  
; Sequence 21, Application US/08905314A  
; Patent No. 5827695  
; GENERAL INFORMATION:  
; APPLICANT: Beck, James J.  
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS  
; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5827695artis Corporation Patent Department  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 20779-2257  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/905,314A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC 1944  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8587  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 545 base pairs  
; TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Fusarium moniliforme  
INDIVIDUAL ISOLATE: 4551  
IMMEDIATE SOURCE:  
CLONE: PCRPMON1  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..30  
OTHER INFORMATION: /note= "3' end of small subunit"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 31..178  
OTHER INFORMATION: /note= "ITS 1"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 179..335  
OTHER INFORMATION: /note= "5.8S rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 336..488  
OTHER INFORMATION: /note= "ITS 2"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 489..545  
OTHER INFORMATION: /note= "5' end of large subunit"  
OTHER INFORMATION: rRNA gene"  
US-08-905-314A-21

Query Match 100.0%; Score 18; DB 1; Length 545;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCCAAGTTCTGATGTTG 18  
Db 473 CCCAAGTTCTGATGTTG 490

RESULT 15  
US-08-887-480-96  
Sequence 96, Application US/08887480  
Patent No. 5814453  
GENERAL INFORMATION:  
APPLICANT: Beck, James J  
TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
TITLE OF INVENTION: Polymerase Chain Reaction  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5814453artis Corporation  
STREET: 520 White Plains Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,480  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/722,187  
FILING DATE: 15-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
FAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 546 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: Fusarium poae  
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus  
INDIVIDUAL ISOLATE: sequence)  
IMMEDIATE SOURCE:  
CLONE: PCRPMON1427(1-2), PCRPMON1534(2-2), and  
CLONE: PCRPMON1756(3-1)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..30  
OTHER INFORMATION: /note= "3' end of small subunit"  
OTHER INFORMATION: rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 31..180  
OTHER INFORMATION: /note= "ITS 1"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 181..337  
OTHER INFORMATION: /note= "5.8S rRNA gene"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 338..489  
OTHER INFORMATION: /note= "ITS 2"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 490..546  
OTHER INFORMATION: /note= "5' end of large subunit"  
OTHER INFORMATION: rRNA gene"  
US-08-887-480-96

Query Match 100.0%; Score 18; DB 1; Length 546;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCCAAGTTCTGATGTTG 18  
Db 474 CCCAAGTTCTGATGTTG 491

Search completed: October 1, 2004, 08:06:06  
Job time: 7.93182 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:20:11 ; Search time 73.304 Seconds  
(without alignments)  
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Title: US-10-046-955-59

Perfect score: 18

Sequence: 1 cccacttcgcatgttg 18

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6661306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-046-955-59	Sequence 59, Appl
2	18	100.0	310	US-10-046-955-7	Sequence 6, Appl
3	18	100.0	319	US-10-046-955-6	Sequence 6, Appl
4	18	100.0	521	US-09-961-755A-6	Sequence 6, Appl
5	18	100.0	522	US-09-961-755A-5	Sequence 5, Appl
6	18	100.0	522	US-09-961-755A-7	Sequence 8, Appl
7	18	100.0	534	US-09-961-755A-8	Sequence 7, Appl
8	17	94.4	666	US-10-027-632-229494	Sequence 229494,
9	17	94.4	666	US-10-027-632-229494	Sequence 229494,
10	16.4	91.1	382	US-10-424-599-66950	Sequence 66950, A
11	16.4	91.1	879	US-10-767-701-4881	Sequence 4881, Ap
12	16.4	91.1	906	US-10-437-963-82909	Sequence 82909, A
13	16.4	91.1	1566	US-10-437-963-82910	Sequence 82910, A
14	16.4	91.1	13444	US-09-764-877-3660	Sequence 3660, Ap

15	16.4	91.1	13444	US-10-242-515-3660	Sequence 3660, Ap
16	16.4	91.1	67674	US-10-316-242-11	Sequence 11, Appl
17	15.4	85.6	332	US-10-424-599-19065	Sequence 19065, A
18	15.4	85.6	340	US-10-198-846-11981	Sequence 11981, A
19	15.4	85.6	385	US-10-424-599-120953	Sequence 120953, A
20	15.4	85.6	476	US-10-424-599-70014	Sequence 70014, A
21	15.4	85.6	579	US-10-424-599-57294	Sequence 57294, A
22	15.4	85.6	617	US-10-027-632-94609	Sequence 94609, A
23	15.4	85.6	617	US-10-027-632-305503	Sequence 305503, A
24	15.4	85.6	617	US-10-027-632-94609	Sequence 94609, A
25	15.4	85.6	617	US-10-027-632-305503	Sequence 305503, A
26	15.4	85.6	660	US-10-767-701-24598	Sequence 24598, A
27	15.4	85.6	739	US-10-198-846-13876	Sequence 13876, Ap
28	15.4	85.6	828	US-10-424-599-4529	Sequence 4529, Ap
29	15.4	85.6	1500	US-10-369-493-27922	Sequence 27922, A
30	15.4	85.6	1582	US-10-424-599-114901	Sequence 114901, A
31	15.4	85.6	1599	US-10-282-122A-12302	Sequence 12302, A
32	15.4	85.6	3607	US-10-424-599-19067	Sequence 19067, A
33	15.4	85.6	23640	US-10-087-192-12439	Sequence 12439, Ap
34	15.4	85.6	46030	US-10-367-094-1	Sequence 1, Appl
35	15.4	85.6	55135	US-09-735-933-1	Sequence 3, Appl
36	15.4	85.6	89213	US-10-322-281-843	Sequence 843, App
37	15.4	85.6	90100	US-09-997-722-295	Sequence 295, App
38	15.4	85.6	188794	US-10-322-696-112	Sequence 112, App
39	15	83.3	211	US-10-085-783A-33208	Sequence 33208, A
40	15	83.3	211	US-10-242-535A-33208	Sequence 33208, A
41	15	83.3	309	US-10-085-783A-55973	Sequence 55973, A
42	15	83.3	309	US-10-242-535A-55973	Sequence 55973, A
43	15	83.3	350	US-10-085-783A-9757	Sequence 9757, Ap
44	15	83.3	350	US-10-242-535A-9757	Sequence 9757, Ap
45	15	83.3	575	US-10-424-599-47112	Sequence 47112, A

#### ALIGNMENTS

##### RESULT 1

US-10-046-955-59  
Sequence 59, Application US/10046955  
Publication No. US20030129600A1  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America, as Represented by the  
Secretary of the Department of Health and Human Services, Centers for Disease  
Control and Prevention  
APPLICANT: Morrison, Christine J.  
APPLICANT: Reiss, Errol  
APPLICANT: Aldorevich, Lilianna  
APPLICANT: Choi, Jong Soo  
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
TITLE OF INVENTION: Other Filamentous Fungi  
FILE REFERENCE: 6395-62064  
CURRENT APPLICATION NUMBER: US/10/046,955  
CURRENT FILING DATE: 2002-06-04  
PRIOR APPLICATION NUMBER: US 09/423,233  
PRIOR FILING DATE: 2000-06-27  
PRIOR APPLICATION NUMBER: PCT/US98/08926  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: US 60/045,400  
PRIOR FILING DATE: 1997-05-02  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 59  
TYPE: DNA  
LENGTH: 18  
ORGANISM: Fusarium sp.  
US-10-046-955-59

Query Match 100.0%, Score 18, DB 15, Length 18,  
Best Local Similarity 100.0%, Pred. No. 12,  
Matches 18, Conservative 0, Mismatches 0, Indels 0, Gaps 0,  
1 CCCACTTCGATGTG 18  
|||||

Db 1 CCCAACTTCTGAATGTTG 18

## RESULT 2

US-10-046-955-7  
; Sequence 7, Application US/10046955  
; Publication No. US20030128600A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as Represented by the  
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis  
; APPLICANT: Control and Prevention  
; APPLICANT: Morrison, Christine J.  
; APPLICANT: Reiss, Errol  
; APPLICANT: Aidorevich, Liliانا  
; APPLICANT: Choi, Jong Soo  
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
; FILE REFERENCE: 6395-62064  
; CURRENT APPLICATION NUMBER: US/10/046,955  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 09/423,233  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: PCT/US98/08926  
; PRIOR FILING DATE: 1998-05-01  
; PRIOR APPLICATION NUMBER: US 60/045,400  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 310  
; TYPE: DNA  
; ORGANISM: Fusarium moniliforme  
US-10-046-955-7

Query Match 100.0%; Score 18; DB 15; Length 310;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18

Db 258 CCCAACTTCTGAATGTTG 275

## RESULT 3

US-10-046-955-6  
; Sequence 6, Application US/10046955  
; Publication No. US20030129600A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as Represented by the  
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis  
; APPLICANT: Control and Prevention  
; APPLICANT: Morrison, Christine J.  
; APPLICANT: Reiss, Errol  
; APPLICANT: Aidorevich, Liliانا  
; APPLICANT: Choi, Jong Soo  
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
; FILE REFERENCE: 6395-62064  
; CURRENT APPLICATION NUMBER: US/10/046,955  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 09/423,233  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: PCT/US98/08926  
; PRIOR FILING DATE: 1998-05-01  
; PRIOR APPLICATION NUMBER: US 60/045,400  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 319  
; TYPE: DNA  
; ORGANISM: Fusarium solani  
US-10-046-955-6

Query Match 100.0%; Score 18; DB 15; Length 319;

Best Local Similarity 100.0%; Pred. No. 19;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18  
Db 267 CCCAACTTCTGAATGTTG 284

## RESULT 4

US-09-961-755A-6  
; Sequence 6, Application US/09961755A  
; Publication No. US20030113722A1  
; GENERAL INFORMATION:  
; APPLICANT: Beck, Jim  
; APPLICANT: Barnett, Jason  
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the  
; FILE REFERENCE: 60055  
; CURRENT APPLICATION NUMBER: US/09/961,755A  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 521  
; TYPE: DNA  
; ORGANISM: Gibberella zeae  
US-09-961-755A-6

Query Match 100.0%; Score 18; DB 10; Length 521;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18  
Db 473 CCCAACTTCTGAATGTTG 490

## RESULT 5

US-09-961-755A-5  
; Sequence 5, Application US/09961755A  
; Publication No. US20030113722A1  
; GENERAL INFORMATION:  
; APPLICANT: Beck, Jim  
; APPLICANT: Barnett, Jason  
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the  
; FILE REFERENCE: 60055  
; CURRENT APPLICATION NUMBER: US/09/961,755A  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 522  
; TYPE: DNA  
; ORGANISM: Fusarium subglutinans  
US-09-961-755A-5

Query Match 100.0%; Score 18; DB 10; Length 522;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGAATGTTG 18  
Db 474 CCCAACTTCTGAATGTTG 491

## RESULT 6

US-09-961-755A-8  
; Sequence 8, Application US/09961755A  
; Publication No. US20030113722A1  
; GENERAL INFORMATION:



```

; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
US-09-961-755A-8

Query Match          100.0%; Score 18; DB 10; Length 522;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCAACTTCTGAATGTTG 18
Db      474 CCAACTTCTGAATGTTG 491

RESULT 7
US-09-961-755A-7
; Sequence 7, Application US/09961755A
; Publication No. US20030113722A1
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7

Query Match          100.0%; Score 18; DB 10; Length 534;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCAACTTCTGAATGTTG 18
Db      486 CCAACTTCTGAATGTTG 503

RESULT 8
US-10-027-632-229494/c
; Sequence 229494, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
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; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 229494
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(666)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-229494

Query Match          94.4%; Score 17; DB 13; Length 666;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  CCAACTTCTGAATGTTG 18
Db      434 CCAACTTCTGAATGTTG 418

RESULT 9
US-10-027-632-229494/c
; Sequence 229494, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 229494
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(666)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-229494

Query Match          94.4%; Score 17; DB 16; Length 666;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  CCAACTTCTGAATGTTG 18
Db      434 CCAACTTCTGAATGTTG 418

RESULT 10
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US-10-424-599-66950/c
; Sequence 66950, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 66950
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31471C.1
US-10-424-599-66950
Query Match          91.1%; Score 16.4; DB 13; Length 382;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18
DB 72 CCCAACTTATGAATGTTG 55

RESULT 11
US-10-767-701-4881
; Sequence 4881, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4881
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS91898_1
US-10-767-701-4881
Query Match          91.1%; Score 16.4; DB 17; Length 879;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18
DB 809 CTCAACTTCTGAATGTTG 826

RESULT 12
US-10-437-963-82909/c
; Sequence 82909, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 82909
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(906)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_82292C.1
US-10-437-963-82909
Query Match          91.1%; Score 16.4; DB 17; Length 906;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18
DB 539 CCCAACTTCTGAATGTCG 522

RESULT 13
US-10-437-963-82910/c
; Sequence 82910, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 82910
; LENGTH: 1566
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_82293C.1
US-10-437-963-82910
Query Match          91.1%; Score 16.4; DB 17; Length 1566;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18
DB 879 CCCAACTTCTGAATGTCG 862

RESULT 14
US-09-764-877-3660
; Sequence 3660, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
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; CURRENT APPLICATION NUMBER: US/09/764,877  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3660  
; LENGTH: 13444  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-877-3660

Query Match 91.1%; Score 16.4; DB 9; Length 13444;  
Best Local Similarity 94.4%; Pred. No. 2.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGATGTTG 18  
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Db 299 CCCAACTTATGATGTTG 316

RESULT 15  
US-10-242-515-3660  
; Sequence 3660, Application US/10242515  
; Publication No. US2004009488A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OR INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC005C1  
; CURRENT APPLICATION NUMBER: US/10/242,515  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/764,877  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3660  
; LENGTH: 13444  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-242-515-3660

Query Match 91.1%; Score 16.4; DB 16; Length 13444;  
Best Local Similarity 94.4%; Pred. No. 2.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGATGTTG 18  
|||  
Db 299 CCCAACTTATGATGTTG 316

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 03:03:48 ; Search time 282 Seconds

(without alignments)  
2133.013 Million cell updates/sec

Title: US-10-046-955-59

Perfect score: 18

Sequence: 1 cccacatcgcgaatgctg 18

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Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

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1: em\_estba:\*  
2: em\_esthum:\*  
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6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estc1:\*  
10: gb\_estc2:\*  
11: gb\_hic:\*  
12: gb\_estc3:\*  
13: gb\_estc4:\*  
14: gb\_estc5:\*  
15: em\_estum:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rnd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrt1:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	379	9	AA112191
2	16.4	91.1	403	14	AA112191 zn60e02.r
3	16.4	91.1	473	10	W19631 w19631
4	16.4	91.1	523	13	BU713295 BU713295

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
AA112191	zn60e02.r1	Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562586 5' similar to WP:F08C6.3 CE02592 ;, mRNA sequence.	AA112191	1	GI:1664478	EST.	Homo sapiens (human)	1 (bases 1 to 379)	Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B., Chisone, S., Dietrich, N., Dubuque, T., Favell, A., Gib, W., Hawkins, M., Hulman, M., Kucaba, T., Lacy, M., Le, N., Maridis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Maria, M.	Generation and analysis of 280,000 human expressed sequence tags	Genome Res. 6 (9), 807-828 (1996)	97044478	8889549
AA112191	zn60e02.r1	Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562586 5' similar to WP:F08C6.3 CE02592 ;, mRNA sequence.	AA112191	1	GI:1664478	EST.	Homo sapiens (human)	1 (bases 1 to 379)	Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B., Chisone, S., Dietrich, N., Dubuque, T., Favell, A., Gib, W., Hawkins, M., Hulman, M., Kucaba, T., Lacy, M., Le, N., Maridis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Maria, M.	Generation and analysis of 280,000 human expressed sequence tags	Genome Res. 6 (9), 807-828 (1996)	97044478	8889549

## ALIGNMENTS

AA112191 379 bp mRNA linear EST 01-AUG-1997  
zn60e02.r1 Stratagene muscle 937209 Homo sapiens cDNA clone  
IMAGE:562586 5' similar to WP:F08C6.3 CE02592 ;, mRNA sequence.

AA112191  
AA112191.1 GI:1664478

EST.  
Homo sapiens (human)

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 379)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B., Chisone, S., Dietrich, N., Dubuque, T., Favell, A., Gib, W., Hawkins, M., Hulman, M., Kucaba, T., Lacy, M., Le, N., Maridis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Maria, M.

Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
97044478  
8889549

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 768 Std Error: 0.00  
 Seq primer: -28M13 rev2 from Amerisham  
 High quality sequence stop: 287.  
 Location/Qualifiers

## FEATURES

## source

1. 379  
 /organism="Homo sapiens"  
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 /db\_xref="GDB:4595876"  
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 /clone="IMAGE:562586"  
 /tissue\_type="muscle"  
 /dev\_stage="adult"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="Stratagene muscle 937209"  
 /note="Organ: skeletal muscle; Vector: pBluescript SK-;  
 Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally.  
 Primer: Oligo dt. Skeletal muscle from patient with  
 malignant hyperthermia. Average insert size: 1.0 kb;  
 Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGACGACG  
 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'"

## ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 379;  
 Best Local Similarity 94.4%; Pred. No. 2.1e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGTTTCGATGTTG 18  
 |||||  
 Db 361 CCCAAGTTTCGATGTTG 378

RESULT 2 403 bp mRNA linear EST 03-MAY-1996  
 W19631 2b55d09.r1 Soares Parathyroid tumor\_NbHRA Homo sapiens cDNA clone  
 IMAGE:305585 5', mRNA sequence.  
 W19631  
 W19631.1 GI:1295540

EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 403)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, P.,  
 Trevaethick, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

Unpublished (1995)  
 The Mashu-Merck EST Project  
 Contact: Wilson RK

Washington University School of Medicine  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Seq primer: mob.NEGA+ET  
 High quality sequence stop: 264.  
 Location/Qualifiers

## FEATURES

## source

1. 403  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1248995"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:305585"

## ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 403;  
 Best Local Similarity 94.4%; Pred. No. 2.1e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGTTTCGATGTTG 18  
 |||||  
 Db 94 CCCAAGTTTCGATGTTG 77

RESULT 3 473 bp mRNA linear EST 18-AUG-2000  
 BE592535 W51.94.C12.bl\_A002 Water-stressed 1 (W51) Sorghum bicolor cDNA,  
 LOCUS mRNA sequence.  
 BE592535  
 BE592535.1 GI:9847608

EST.  
 Sorghum bicolor (sorghum)  
 Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 473)  
 Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and  
 Pratt, L.H.

An EST database from Sorghum: water-stressed plants  
 Unpublished (2000)  
 Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210

Email: ampratenga.edu  
 Sequences have been trimmed to exclude PolyA, vector and regions  
 below Phred quality 16. The threshold for highest quality sequence  
 is 20.  
 Seq primer: JEN REV  
 High quality sequence stop: 464  
 PolyA=No.

Location/Qualifiers

## FEATURES

## source

1. 473  
 /organism="Sorghum bicolor"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4558"  
 /clone\_lib="Water-stressed 1 (W51)"  
 /note="Organ: Mix of 5-week old plants on days 7 & 8 after  
 water was withheld; Vector: lambda Zap; Site 1: XhoI;  
 Site 2: EcoRI; The library was made from poly-A RNA in the  
 cloning vector lambda Zap II. Clones to be sequenced were  
 prepared by mass excision."

## ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 473;  
 Best Local Similarity 94.4%; Pred. No. 2.2e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGTTGATGATTTG 18  
 |||||  
 403 CTCACCTTCGATGATTTG 420

RESULT 4  
 BU713295 523 bp mRNA linear EST 23-OCT-2003  
 LOCUS SJRABOB11 Adult SJC 7/94 Schistosoma japonicum cDNA, mRNA sequence.  
 DEFINITION BU713295  
 ACCESSION BU713295.1 GI:28320657  
 VERSION EST.  
 KEYWORDS Schistosoma japonicum  
 SOURCE Schistosoma japonicum  
 ORGANISM Schistosoma japonicum  
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
 Strigidae; Schistosomatidae; Schistosomatidae; Schistosoma.  
 1 (bases 1 to 523)  
 Hu, W., Yan, Q., Shen, D. K., Liu, F., Zhu, Z. D., Song, H. D., Xu, X. R.,  
 Wang, Z. J., Rong, Y. P., Zeng, L. C., Wu, J., Zhang, X., Wang, J. J.,  
 Xu, X. N., Wang, S. Y., Fu, G., Zhang, X. L., Wang, Z. Q., Brindley, P. J.,  
 McManus, D. P., Xue, C. L., Feng, Z., Chen, Z., and Han, Z. G.  
 Evolutionary and biomedical implications of a Schistosoma japonicum  
 complementary DNA resource  
 Nat. Genet. 35 (2), 139-147 (2003)  
 22879925  
 Contact: Zeguang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China  
 Tel: 86-21-50801919 (ex. 45)  
 Fax: 86-21-50801922  
 Email: hanzg@chgc.sh.cn.  
 Location/Qualifiers  
 1..523  
 /organism="Schistosoma japonicum"  
 /mol\_type="mRNA"  
 /strain="Chinese (Anhui) strain"  
 /db\_xref="taxon:6182"  
 /sex="Male and female"  
 /tissue\_type="Whole body"  
 /dev\_stage="Adult worms"  
 /lab\_host="Mouse and rabbit"  
 /clone\_id="Adult SJC 7/94"  
 /note="Vector: Lambda ZAP-II XR.; Site 1: EcoR I; Site 2:  
 XhoI I; Several hundred adult Schistosoma japonicum  
 (Anhui, P. R. China, strain), of mixed sex, were perfused  
 from the mesenteries of experimentally infected mice and  
 rabbits at the Queensland Institute of Medical Research,  
 Brisbane, Australia (QIMR), and stored for several months  
 in liquid nitrogen. Subsequently, mRNA was isolated at the  
 QIMR from lysates of these worms by oligo dt  
 chromatography, using a kit from Pharmacia. The mRNA was  
 then shipped to Clontech, Palo Alto, CA, USA, who  
 constructed a cDNA library. First strand synthesis was  
 primed with an oligo-dt-XhoI-primer and synthesized using  
 M-MLV reverse transcriptase. Second strand synthesis was  
 accomplished with RNase H and T4 DNA polymerase. The  
 double stranded cDNA was ligated to EcoRI linkers,  
 digested with EcoRI and XhoI, and ligated into the  
 phagemid vector lambda ZAP II XR. After construction of  
 this directional library by Clontech, it was returned to  
 the QIMR. During analysis of the library at the QIMR, we  
 have found that a small percentage, 2% to 3%, of the  
 clones contain inserts that appear to be highly homologous  
 to sequences from salmonid fishes, as determined by  
 homology comparisons using BLAST and by Southern  
 hybridization analysis to genomic DNA from salmon (Sigma  
 Chemical Co., St. Louis, MO) under stringent washing  
 conditions. The remainder of the clones appear to contain

ORIGIN S. japonicum sequences."

Query Match 91.1%; Score 16.4; DB 13; Length 523;  
 Best Local Similarity 94.4%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGTTGATGATTTG 18  
 |||||  
 489 CACACCTTCGATGATTTG 506

RESULT 5  
 CD885707 524 bp mRNA linear EST 14-JUL-2003  
 LOCUS G118.100C21F010423 G118 Triticum aestivum cDNA clone G118100C21,  
 DEFINITION mRNA sequence.  
 ACCESSION CD885707  
 VERSION CD885707.1 GI:32651023  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 524)  
 Genoplane.  
 Genoplane, a major partnership french program in plant genomics  
 Unpublished (2003)  
 Contact: Genoplane  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplane' (<http://www.genoplane.com>  
 and <http://genoplane-info.infobiogen.fr>).  
 Location/Qualifiers  
 1..524  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="rectal"  
 /db\_xref="taxon:4565"  
 /clone="G118100C21"  
 /tissue\_type="grain (118 degrees per day after  
 pollination)"  
 /clone\_id="G118"

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 524;  
 Best Local Similarity 94.4%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGTTGATGATTTG 18  
 |||||  
 226 CCCAAGTTGATGATTTG 209

RESULT 6  
 BJ108367 548 bp mRNA linear EST 30-MAY-2003  
 LOCUS BJ108367/c  
 DEFINITION BJ108367 unpublished oligo-capped cDNA library, C. elegans L1 stage  
 Caenorhabditis elegans cDNA clone Yk1107a11 5', mRNA sequence.  
 ACCESSION BJ108367  
 VERSION BJ108367.2 GI:31243821  
 KEYWORDS EST.  
 SOURCE Caenorhabditis elegans  
 ORGANISM Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.  
 1 (bases 1 to 548)  
 Kohara, Y., Shih, I. T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.  
 and Sugano, S.

TITLE A complementary view of the C.elegans genome  
JOURNAL Unpublished (2002)  
COMMENT On Jan 23, 2002 this sequence version replaced gi:18268395.  
Contact: Tadasu Shin-1  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.

FEATURES  
source  
1. .548  
Location/Qualifiers  
/organism="Caenorhabditis elegans"  
/mol\_type="mRNA"  
/strain="N2"  
/db\_xref="taxon:6239"  
/clone="YK107a11"  
/sex="hermaphrodite"  
/tissue\_type="whole animal"  
/dev\_stage="L1"  
/clone\_lib="unpublished oligo-capped cDNA library, C.  
elegans L1 stage"

## ORIGIN

Query Match 91.1%; Score 16.4; DB 12; Length 548;  
Best Local Similarity 94.4%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18  
152 CCCAACTTCTGAATGTTG 135

RESULT 7  
CE323958 555 bp DNA linear GSS 26-SEP-2003  
LOCUS tigr-gss-dog-17000360306070 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CE323958 GI:36133381  
VERSION  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 555)  
Kirchness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
JOURNAL MEDLINE  
PUBMED 22875432  
14512627

COMMENT Contact: Kirkness EF

The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: Shotgun.

FEATURES  
source  
Location/Qualifiers  
1. .555  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

## ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 555;

Best Local Similarity 94.4%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18  
188 CCCAACTTCTGAATGTTG 171

RESULT 8  
AQ665757 579 bp DNA linear GSS 23-JUN-1999  
LOCUS HS 5354 B2 E01 T7A RPCI-11 Human Male BAC library Homo sapiens  
DEFINITION genomic clone Plate=930 Col=2 Row=J, genomic survey sequence.  
ACCESSION AQ665757  
VERSION AQ665757.1 GI:5173525  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 579)  
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,W.D. and  
Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
99380589  
10449764  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm))  
or from Resear h Genetics (info@resgen.com). BAC end web server:  
<http://www.htsc.washington.edu>  
Plate: 930 row: J column: 2  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 579.

FEATURES  
source  
Location/Qualifiers  
1. .579  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=930 Col=2 Row=J"  
/sex="male"  
/clone\_lib="RPCI-11 Human Male BAC Library"  
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI methylase. Size selected DNA was cloned into the  
pBAC3.6 vector at EcoRI sites"

## ORIGIN

Query Match 91.1%; Score 16.4; DB 28; Length 579;  
Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAACTTCTGAATGTTG 18  
426 CCCAACTTCTGAATGTTG 443

RESULT 9  
CA032813/c 584 bp mRNA linear EST 24-OCT-2002  
LOCUS CA032813



DEFINITION HX14E13r HX Hordeum vulgare subsp. vulgare cDNA clone HX14E13  
 5-PRIME, mRNA sequence.  
 ACCESSION CA032813  
 VERSION CA032813.1 GI:24329571  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooideae; Triticeae; Hordeum.  
 1 (bases 1 to 584)  
 REFERENCE 1 (bases 1 to 584)  
 AUTHORS Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.  
 TITLE EST sequencing and analysis in barley (2002)  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Stein Nils  
 Molecular Markers Group, Department Genbank  
 Institute of Plant Genetics and Crop Plant Research (IPK)  
 Corrensstr. 3, 06466, Gatersleben, Germany  
 Tel: 039482-5522  
 Fax: 039482-5595  
 Email: stein@ipk-gatersleben.de  
 Insert Length: 584 Std Error: 0.00  
 Plate: 14 row: E column: 13  
 Seq primer: M3rev.  
 Location/Qualifiers  
 1..584  
 /organism="Hordeum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /cultivar="barke"  
 /sub\_species="vulgare"  
 /db\_xref="GABI:273489"  
 /db\_xref="taxon:112509"  
 /clone="HX14E13"  
 /tissue\_type="apex"  
 /dev\_stage="apex (3-5 mm in size)"  
 /lab\_host="XL10-Gold"  
 /clone\_1lb="HX"  
 /note="Vector: pBluescript SK+; Site\_1: EcoRI (5'-end of cDNA); Site\_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN  
 Query Match 91.1%; Score 16.4; DB 13; Length 584;  
 Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGCTTCGAGATGTTG 18  
 |||||  
 Db 396 CCCAGCTTCTGATGTTG 379

RESULT 10  
 BUI26336 587 bp mRNA linear EST 23-JAN-2002  
 LOCUS BUI26336 unpublished oligo-capped cDNA library, C. elegans L1 stage  
 DEFINITION Caenorhabditis elegans cDNA clone yk1333h08 5', mRNA sequence.  
 ACCESSION BUI26336  
 VERSION BUI26336.1 GI:18286488  
 KEYWORDS EST.  
 SOURCE Caenorhabditis elegans  
 ORGANISM Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 Rhabditioidea; Rhabditidae; Rhabditinae; Caenorhabditis.  
 1 (bases 1 to 587)  
 REFERENCE Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.  
 and Sugano, S.  
 TITLE A complementary view of the C. elegans genome  
 JOURNAL Unpublished (2002)

COMMENT Contact: Tadasu Shin-i  
 Center for Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@gene.nig.ac.jp.  
 Location/Qualifiers  
 1..587  
 /organism="Caenorhabditis elegans"  
 /mol\_type="mRNA"  
 /strain="N2"  
 /db\_xref="taxon:6239"  
 /clone="yk1333h08"  
 /sex="hermaphrodite"  
 /tissue\_type="whole animal"  
 /dev\_stage="L1"  
 /clone\_1lb="unpublished oligo-capped cDNA library, C. elegans L1 stage"

ORIGIN  
 Query Match 91.1%; Score 16.4; DB 12; Length 587;  
 Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGCTTCGAGATGTTG 18  
 |||||  
 Db 401 CCCAAGCTTCGAGATGTTG 384

RESULT 11  
 CD910198 604 bp mRNA linear EST 14-JUL-2003  
 LOCUS CD910198 G468.114K19F010821 G468 Triticum aestivum cDNA clone G468114K19,  
 DEFINITION mRNA sequence.  
 ACCESSION CD910198  
 VERSION CD910198.1 GI:32684522  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooideae; Triticeae; Triticum.  
 1 (bases 1 to 604)  
 REFERENCE 1 (bases 1 to 604)  
 AUTHORS Genoplane.  
 TITLE Genoplane, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Genoplane  
 Genoplane  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplane' (<http://www.genoplane.com>  
 and <http://genoplane-info.infobiogen.fr>).  
 Location/Qualifiers  
 1..604  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="rectal"  
 /db\_xref="taxon:4565"  
 /clone="G468114K19"  
 /tissue\_type="grain (468 degrees per day after  
 pollination)"  
 /clone\_1lb="G468"

ORIGIN  
 Query Match 91.1%; Score 16.4; DB 14; Length 604;  
 Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCAAGCTTCGAGATGTTG 18  
 |||||

Db 343 CCCAGCTTCTGAATGTTG 326

RESULT 12  
AM857324/c 606 bp mRNA linear EST 19-MAY-2000  
DEFINITION CM1-CT0309-071299-057-b10 CT0309 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AM857324  
VERSION AM857324.1 GI:7953017  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 606)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,F.S., Bucher,F., Jorgensen,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL MEDLINE 20202863  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2-cml-CT0309-071299-057-b10&ct3=1999-12-07&ct4=1)  
299-057-b10&ct3=1999-12-07&ct4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 606.  
Location/Qualifiers  
1..606  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="CT0309"  
/note="Organ: colon; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 606;  
Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 361 CCCACTTCTGAATGTTG 344

RESULT 13  
CA220452 616 bp mRNA linear EST 25-SEP-2003  
LOCUS SCSPFL4014F10.g FL4 Saccharum officinarum cDNA clone SCSPFL4014F10  
DEFINITION 5', mRNA sequence.  
ACCESSION CA220452  
VERSION CA220452.1 GI:35273771  
KEYWORDS EST.

SOURCE  
ORGANISM Saccharum officinarum  
Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.  
REFERENCE 1 (bases 1 to 616)  
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
The libraries that made SUCEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
JOURNAL Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: patricia@unicamp.br  
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br  
Plate: 014 row: F column: 10  
Seq primer: 17 Promoter Primer.  
Location/Qualifiers  
1..616  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCSPFL4014F10"  
/lab\_host="DH10B"  
/clone\_lib="FL4"  
/note="Organ: Developed inflorescence and rachis (20cm-long); Vector: pSPORT1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Developed inflorescence and rachis (20cm-long)]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a Sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 616;  
Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCACTTCTGAATGTTG 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 330 CTCACCTTCTGAATGTTG 347

RESULT 14  
B1111174 631 bp mRNA linear EST 26-JUN-2001  
LOCUS 60289366F1 NCI\_CGAP\_Mams Mus musculus cDNA clone IMAGE:5029192 5', mRNA sequence.  
ACCESSION B1111174  
VERSION B1111174.1 GI:14562075  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.lnl.gov  
 Plate: LMAN1082 row: C column: 17  
 High quality sequence stop: 620.

## FEATURES

source

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/strain="C57BL/6J"
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/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_idb="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

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## ORIGIN

Query Match 91.1%; Score 16.4; DB 12; Length 631;  
 Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCAACTTCTGATGTTG 18  
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 Db 458 CCCAACTTCAGATGTTG 441

## RESULT 15

AW857329/c 632 bp mRNA linear EST 19-MAY-2000  
 LOCUS CM1-CT0309-071299-057-g11 CT0309 Homo sapiens cDNA, mRNA sequence.

DEFINITION AW857329  
 ACCESSION AW857329  
 VERSION AW857329.1 GI:7953022  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 632)  
 Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.G.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=ct2=CM1-CT0309-071299-057-g11&t3=1999-12-07&t4=1)

Seq primer: puc 18 forward  
 High quality sequence stop: 630.

## FEATURES

source

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/mol_type="mRNA"

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/db_xref="taxon:9606"
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## ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 632;  
 Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
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 Db 361 CCCAACTTCTGATGTTG 344

Search completed: October 1, 2004, 08:02:06  
 Job time : 259.333 secs

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